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PATENT APPLICATION

FOR

Human Genes and Gene Expression Products

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HUMAN GENES AND GENE EXPRESSION PRODUCTS

Cross-Reference to Related Applications

5 This application claims the benefit of U.S. provisional application serial no. 60/188,609, filed March 9, 2000, which application is incorporated herein by reference in its entirety.

Field of the Invention

The present invention relates to polynucleotides of human origin and the encoded gene products.

Background of the Invention

10 Identification of novel polynucleotides, particularly those that encode an expressed gene product, is important in the advancement of drug discovery, diagnostic technologies, and the understanding of the progression and nature of complex diseases such as cancer. Identification of genes expressed in different cell types isolated from sources that differ in disease state or stage, developmental stage, exposure to various environmental factors, the tissue of origin, the species from which the tissue was isolated, and the like is key to identifying the genetic factors that are responsible for the phenotypes associated with these various differences.

This invention provides novel human polynucleotides, the polypeptides encoded by these polynucleotides, and the genes and proteins corresponding to these novel polynucleotides.

Summary of the Invention

20 This invention relates to novel human polynucleotides and variants thereof, their encoded polypeptides and variants thereof, to genes corresponding to these polynucleotides and to proteins expressed by the genes. The invention also relates to diagnostics and therapeutics comprising such novel human polynucleotides, their corresponding genes or gene products, including probes, antisense nucleotides, and antibodies. The polynucleotides of the invention correspond to a
25 polynucleotide comprising the sequence information of at least one of SEQ ID NOS:1-2396.

Various aspects and embodiments of the invention will be readily apparent to the ordinarily skilled artisan upon reading the description provided herein.

Detailed Description of the Invention

30 The invention relates to polynucleotides comprising the disclosed nucleotide sequences, to full length cDNA, mRNA genomic sequences, and genes corresponding to these sequences and degenerate variants thereof, and to polypeptides encoded by the polynucleotides of the invention and polypeptide variants. The following detailed description describes the polynucleotide compositions encompassed by the invention, methods for obtaining cDNA or genomic DNA encoding a full-length gene product, expression of these polynucleotides and genes, identification of structural
35 motifs of the polynucleotides and genes, identification of the function of a gene product encoded by

a gene corresponding to a polynucleotide of the invention, use of the provided polynucleotides as probes and in mapping and in tissue profiling, use of the corresponding polypeptides and other gene products to raise antibodies, and use of the polynucleotides and their encoded gene products for therapeutic and diagnostic purposes.

5 Polynucleotide Compositions

10 The scope of the invention with respect to polynucleotide compositions includes, but is not necessarily limited to, polynucleotides having a sequence set forth in any one of SEQ ID NOS:1-2396; polynucleotides obtained from the biological materials described herein or other biological sources (particularly human sources) by hybridization under stringent conditions (particularly
15 conditions of high stringency); genes corresponding to the provided polynucleotides; variants of the provided polynucleotides and their corresponding genes, particularly those variants that retain a biological activity of the encoded gene product (*e.g.*, a biological activity ascribed to a gene product corresponding to the provided polynucleotides as a result of the assignment of the gene product to a protein family(ies) and/or identification of a functional domain present in the gene product). Other
20 nucleic acid compositions contemplated by and within the scope of the present invention will be readily apparent to one of ordinary skill in the art when provided with the disclosure here. "Polynucleotide" and "nucleic acid" as used herein with reference to nucleic acids of the composition is not intended to be limiting as to the length or structure of the nucleic acid unless specifically indicted.

25 The invention features polynucleotides that are expressed in human tissue, specifically human colon, breast, and/or lung tissue. Novel nucleic acid compositions of the invention of particular interest comprise a sequence set forth in any one of SEQ ID NOS:1-2396 or an identifying sequence thereof. An "identifying sequence" is a contiguous sequence of residues at least about 10 nt to about 20 nt in length, usually at least about 50 nt to about 100 nt in length, that uniquely
30 identifies a polynucleotide sequence, *e.g.*, exhibits less than 90%, usually less than about 80% to about 85% sequence identity to any contiguous nucleotide sequence of more than about 20 nt. Thus, the subject novel nucleic acid compositions include full length cDNAs or mRNAs that encompass an identifying sequence of contiguous nucleotides from any one of SEQ ID NOS: 1-2396.

35 The polynucleotides of the invention also include polynucleotides having sequence similarity or sequence identity. Nucleic acids having sequence similarity are detected by hybridization under low stringency conditions, for example, at 50°C and 10XSSC (0.9 M saline/0.09 M sodium citrate) and remain bound when subjected to washing at 55°C in 1XSSC. Sequence identity can be determined by hybridization under stringent conditions, for example, at 50°C or higher and 0.1XSSC (9 mM saline/0.9 mM sodium citrate). Hybridization methods and conditions are well known in the art, see, *e.g.*, USPN 5,707,829. Nucleic acids that are substantially identical

to the provided polynucleotide sequences, *e.g.* allelic variants, genetically altered versions of the gene, *etc.*, bind to the provided polynucleotide sequences (SEQ ID NOS:1-2396) under stringent hybridization conditions. By using probes, particularly labeled probes of DNA sequences, one can isolate homologous or related genes. The source of homologous genes can be any species, *e.g.* primate species, particularly human; rodents, such as rats and mice; canines, felines, bovines, ovines, equines, yeast, nematodes, *etc.*

Preferably, hybridization is performed using at least 15 contiguous nucleotides (nt) of at least one of SEQ ID NOS:1-2396. That is, when at least 15 contiguous nt of one of the disclosed SEQ ID NOS. is used as a probe, the probe will preferentially hybridize with a nucleic acid comprising the complementary sequence, allowing the identification and retrieval of the nucleic acids that uniquely hybridize to the selected probe. Probes from more than one SEQ ID NO. can hybridize with the same nucleic acid if the cDNA from which they were derived corresponds to one mRNA. Probes of more than 15 nt can be used, *e.g.*, probes of from about 18 nt to about 100 nt, but 15 nt represents sufficient sequence for unique identification.

The polynucleotides of the invention also include naturally occurring variants of the nucleotide sequences (*e.g.*, degenerate variants, allelic variants, *etc.*). Variants of the polynucleotides of the invention are identified by hybridization of putative variants with nucleotide sequences disclosed herein, preferably by hybridization under stringent conditions. For example, by using appropriate wash conditions, variants of the polynucleotides of the invention can be identified where the allelic variant exhibits at most about 25-30% base pair (bp) mismatches relative to the selected polynucleotide probe. In general, allelic variants contain 15-25% bp mismatches, and can contain as little as even 5-15%, or 2-5%, or 1-2% bp mismatches, as well as a single bp mismatch.

The invention also encompasses homologs corresponding to the polynucleotides of SEQ ID NOS:1-2396, where the source of homologous genes can be any mammalian species, *e.g.*, primate species, particularly human; rodents, such as rats; canines, felines, bovines, ovines, equines, yeast, nematodes, *etc.* Between mammalian species, *e.g.*, human and mouse, homologs generally have substantial sequence similarity, *e.g.*, at least 75% sequence identity, usually at least 90%, more usually at least 95% between nucleotide sequences. Sequence similarity is calculated based on a reference sequence, which may be a subset of a larger sequence, such as a conserved motif, coding region, flanking region, *etc.* A reference sequence will usually be at least about 18 contiguous nt long, more usually at least about 30 nt long, and may extend to the complete sequence that is being compared. Algorithms for sequence analysis are known in the art, such as gapped BLAST, described in Altschul, et al. *Nucleic Acids Res.* (1997) 25:3389-3402.

In general, variants of the invention have a sequence identity greater than at least about 65%, preferably at least about 75%, more preferably at least about 85%, and can be greater than at

least about 90% or more as determined by the Smith-Waterman homology search algorithm as implemented in MPSRCH program (Oxford Molecular). For the purposes of this invention, a preferred method of calculating percent identity is the Smith-Waterman algorithm, using the following. Global DNA sequence identity must be greater than 65% as determined by the Smith-Waterman homology search algorithm as implemented in MPSRCH program (Oxford Molecular) using an affine gap search with the following search parameters: gap open penalty, 12; and gap extension penalty, 1.

The subject nucleic acids can be cDNAs or genomic DNAs, as well as fragments thereof, particularly fragments that encode a biologically active gene product and/or are useful in the methods disclosed herein (*e.g.*, in diagnosis, as a unique identifier of a differentially expressed gene of interest, *etc.*). The term "cDNA" as used herein is intended to include all nucleic acids that share the arrangement of sequence elements found in native mature mRNA species, where sequence elements are exons and 3' and 5' non-coding regions. Normally mRNA species have contiguous exons, with the intervening introns, when present, being removed by nuclear RNA splicing, to create a continuous open reading frame encoding a polypeptide of the invention.

A genomic sequence of interest comprises the nucleic acid present between the initiation codon and the stop codon, as defined in the listed sequences, including all of the introns that are normally present in a native chromosome. It can further include the 3' and 5' untranslated regions found in the mature mRNA. It can further include specific transcriptional and translational regulatory sequences, such as promoters, enhancers, *etc.*, including about 1 kb, but possibly more, of flanking genomic DNA at either the 5' and 3' end of the transcribed region. The genomic DNA can be isolated as a fragment of 100 kbp or smaller; and substantially free of flanking chromosomal sequence. The genomic DNA flanking the coding region, either 3' and 5', or internal regulatory sequences as sometimes found in introns, contains sequences required for proper tissue, stage-specific, or disease-state specific expression.

The nucleic acid compositions of the subject invention can encode all or a part of the subject polypeptides. Double or single stranded fragments can be obtained from the DNA sequence by chemically synthesizing oligonucleotides in accordance with conventional methods, by restriction enzyme digestion, by PCR amplification, *etc.* Isolated polynucleotides and polynucleotide fragments of the invention comprise at least about 10, about 15, about 20, about 35, about 50, about 100, about 150 to about 200, about 250 to about 300, or about 350 contiguous nt selected from the polynucleotide sequences as shown in SEQ ID NOS:1-2396. For the most part, fragments will be of at least 15 nt, usually at least 18 nt or 25 nt, and up to at least about 50 contiguous nt in length or more. In a preferred embodiment, the polynucleotide molecules comprise a contiguous sequence of

at least 12 nt selected from the group consisting of the polynucleotides shown in SEQ ID NOS:1-2396.

Probes specific to the polynucleotides of the invention can be generated using the polynucleotide sequences disclosed in SEQ ID NOS:1-2396. The probes are preferably at least about a 12, 15, 16, 18, 20, 22, 24, or 25 nt fragment of a corresponding contiguous sequence of SEQ ID NOS:1-2396, and can be less than 2, 1, 0.5, 0.1, or 0.05 kb in length. The probes can be synthesized chemically or can be generated from longer polynucleotides using restriction enzymes. The probes can be labeled, for example, with a radioactive, biotinylated, or fluorescent tag. Preferably, probes are designed based upon an identifying sequence of a polynucleotide of one of SEQ ID NOS:1-2396. More preferably, probes are designed based on a contiguous sequence of one of the subject polynucleotides that remain unmasked following application of a masking program for masking low complexity (*e.g.*, XBLAST) to the sequence., *i.e.*, one would select an unmasked region, as indicated by the polynucleotides outside the poly-n stretches of the masked sequence produced by the masking program.

The polynucleotides of the subject invention are isolated and obtained in substantial purity, generally as other than an intact chromosome. Usually, the polynucleotides, either as DNA or RNA, will be obtained substantially free of other naturally-occurring nucleic acid sequences, generally being at least about 50%, usually at least about 90% pure and are typically "recombinant", *e.g.*, flanked by one or more nucleotides with which it is not normally associated on a naturally occurring chromosome.

The polynucleotides of the invention can be provided as a linear molecule or within a circular molecule, and can be provided within autonomously replicating molecules (vectors) or within molecules without replication sequences. Expression of the polynucleotides can be regulated by their own or by other regulatory sequences known in the art. The polynucleotides of the invention can be introduced into suitable host cells using a variety of techniques available in the art, such as transferrin polycation-mediated DNA transfer, transfection with naked or encapsulated nucleic acids, liposome-mediated DNA transfer, intracellular transportation of DNA-coated latex beads, protoplast fusion, viral infection, electroporation, gene gun, calcium phosphate-mediated transfection, and the like.

The subject nucleic acid compositions can be used to, for example, produce polypeptides, as probes for the detection of mRNA of the invention in biological samples (*e.g.*, extracts of human cells) to generate additional copies of the polynucleotides, to generate ribozymes or antisense oligonucleotides, and as single stranded DNA probes or as triple-strand forming oligonucleotides. The probes described herein can be used to, for example, determine the presence or absence of the

polynucleotide sequences as shown in SEQ ID NOS:1-2396 or variants thereof in a sample. These and other uses are described in more detail below.

Use of Polynucleotides to Obtain Full-Length cDNA, Gene, and Promoter Region

Full-length cDNA molecules comprising the disclosed polynucleotides are obtained as follows. A polynucleotide having a sequence of one of SEQ ID NOS:1-2396, or a portion thereof comprising at least 12, 15, 18, or 20 nt, is used as a hybridization probe to detect hybridizing members of a cDNA library using probe design methods, cloning methods, and clone selection techniques such as those described in USPN 5,654,173. Libraries of cDNA are made from selected tissues, such as normal or tumor tissue, or from tissues of a mammal treated with, for example, a pharmaceutical agent. Preferably, the tissue is the same as the tissue from which the polynucleotides of the invention were isolated, as both the polynucleotides described herein and the cDNA represent expressed genes. Most preferably, the cDNA library is made from the biological material described herein in the Examples. The choice of cell type for library construction can be made after the identity of the protein encoded by the gene corresponding to the polynucleotide of the invention is known. This will indicate which tissue and cell types are likely to express the related gene, and thus represent a suitable source for the mRNA for generating the cDNA. Where the provided polynucleotides are isolated from cDNA libraries, the libraries are prepared from mRNA of human colon cells, more preferably, human colon cancer cells, even more preferably, from a highly metastatic colon cell, Km12L4.

Techniques for producing and probing nucleic acid sequence libraries are described, for example, in Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual*, 2nd Ed., (1989) Cold Spring Harbor Press, Cold Spring Harbor, NY. The cDNA can be prepared by using primers based on sequence from SEQ ID NOS:1-2396. In one embodiment, the cDNA library can be made from only poly-adenylated mRNA. Thus, poly-T primers can be used to prepare cDNA from the mRNA.

Members of the library that are larger than the provided polynucleotides, and preferably that encompass the complete coding sequence of the native message, are obtained. In order to confirm that the entire cDNA has been obtained, RNA protection experiments are performed as follows. Hybridization of a full-length cDNA to an mRNA will protect the RNA from RNase degradation. If the cDNA is not full length, then the portions of the mRNA that are not hybridized will be subject to RNase degradation. This is assayed, as is known in the art, by changes in electrophoretic mobility on polyacrylamide gels, or by detection of released monoribonucleotides. Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual*, 2nd Ed., (1989) Cold Spring Harbor Press, Cold Spring Harbor, NY. In order to obtain additional sequences 5' to the end of a partial cDNA, 5' RACE (*PCR Protocols: A Guide to Methods and Applications*, (1990) Academic Press, Inc.) can be performed.

Genomic DNA is isolated using the provided polynucleotides in a manner similar to the isolation of full-length cDNAs. Briefly, the provided polynucleotides, or portions thereof, are used as probes to libraries of genomic DNA. Preferably, the library is obtained from the cell type that was used to generate the polynucleotides of the invention, but this is not essential. Most preferably, the genomic DNA is obtained from the biological material described herein in the Examples. Such libraries can be in vectors suitable for carrying large segments of a genome, such as P1 or YAC, as described in detail in Sambrook *et al.*, 9.4-9.30. In addition, genomic sequences can be isolated from human BAC libraries, which are commercially available from Research Genetics, Inc., Huntsville, Alabama, USA, for example. In order to obtain additional 5' or 3' sequences, chromosome walking is performed, as described in Sambrook *et al.*, such that adjacent and overlapping fragments of genomic DNA are isolated. These are mapped and pieced together, as is known in the art, using restriction digestion enzymes and DNA ligase.

Using the polynucleotide sequences of the invention, corresponding full-length genes can be isolated using both classical and PCR methods to construct and probe cDNA libraries. Using either method, Northern blots, preferably, are performed on a number of cell types to determine which cell lines express the gene of interest at the highest level. Classical methods of constructing cDNA libraries are taught in Sambrook *et al.*, *supra*. With these methods, cDNA can be produced from mRNA and inserted into viral or expression vectors. Typically, libraries of mRNA comprising poly(A) tails can be produced with poly(T) primers. Similarly, cDNA libraries can be produced using the instant sequences as primers.

PCR methods are used to amplify the members of a cDNA library that comprise the desired insert. In this case, the desired insert will contain sequence from the full length cDNA that corresponds to the instant polynucleotides. Such PCR methods include gene trapping and RACE methods. Gene trapping entails inserting a member of a cDNA library into a vector. The vector then is denatured to produce single stranded molecules. Next, a substrate-bound probe, such as a biotinylated oligo, is used to trap cDNA inserts of interest. Biotinylated probes can be linked to an avidin-bound solid substrate. PCR methods can be used to amplify the trapped cDNA. To trap sequences corresponding to the full length genes, the labeled probe sequence is based on the polynucleotide sequences of the invention. Random primers or primers specific to the library vector can be used to amplify the trapped cDNA. Such gene trapping techniques are described in Gruber *et al.*, WO 95/04745 and Gruber *et al.*, USPN 5,500,356. Kits are commercially available to perform gene trapping experiments from, for example, Life Technologies, Gaithersburg, Maryland, USA.

"Rapid amplification of cDNA ends," or RACE, is a PCR method of amplifying cDNAs from a number of different RNAs. The cDNAs are ligated to an oligonucleotide linker, and amplified by PCR using two primers. One primer is based on sequence from the instant

polynucleotides, for which full length sequence is desired, and a second primer comprises sequence that hybridizes to the oligonucleotide linker to amplify the cDNA. A description of this methods is reported in WO 97/19110. In preferred embodiments of RACE, a common primer is designed to anneal to an arbitrary adaptor sequence ligated to cDNA ends (Apte and Siebert, *Biotechniques* (1993) 15:890-893; Edwards *et al.*, *Nuc. Acids Res.* (1991) 19:5227-5232). When a single gene-specific RACE primer is paired with the common primer, preferential amplification of sequences between the single gene specific primer and the common primer occurs. Commercial cDNA pools modified for use in RACE are available.

Another PCR-based method generates full-length cDNA library with anchored ends without needing specific knowledge of the cDNA sequence. The method uses lock-docking primers (I-VI), where one primer, poly TV (I-III) locks over the polyA tail of eukaryotic mRNA producing first strand synthesis and a second primer, polyGH (IV-VI) locks onto the polyC tail added by terminal deoxynucleotidyl transferase (TdT)(see, e.g., WO 96/40998).

The promoter region of a gene generally is located 5' to the initiation site for RNA polymerase II. Hundreds of promoter regions contain the "TATA" box, a sequence such as TATTA or TATAA, which is sensitive to mutations. The promoter region can be obtained by performing 5' RACE using a primer from the coding region of the gene. Alternatively, the cDNA can be used as a probe for the genomic sequence, and the region 5' to the coding region is identified by "walking up." If the gene is highly expressed or differentially expressed, the promoter from the gene can be of use in a regulatory construct for a heterologous gene.

Once the full-length cDNA or gene is obtained, DNA encoding variants can be prepared by site-directed mutagenesis, described in detail in Sambrook *et al.*, 15.3-15.63. The choice of codon or nucleotide to be replaced can be based on disclosure herein on optional changes in amino acids to achieve altered protein structure and/or function.

As an alternative method to obtaining DNA or RNA from a biological material, nucleic acid comprising nucleotides having the sequence of one or more polynucleotides of the invention can be synthesized. Thus, the invention encompasses nucleic acid molecules ranging in length from 15 nt (corresponding to at least 15 contiguous nt of one of SEQ ID NOS:1-2396) up to a maximum length suitable for one or more biological manipulations, including replication and expression, of the nucleic acid molecule. The invention includes but is not limited to (a) nucleic acid having the size of a full gene, and comprising at least one of SEQ ID NOS:1-2396; (b) the nucleic acid of (a) also comprising at least one additional gene, operably linked to permit expression of a fusion protein; (c) an expression vector comprising (a) or (b); (d) a plasmid comprising (a) or (b) ; and (e) a recombinant viral particle comprising (a) or (b). Once provided with the polynucleotides disclosed herein, construction or preparation of (a) - (e) are well within the skill in the art.

The sequence of a nucleic acid comprising at least 15 contiguous nt of at least any one of SEQ ID NOS:1-2396, preferably the entire sequence of at least any one of SEQ ID NOS:1-2396, is not limited and can be any sequence of A, T, G, and/or C (for DNA) and A, U, G, and/or C (for RNA) or modified bases thereof, including inosine and pseudouridine. The choice of sequence will depend on the desired function and can be dictated by coding regions desired, the intron-like regions desired, and the regulatory regions desired. Where the entire sequence of any one of SEQ ID NOS:1-2396 is within the nucleic acid, the nucleic acid obtained is referred to herein as a polynucleotide comprising the sequence of any one of SEQ ID NOS:1-2396.

Expression of Polypeptide Encoded by Full-Length cDNA or Full-Length Gene

The provided polynucleotides (e.g., a polynucleotide having a sequence of one of SEQ ID NOS:1-2396), the corresponding cDNA, or the full-length gene is used to express a partial or complete gene product. Constructs of polynucleotides having sequences of SEQ ID NOS:1-2396 can also be generated synthetically. Alternatively, single-step assembly of a gene and entire plasmid from large numbers of oligodeoxyribonucleotides is described by, e.g., Stemmer *et al.*, *Gene (Amsterdam)* (1995) 164(1):49-53. In this method, assembly PCR (the synthesis of long DNA sequences from large numbers of oligodeoxyribonucleotides (oligos)) is described. The method is derived from DNA shuffling (Stemmer, *Nature* (1994) 370:389-391), and does not rely on DNA ligase, but instead relies on DNA polymerase to build increasingly longer DNA fragments during the assembly process.

Appropriate polynucleotide constructs are purified using standard recombinant DNA techniques as described in, for example, Sambrook *et al.*, *Molecular Cloning: A Laboratory Manual, 2nd Ed.*, (1989) Cold Spring Harbor Press, Cold Spring Harbor, NY, and under current regulations described in United States Dept. of HHS, National Institute of Health (NIH) Guidelines for Recombinant DNA Research. The gene product encoded by a polynucleotide of the invention is expressed in any expression system, including, for example, bacterial, yeast, insect, amphibian and mammalian systems. Vectors, host cells and methods for obtaining expression in same are well known in the art. Suitable vectors and host cells are described in USPN 5,654,173.

Polynucleotide molecules comprising a polynucleotide sequence provided herein are generally propagated by placing the molecule in a vector. Viral and non-viral vectors are used, including plasmids. The choice of plasmid will depend on the type of cell in which propagation is desired and the purpose of propagation. Certain vectors are useful for amplifying and making large amounts of the desired DNA sequence. Other vectors are suitable for expression in cells in culture. Still other vectors are suitable for transfer and expression in cells in a whole animal or person. The choice of appropriate vector is well within the skill of the art. Many such vectors are available

commercially. Methods for preparation of vectors comprising a desired sequence are well known in the art.

The polynucleotides set forth in SEQ ID NOS:1-2396 or their corresponding full-length polynucleotides are linked to regulatory sequences as appropriate to obtain the desired expression properties. These can include promoters (attached either at the 5' end of the sense strand or at the 3' end of the antisense strand), enhancers, terminators, operators, repressors, and inducers. The promoters can be regulated or constitutive. In some situations it may be desirable to use conditionally active promoters, such as tissue-specific or developmental stage-specific promoters. These are linked to the desired nucleotide sequence using the techniques described above for linkage to vectors. Any techniques known in the art can be used.

When any of the above host cells, or other appropriate host cells or organisms, are used to replicate and/or express the polynucleotides or nucleic acids of the invention, the resulting replicated nucleic acid, RNA, expressed protein or polypeptide, is within the scope of the invention as a product of the host cell or organism. The product is recovered by any appropriate means known in the art.

Once the gene corresponding to a selected polynucleotide is identified, its expression can be regulated in the cell to which the gene is native. For example, an endogenous gene of a cell can be regulated by an exogenous regulatory sequence as disclosed in USPN 5,641,670.

Identification of Functional and Structural Motifs of Novel Genes Screening Against Publicly Available Databases

Translations of the nucleotide sequence of the provided polynucleotides, cDNAs or full genes can be aligned with individual known sequences. Similarity with individual sequences can be used to determine the activity of the polypeptides encoded by the polynucleotides of the invention. Also, sequences exhibiting similarity with more than one individual sequence can exhibit activities that are characteristic of either or both individual sequences.

The full length sequences and fragments of the polynucleotide sequences of the nearest neighbors can be used as probes and primers to identify and isolate the full length sequence corresponding to provided polynucleotides. The nearest neighbors can indicate a tissue or cell type to be used to construct a library for the full-length sequences corresponding to the provided polynucleotides.

Typically, a selected polynucleotide is translated in all six frames to determine the best alignment with the individual sequences. The sequences disclosed herein in the Sequence Listing are in a 5' to 3' orientation and translation in three frames can be sufficient (with a few specific exceptions as described in the Examples). These amino acid sequences are referred to, generally, as

query sequences, which will be aligned with the individual sequences. Databases with individual sequences are described in "Computer Methods for Macromolecular Sequence Analysis" *Methods in Enzymology* (1996) 266, Doolittle, Academic Press, Inc., a division of Harcourt Brace & Co., San Diego, California, USA. Databases include GenBank, EMBL, and DNA Database of Japan (DDBJ).

Query and individual sequences can be aligned using the methods and computer programs described above, and include BLAST 2.0 ((National Center for Biotechnology Information, Bethesda, Maryland). See also Altschul, et al. *Nucleic Acids Res.* (1997) 25:3389-3402. Another alignment algorithm is Fasta, available in the Genetics Computing Group (GCG) package, Madison, Wisconsin, USA, a wholly owned subsidiary of Oxford Molecular Group, Inc. Other techniques for alignment are described in Doolittle, *supra*. Preferably, an alignment program that permits gaps in the sequence is utilized to align the sequences. The Smith-Waterman is one type of algorithm that permits gaps in sequence alignments. See *Meth. Mol. Biol.* (1997) 70: 173-187. Also, the GAP program using the Needleman and Wunsch alignment method can be utilized to align sequences. An alternative search strategy uses MPSRCH software, which runs on a MASPAR computer. MPSRCH uses a Smith-Waterman algorithm to score sequences on a massively parallel computer. This approach improves ability to identify sequences that are distantly related matches, and is especially tolerant of small gaps and nucleotide sequence errors. Amino acid sequences encoded by the provided polynucleotides can be used to search both protein and DNA databases. Incorporated herein by reference are all sequences that have been made public as of the filing date of this application by any of the DNA or protein sequence databases, including the patent databases (*e.g.*, GeneSeq). Also incorporated by reference are those sequences that have been submitted to these databases as of the filing date of the present application but not made public until after the filing date of the present application.

Results of individual and query sequence alignments can be divided into three categories: high similarity, weak similarity, and no similarity. Individual alignment results ranging from high similarity to weak similarity provide a basis for determining polypeptide activity and/or structure. Parameters for categorizing individual results include: percentage of the alignment region length where the strongest alignment is found, percent sequence identity, and p value. The percentage of the alignment region length is calculated by counting the number of residues of the individual sequence found in the region of strongest alignment, *e.g.*, contiguous region of the individual sequence that contains the greatest number of residues that are identical to the residues of the corresponding region of the aligned query sequence. This number is divided by the total residue length of the query sequence to calculate a percentage. For example, a query sequence of 20 amino acid residues might be aligned with a 20 amino acid region of an individual sequence. The

individual sequence might be identical to amino acid residues 5, 9-15, and 17-19 of the query sequence. The region of strongest alignment is thus the region stretching from residue 9-19, an 11 amino acid stretch. The percentage of the alignment region length is: 11 (length of the region of strongest alignment) divided by (query sequence length) 20 or 55%.

Percent sequence identity is calculated by counting the number of amino acid matches between the query and individual sequence and dividing total number of matches by the number of residues of the individual sequences found in the region of strongest alignment. Thus, the percent identity in the example above would be 10 matches divided by 11 amino acids, or approximately, 90.9%

P value is the probability that the alignment was produced by chance. For a single alignment, the p value can be calculated according to Karlin *et al.*, *Proc. Natl. Acad. Sci.* (1990) 87:2264 and Karlin *et al.*, *Proc. Natl. Acad. Sci.* (1993) 90. The p value of multiple alignments using the same query sequence can be calculated using an heuristic approach described in Altschul *et al.*, *Nat. Genet.* (1994) 6:119. Alignment programs such as BLAST program can calculate the p value. See also Altschul *et al.*, *Nucleic Acids Res.* (1997) 25:3389-3402.

Another factor to consider for determining identity or similarity is the location of the similarity or identity. Strong local alignment can indicate similarity even if the length of alignment is short. Sequence identity scattered throughout the length of the query sequence also can indicate a similarity between the query and profile sequences. The boundaries of the region where the sequences align can be determined according to Doolittle, *supra*; BLAST 2.0 (see, *e.g.*, Altschul, *et al.* *Nucleic Acids Res.* (1997) 25:3389-3402) or FAST programs; or by determining the area where sequence identity is highest.

High Similarity. In general, in alignment results considered to be of high similarity, the percent of the alignment region length is typically at least about 55% of total length query sequence; more typically, at least about 58%; even more typically; at least about 60% of the total residue length of the query sequence. Usually, percent length of the alignment region can be as much as about 62%; more usually, as much as about 64%; even more usually, as much as about 66%. Further, for high similarity, the region of alignment, typically, exhibits at least about 75% of sequence identity; more typically, at least about 78%; even more typically; at least about 80% sequence identity.

Usually, percent sequence identity can be as much as about 82%; more usually, as much as about 84%; even more usually, as much as about 86%.

The p value is used in conjunction with these methods. If high similarity is found, the query sequence is considered to have high similarity with a profile sequence when the p value is less than or equal to about 10^{-2} ; more usually; less than or equal to about 10^{-3} ; even more usually; less than

or equal to about 10^{-4} . More typically, the p value is no more than about 10^{-5} ; more typically; no

more than or equal to about 10^{-10} ; even more typically; no more than or equal to about 10^{-15} for the query sequence to be considered high similarity.

Weak Similarity. In general, where alignment results considered to be of weak similarity, there is no minimum percent length of the alignment region nor minimum length of alignment. A better showing of weak similarity is considered when the region of alignment is, typically, at least about 15 amino acid residues in length; more typically, at least about 20; even more typically; at least about 25 amino acid residues in length. Usually, length of the alignment region can be as much as about 30 amino acid residues; more usually, as much as about 40; even more usually, as much as about 60 amino acid residues. Further, for weak similarity, the region of alignment, typically, exhibits at least about 35% of sequence identity; more typically, at least about 40%; even more typically; at least about 45% sequence identity. Usually, percent sequence identity can be as much as about 50%; more usually, as much as about 55%; even more usually, as much as about 60%.

If low similarity is found, the query sequence is considered to have weak similarity with a profile sequence when the p value is usually less than or equal to about 10^{-2} ; more usually; less than or equal to about 10^{-3} ; even more usually; less than or equal to about 10^{-4} . More typically, the p value is no more than about 10^{-5} ; more usually; no more than or equal to about 10^{-10} ; even more usually; no more than or equal to about 10^{-15} for the query sequence to be considered weak similarity.

Similarity Determined by Sequence Identity Alone. Sequence identity alone can be used to determine similarity of a query sequence to an individual sequence and can indicate the activity of the sequence. Such an alignment, preferably, permits gaps to align sequences. Typically, the query sequence is related to the profile sequence if the sequence identity over the entire query sequence is at least about 15%; more typically, at least about 20%; even more typically, at least about 25%; even more typically, at least about 50%. Sequence identity alone as a measure of similarity is most useful when the query sequence is usually, at least 80 residues in length; more usually, 90 residues; even more usually, at least 95 amino acid residues in length. More typically, similarity can be concluded based on sequence identity alone when the query sequence is preferably 100 residues in length; more preferably, 120 residues in length; even more preferably, 150 amino acid residues in length.

Alignments with Profile and Multiple Aligned Sequences. Translations of the provided polynucleotides can be aligned with amino acid profiles that define either protein families or common motifs. Also, translations of the provided polynucleotides can be aligned to multiple sequence alignments (MSA) comprising the polypeptide sequences of members of protein families or motifs. Similarity or identity with profile sequences or MSAs can be used to determine the

activity of the gene products (*e.g.*, polypeptides) encoded by the provided polynucleotides or corresponding cDNA or genes. For example, sequences that show an identity or similarity with a chemokine profile or MSA can exhibit chemokine activities.

Profiles can be designed manually by (1) creating an MSA, which is an alignment of the amino acid sequence of members that belong to the family and (2) constructing a statistical representation of the alignment. Such methods are described, for example, in Birney *et al.*, *Nucl. Acid Res.* (1996) 24(14): 2730-2739. MSAs of some protein families and motifs are publicly available. For example, the Pfam database available from Washington University (St. Louis, Missouri) includes MSAs of 547 different families and motifs. These MSAs are described also in Sonnhammer *et al.*, *Proteins* (1997) 28: 405-420. Other publically available sources include those over the world wide web provided by the European Molecular Biology Laboratory (Heidelberg, Germany). A brief description of these MSAs is reported in Pascarella *et al.*, *Prot. Eng.* (1996) 9(3):249-251.

Techniques for building profiles from MSAs are described in Sonnhammer *et al.*, *supra*; Birney *et al.*, *supra*; and "Computer Methods for Macromolecular Sequence Analysis," *Methods in Enzymology* (1996) 266, Doolittle, Academic Press, Inc., San Diego, California, USA.

Similarity between a query sequence and a protein family or motif can be determined by (a) comparing the query sequence against the profile and/or (b) aligning the query sequence with the members of the family or motif. Typically, a program such as Searchwise is used to compare the query sequence to the statistical representation of the multiple alignment, also known as a profile (see Birney *et al.*, *supra*). Other techniques to compare the sequence and profile are described in Sonnhammer *et al.*, *supra* and Doolittle, *supra*.

Next, methods described by Feng *et al.*, *J. Mol. Evol.* (1987) 25:351 and Higgins *et al.*, *CABIOS* (1989) 5:151 can be used to align the query sequence with the members of a family or motif, also known as a MSA. Sequence alignments can be generated using any of a variety of software tools. Examples include PileUp, which creates a multiple sequence alignment, and is described in Feng *et al.*, *J. Mol. Evol.* (1987) 25:351. Another method, GAP, uses the alignment method of Needleman *et al.*, *J. Mol. Biol.* (1970) 48:443. GAP is best suited for global alignment of sequences. A third method, BestFit, functions by inserting gaps to maximize the number of matches using the local homology algorithm of Smith *et al.*, *Adv. Appl. Math.* (1981) 2:482. In general, the following factors are used to determine if a similarity between a query sequence and a profile or MSA exists: (1) number of conserved residues found in the query sequence, (2) percentage of conserved residues found in the query sequence, (3) number of frameshifts, and (4) spacing between conserved residues.

Some alignment programs that both translate and align sequences can make any number of frameshifts when translating the nucleotide sequence to produce the best alignment. The fewer

frameshifts needed to produce an alignment, the stronger the similarity or identity between the query and profile or MSAs. For example, a weak similarity resulting from no frameshifts can be a better indication of activity or structure of a query sequence, than a strong similarity resulting from two frameshifts. Preferably, three or fewer frameshifts are found in an alignment; more preferably two or fewer frameshifts; even more preferably, one or fewer frameshifts; even more preferably, no frameshifts are found in an alignment of query and profile or MSAs.

Conserved residues are those amino acids found at a particular position in all or some of the family or motif members. Alternatively, a position is considered conserved if only a certain class of amino acids is found in a particular position in all or some of the family members. For example, the N-terminal position can contain a positively charged amino acid, such as lysine, arginine, or histidine.

Typically, a residue of a polypeptide is conserved when a class of amino acids or a single amino acid is found at a particular position in at least about 40% of all class members; more typically, at least about 50%; even more typically, at least about 60% of the members. Usually, a residue is conserved when a class or single amino acid is found in at least about 70% of the members of a family or motif; more usually, at least about 80%; even more usually, at least about 90%; even more usually, at least about 95%.

A residue is considered conserved when three unrelated amino acids are found at a particular position in the some or all of the members; more usually, two unrelated amino acids. These residues are conserved when the unrelated amino acids are found at particular positions in at least about 40% of all class member; more typically, at least about 50%; even more typically, at least about 60% of the members. Usually, a residue is conserved when a class or single amino acid is found in at least about 70% of the members of a family or motif; more usually, at least about 80%; even more usually, at least about 90%; even more usually, at least about 95%.

A query sequence has similarity to a profile or MSA when the query sequence comprises at least about 25% of the conserved residues of the profile or MSA; more usually, at least about 30%; even more usually; at least about 40%. Typically, the query sequence has a stronger similarity to a profile sequence or MSA when the query sequence comprises at least about 45% of the conserved residues of the profile or MSA; more typically, at least about 50%; even more typically; at least about 55%.

Identification of Secreted & Membrane-Bound Polypeptides

Both secreted and membrane-bound polypeptides of the present invention are of particular interest. For example, levels of secreted polypeptides can be assayed in body fluids that are convenient, such as blood, plasma, serum, and other body fluids such as urine, prostatic fluid and semen. Membrane-bound polypeptides are useful for constructing vaccine antigens or inducing an

immune response. Such antigens would comprise all or part of the extracellular region of the membrane-bound polypeptides. Because both secreted and membrane-bound polypeptides comprise a fragment of contiguous hydrophobic amino acids, hydrophobicity predicting algorithms can be used to identify such polypeptides.

5 A signal sequence is usually encoded by both secreted and membrane-bound polypeptide genes to direct a polypeptide to the surface of the cell. The signal sequence usually comprises a stretch of hydrophobic residues. Such signal sequences can fold into helical structures. Membrane-bound polypeptides typically comprise at least one transmembrane region that possesses a stretch of hydrophobic amino acids that can transverse the membrane. Some transmembrane regions also
10 exhibit a helical structure. Hydrophobic fragments within a polypeptide can be identified by using computer algorithms. Such algorithms include Hopp & Woods, *Proc. Natl. Acad. Sci. USA* (1981) 78:3824-3828; Kyte & Doolittle, *J. Mol. Biol.* (1982) 157: 105-132; and RAOAR algorithm, Degli Esposti *et al.*, *Eur. J. Biochem.* (1990) 190: 207-219.

15 Another method of identifying secreted and membrane-bound polypeptides is to translate the polynucleotides of the invention in all six frames and determine if at least 8 contiguous hydrophobic amino acids are present. Those translated polypeptides with at least 8; more typically, 10; even more typically, 12 contiguous hydrophobic amino acids are considered to be either a putative secreted or membrane bound polypeptide. Hydrophobic amino acids include alanine, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, threonine, tryptophan, tyrosine, and
20 valine

Identification of the Function of an Expression Product of a Full-Length Gene

Ribozymes, antisense constructs, and dominant negative mutants can be used to determine
function of the expression product of a gene corresponding to a polynucleotide provided herein. These methods and compositions are particularly useful where the provided novel polynucleotide
25 exhibits no significant or substantial homology to a sequence encoding a gene of known function. Antisense molecules and ribozymes can be constructed from synthetic polynucleotides. Typically, the phosphoramidite method of oligonucleotide synthesis is used. See Beaucage *et al.*, *Tet. Lett.* (1981) 22:1859 and USPN 4,668,777. Automated devices for synthesis are available to create oligonucleotides using this chemistry. Examples of such devices include Biosearch 8600, Models
30 392 and 394 by Applied Biosystems, a division of Perkin-Elmer Corp., Foster City, California, USA; and Expedite by Perceptive Biosystems, Framingham, Massachusetts, USA. Synthetic RNA, phosphate analog oligonucleotides, and chemically derivatized oligonucleotides can also be produced, and can be covalently attached to other molecules. RNA oligonucleotides can be synthesized, for example, using RNA phosphoramidites. This method can be performed on an

automated synthesizer, such as Applied Biosystems, Models 392 and 394, Foster City, California, USA.

Phosphorothioate oligonucleotides can also be synthesized for antisense construction. A sulfurizing reagent, such as tetraethylthiuram disulfide (TETD) in acetonitrile can be used to convert the internucleotide cyanoethyl phosphite to the phosphorothioate triester within 15 minutes at room temperature. TETD replaces the iodine reagent, while all other reagents used for standard phosphoramidite chemistry remain the same. Such a synthesis method can be automated using Models 392 and 394 by Applied Biosystems, for example.

Oligonucleotides of up to 200 nt can be synthesized, more typically, 100 nt, more typically 50 nt; even more typically 30 to 40 nt. These synthetic fragments can be annealed and ligated together to construct larger fragments. See, for example, Sambrook *et al.*, *supra*. Trans-cleaving catalytic RNAs (ribozymes) are RNA molecules possessing endoribonuclease activity. Ribozymes are specifically designed for a particular target, and the target message must contain a specific nucleotide sequence. They are engineered to cleave any RNA species site-specifically in the background of cellular RNA. The cleavage event renders the mRNA unstable and prevents protein expression. Importantly, ribozymes can be used to inhibit expression of a gene of unknown function for the purpose of determining its function in an in vitro or in vivo context, by detecting the phenotypic effect. One commonly used ribozyme motif is the hammerhead, for which the substrate sequence requirements are minimal. Design of the hammerhead ribozyme, as well as therapeutic uses of ribozymes, are disclosed in Usman *et al.*, *Current Opin. Struct. Biol.* (1996) 6:527. Methods for production of ribozymes, including hairpin structure ribozyme fragments, methods of increasing ribozyme specificity, and the like are known in the art.

The hybridizing region of the ribozyme can be modified or can be prepared as a branched structure as described in Horn and Urdea, *Nucleic Acids Res.* (1989) 17:6959. The basic structure of the ribozymes can also be chemically altered in ways familiar to those skilled in the art, and chemically synthesized ribozymes can be administered as synthetic oligonucleotide derivatives modified by monomeric units. In a therapeutic context, liposome mediated delivery of ribozymes improves cellular uptake, as described in Birikh *et al.*, *Eur. J. Biochem.* (1997) 245:1.

Antisense nucleic acids are designed to specifically bind to RNA, resulting in the formation of RNA-DNA or RNA-RNA hybrids, with an arrest of DNA replication, reverse transcription or messenger RNA translation. Antisense polynucleotides based on a selected polynucleotide sequence can interfere with expression of the corresponding gene. Antisense polynucleotides are typically generated within the cell by expression from antisense constructs that contain the antisense strand as the transcribed strand. Antisense polynucleotides based on the disclosed polynucleotides will bind and/or interfere with the translation of mRNA comprising a sequence complementary to the

antisense polynucleotide. The expression products of control cells and cells treated with the antisense construct are compared to detect the protein product of the gene corresponding to the polynucleotide upon which the antisense construct is based. The protein is isolated and identified using routine biochemical methods.

Given the extensive background literature and clinical experience in antisense therapy, one skilled in the art can use selected polynucleotides of the invention as additional potential therapeutics. The choice of polynucleotide can be narrowed by first testing them for binding to "hot spot" regions of the genome of cancerous cells. If a polynucleotide is identified as binding to a "hot spot", testing the polynucleotide as an antisense compound in the corresponding cancer cells is warranted.

As an alternative method for identifying function of the gene corresponding to a polynucleotide disclosed herein, dominant negative mutations are readily generated for corresponding proteins that are active as homomultimers. A mutant polypeptide will interact with wild-type polypeptides (made from the other allele) and form a non-functional multimer. Thus, a mutation is in a substrate-binding domain, a catalytic domain, or a cellular localization domain. Preferably, the mutant polypeptide will be overproduced. Point mutations are made that have such an effect. In addition, fusion of different polypeptides of various lengths to the terminus of a protein can yield dominant negative mutants. General strategies are available for making dominant negative mutants (see, *e.g.*, Herskowitz, *Nature* (1987) 329:219). Such techniques can be used to create loss of function mutations, which are useful for determining protein function.

Polypeptides and Variants Thereof

The polypeptides of the invention include those encoded by the disclosed polynucleotides, as well as nucleic acids that, by virtue of the degeneracy of the genetic code, are not identical in sequence to the disclosed polynucleotides. Thus, the invention includes within its scope a polypeptide encoded by a polynucleotide having the sequence of any one of SEQ ID NOS:1-2396 or a variant thereof.

In general, the term "polypeptide" as used herein refers to both the full length polypeptide encoded by the recited polynucleotide, the polypeptide encoded by the gene represented by the recited polynucleotide, as well as portions or fragments thereof. "Polypeptides" also includes variants of the naturally occurring proteins, where such variants are homologous or substantially similar to the naturally occurring protein, and can be of an origin of the same or different species as the naturally occurring protein (*e.g.*, human, murine, or some other species that naturally expresses the recited polypeptide, usually a mammalian species). In general, variant polypeptides have a sequence that has at least about 80%, usually at least about 90%, and more usually at least about 98% sequence identity with a differentially expressed polypeptide of the invention, as measured by

BLAST 2.0 using the parameters described above. The variant polypeptides can be naturally or non-naturally glycosylated, *i.e.*, the polypeptide has a glycosylation pattern that differs from the glycosylation pattern found in the corresponding naturally occurring protein.

The invention also encompasses homologs of the disclosed polypeptides (or fragments thereof) where the homologs are isolated from other species, *i.e.* other animal or plant species, where such homologs, usually mammalian species, *e.g.* rodents, such as mice, rats; domestic animals, *e.g.*, horse, cow, dog, cat; and humans. By “homolog” is meant a polypeptide having at least about 35%, usually at least about 40% and more usually at least about 60% amino acid sequence identity to a particular differentially expressed protein as identified above, where sequence identity is determined using the BLAST 2.0 algorithm, with the parameters described *supra*.

In general, the polypeptides of the subject invention are provided in a non-naturally occurring environment, *e.g.* are separated from their naturally occurring environment. In certain embodiments, the subject protein is present in a composition that is enriched for the protein as compared to a control. As such, purified polypeptide is provided, where by purified is meant that the protein is present in a composition that is substantially free of non-differentially expressed polypeptides, where by substantially free is meant that less than 90%, usually less than 60% and more usually less than 50% of the composition is made up of non-differentially expressed polypeptides.

Also within the scope of the invention are variants; variants of polypeptides include mutants, fragments, and fusions. Mutants can include amino acid substitutions, additions or deletions. The amino acid substitutions can be conservative amino acid substitutions or substitutions to eliminate non-essential amino acids, such as to alter a glycosylation site, a phosphorylation site or an acetylation site, or to minimize misfolding by substitution or deletion of one or more cysteine residues that are not necessary for function. Conservative amino acid substitutions are those that preserve the general charge, hydrophobicity/ hydrophilicity, and/or steric bulk of the amino acid substituted. Variants can be designed so as to retain or have enhanced biological activity of a particular region of the protein (*e.g.*, a functional domain and/or, where the polypeptide is a member of a protein family, a region associated with a consensus sequence). Selection of amino acid alterations for production of variants can be based upon the accessibility (interior vs. exterior) of the amino acid (see, *e.g.*, Go *et al*, *Int. J. Peptide Protein Res.* (1980) 15:211), the thermostability of the variant polypeptide (see, *e.g.*, Querol *et al.*, *Prot. Eng.* (1996) 9:265), desired glycosylation sites (see, *e.g.*, Olsen and Thomsen, *J. Gen. Microbiol.* (1991) 137:579), desired disulfide bridges (see, *e.g.*, Clarke *et al.*, *Biochemistry* (1993) 32:4322; and Wakarchuk *et al.*, *Protein Eng.* (1994) 7:1379), desired metal binding sites (see, *e.g.*, Toma *et al.*, *Biochemistry* (1991) 30:97, and Haezebrouck *et al.*, *Protein Eng.* (1993) 6:643), and desired substitutions with in proline loops (see,

e.g., Masul *et al.*, *Appl. Env. Microbiol.* (1994) 60:3579). Cysteine-depleted muteins can be produced as disclosed in USPN 4,959,314.

Variants also include fragments of the polypeptides disclosed herein, particularly biologically active fragments and/or fragments corresponding to functional domains. Fragments of interest will typically be at least about 10 aa to at least about 15 aa in length, usually at least about 50 aa in length, and can be as long as 300 aa in length or longer, but will usually not exceed about 1000 aa in length, where the fragment will have a stretch of amino acids that is identical to a polypeptide encoded by a polynucleotide having a sequence of any SEQ ID NOS:1-2396, or a homolog thereof. The protein variants described herein are encoded by polynucleotides that are within the scope of the invention. The genetic code can be used to select the appropriate codons to construct the corresponding variants.

Computer-Related Embodiments

In general, a library of polynucleotides is a collection of sequence information, which information is provided in either biochemical form (*e.g.*, as a collection of polynucleotide molecules), or in electronic form (*e.g.*, as a collection of polynucleotide sequences stored in a computer-readable form, as in a computer system and/or as part of a computer program). The sequence information of the polynucleotides can be used in a variety of ways, *e.g.*, as a resource for gene discovery, as a representation of sequences expressed in a selected cell type (*e.g.*, cell type markers), and/or as markers of a given disease or disease state. In general, a disease marker is a representation of a gene product that is present in all cells affected by disease either at an increased or decreased level relative to a normal cell (*e.g.*, a cell of the same or similar type that is not substantially affected by disease). For example, a polynucleotide sequence in a library can be a polynucleotide that represents an mRNA, polypeptide, or other gene product encoded by the polynucleotide, that is either overexpressed or underexpressed in a breast ductal cell affected by cancer relative to a normal (*i.e.*, substantially disease-free) breast cell.

The nucleotide sequence information of the library can be embodied in any suitable form, *e.g.*, electronic or biochemical forms. For example, a library of sequence information embodied in electronic form comprises an accessible computer data file (or, in biochemical form, a collection of nucleic acid molecules) that contains the representative nucleotide sequences of genes that are differentially expressed (*e.g.*, overexpressed or underexpressed) as between, for example, i) a cancerous cell and a normal cell; ii) a cancerous cell and a dysplastic cell; iii) a cancerous cell and a cell affected by a disease or condition other than cancer; iv) a metastatic cancerous cell and a normal cell and/or non-metastatic cancerous cell; v) a malignant cancerous cell and a non-malignant cancerous cell (or a normal cell) and/or vi) a dysplastic cell relative to a normal cell. Other combinations and comparisons of cells affected by various diseases or stages of disease will be

readily apparent to the ordinarily skilled artisan. Biochemical embodiments of the library include a collection of nucleic acids that have the sequences of the genes in the library, where the nucleic acids can correspond to the entire gene in the library or to a fragment thereof, as described in greater detail below.

5 The polynucleotide libraries of the subject invention generally comprise sequence information of a plurality of polynucleotide sequences, where at least one of the polynucleotides has a sequence of any of SEQ ID NOS:1-2396. By plurality is meant at least 2, usually at least 3 and can include up to all of SEQ ID NOS:1-2396. The length and number of polynucleotides in the library will vary with the nature of the library, *e.g.*, if the library is an oligonucleotide array, a cDNA
10 array, a computer database of the sequence information, etc.

Where the library is an electronic library, the nucleic acid sequence information can be present in a variety of media. "Media" refers to a manufacture, other than an isolated nucleic acid molecule, that contains the sequence information of the present invention. Such a manufacture provides the genome sequence or a subset thereof in a form that can be examined by means not
15 directly applicable to the sequence as it exists in a nucleic acid. For example, the nucleotide sequence of the present invention, *e.g.* the nucleic acid sequences of any of the polynucleotides of SEQ ID NOS:1-2396, can be recorded on computer readable media, *e.g.* any medium that can be read and accessed directly by a computer. Such media include, but are not limited to: magnetic storage media, such as a floppy disc, a hard disc storage medium, and a magnetic tape; optical
20 storage media such as CD-ROM; electrical storage media such as RAM and ROM; and hybrids of these categories such as magnetic/optical storage media. One of skill in the art can readily appreciate how any of the presently known computer readable mediums can be used to create a manufacture comprising a recording of the present sequence information. "Recorded" refers to a process for storing information on computer readable medium, using any such methods as known in
25 the art. Any convenient data storage structure can be chosen, based on the means used to access the stored information. A variety of data processor programs and formats can be used for storage, *e.g.* word processing text file, database format, *etc.* In addition to the sequence information, electronic versions of the libraries of the invention can be provided in conjunction or connection with other computer-readable information and/or other types of computer-readable files (*e.g.*, searchable files, executable files, *etc.*, including, but not limited to, for example, search program software, *etc.*).
30

By providing the nucleotide sequence in computer readable form, the information can be accessed for a variety of purposes. Computer software to access sequence information is publicly available. For example, the gapped BLAST (Altschul *et al. Nucleic Acids Res.* (1997) 25:3389-3402) and BLAZE (Brutlag *et al. Comp. Chem.* (1993) 17:203) search algorithms on a Sybase

system can be used to identify open reading frames (ORFs) within the genome that contain homology to ORFs from other organisms.

As used herein, "a computer-based system" refers to the hardware means, software means, and data storage means used to analyze the nucleotide sequence information of the present invention.

5 The minimum hardware of the computer-based systems of the present invention comprises a central processing unit (CPU), input means, output means, and data storage means. A skilled artisan can readily appreciate that any one of the currently available computer-based system are suitable for use in the present invention. The data storage means can comprise any manufacture comprising a recording of the present sequence information as described above, or a memory access means that
10 can access such a manufacture.

"Search means" refers to one or more programs implemented on the computer-based system, to compare a target sequence or target structural motif, or expression levels of a polynucleotide in a sample, with the stored sequence information. Search means can be used to identify fragments or regions of the genome that match a particular target sequence or target motif. A variety of known
15 algorithms are publicly known and commercially available, *e.g.* MacPattern (EMBL), BLASTN and BLASTX (NCBI). A "target sequence" can be any polynucleotide or amino acid sequence of six or more contiguous nucleotides or two or more amino acids, preferably from about 10 to 100 amino acids or from about 30 to 300 nt. A variety of comparing means can be used to accomplish comparison of sequence information from a sample (*e.g.*, to analyze target sequences, target motifs,
20 or relative expression levels) with the data storage means. A skilled artisan can readily recognize that any one of the publicly available homology search programs can be used as the search means for the computer based systems of the present invention to accomplish comparison of target sequences and motifs. Computer programs to analyze expression levels in a sample and in controls are also known in the art.

25 A "target structural motif," or "target motif," refers to any rationally selected sequence or combination of sequences in which the sequence(s) are chosen based on a three-dimensional configuration that is formed upon the folding of the target motif, or on consensus sequences of regulatory or active sites. There are a variety of target motifs known in the art. Protein target motifs include, but are not limited to, enzyme active sites and signal sequences. Nucleic acid target motifs
30 include, but are not limited to, hairpin structures, promoter sequences and other expression elements such as binding sites for transcription factors.

A variety of structural formats for the input and output means can be used to input and output the information in the computer-based systems of the present invention. One format for an output means ranks the relative expression levels of different polynucleotides. Such presentation

provides a skilled artisan with a ranking of relative expression levels to determine a gene expression profile. .

As discussed above, the “library” of the invention also encompasses biochemical libraries of the polynucleotides of SEQ ID NOS:1-2396 , *e.g.*, collections of nucleic acids representing the provided polynucleotides. The biochemical libraries can take a variety of forms, *e.g.*, a solution of cDNAs, a pattern of probe nucleic acids stably associated with a surface of a solid support (*i.e.*, an array) and the like. Of particular interest are nucleic acid arrays in which one or more of SEQ ID NOS:1-2396 is represented on the array. By array is meant a an article of manufacture that has at least a substrate with at least two distinct nucleic acid targets on one of its surfaces, where the number of distinct nucleic acids can be considerably higher, typically being at least 10 nt, usually at least 20 nt and often at least 25 nt. A variety of different array formats have been developed and are known to those of skill in the art. The arrays of the subject invention find use in a variety of applications, including gene expression analysis, drug screening, mutation analysis and the like, as disclosed in the above-listed exemplary patent documents.

In addition to the above nucleic acid libraries, analogous libraries of polypeptides are also provided, where the where the polypeptides of the library will represent at least a portion of the polypeptides encoded by SEQ ID NOS:1-2396.

Utilities

Use of Polynucleotide Probes in Mapping, and in Tissue Profiling

Polynucleotide probes, generally comprising at least 12 contiguous nt of a polynucleotide as shown in the Sequence Listing, are used for a variety of purposes, such as chromosome mapping of the polynucleotide and detection of transcription levels. Additional disclosure about preferred regions of the disclosed polynucleotide sequences is found in the Examples. A probe that hybridizes specifically to a polynucleotide disclosed herein should provide a detection signal at least 5-, 10-, or 20-fold higher than the background hybridization provided with other unrelated sequences.

Detection of Expression Levels. Nucleotide probes are used to detect expression of a gene corresponding to the provided polynucleotide. In Northern blots, mRNA is separated electrophoretically and contacted with a probe. A probe is detected as hybridizing to an mRNA species of a particular size. The amount of hybridization is quantitated to determine relative amounts of expression, for example under a particular condition. Probes are used for in situ hybridization to cells to detect expression. Probes can also be used *in vivo* for diagnostic detection of hybridizing sequences. Probes are typically labeled with a radioactive isotope. Other types of detectable labels can be used such as chromophores, fluors, and enzymes. Other examples of nucleotide hybridization assays are described in WO92/02526 and USPN 5,124,246.

Alternatively, the Polymerase Chain Reaction (PCR) is another means for detecting small amounts of target nucleic acids (see, e.g., Mullis *et al.*, *Meth. Enzymol.* (1987) 155:335; USPN 4,683,195; and USPN 4,683,202). Two primer polynucleotides nucleotides that hybridize with the target nucleic acids are used to prime the reaction. The primers can be composed of sequence within or 3' and 5' to the polynucleotides of the Sequence Listing. Alternatively, if the primers are 3' and 5' to these polynucleotides, they need not hybridize to them or the complements. After amplification of the target with a thermostable polymerase, the amplified target nucleic acids can be detected by methods known in the art, e.g., Southern blot. mRNA or cDNA can also be detected by traditional blotting techniques (e.g., Southern blot, Northern blot, etc.) described in Sambrook *et al.*, "Molecular Cloning: A Laboratory Manual" (New York, Cold Spring Harbor Laboratory, 1989) (e.g., without PCR amplification). In general, mRNA or cDNA generated from mRNA using a polymerase enzyme can be purified and separated using gel electrophoresis, and transferred to a solid support, such as nitrocellulose. The solid support is exposed to a labeled probe, washed to remove any unhybridized probe, and duplexes containing the labeled probe are detected.

Mapping. Polynucleotides of the present invention can be used to identify a chromosome on which the corresponding gene resides. Such mapping can be useful in identifying the function of the polynucleotide-related gene by its proximity to other genes with known function. Function can also be assigned to the polynucleotide-related gene when particular syndromes or diseases map to the same chromosome. For example, use of polynucleotide probes in identification and quantification of nucleic acid sequence aberrations is described in USPN 5,783,387. An exemplary mapping method is fluorescence in situ hybridization (FISH), which facilitates comparative genomic hybridization to allow total genome assessment of changes in relative copy number of DNA sequences (see, e.g., Valdes *et al.*, *Methods in Molecular Biology* (1997) 68:1). Polynucleotides can also be mapped to particular chromosomes using, for example, radiation hybrids or chromosome-specific hybrid panels.

See Leach *et al.*, *Advances in Genetics*, (1995) 33:63-99; Walter *et al.*, *Nature Genetics* (1994) 7:22; Walter and Goodfellow, *Trends in Genetics* (1992) 9:352. Panels for radiation hybrid mapping are available from Research Genetics, Inc., Huntsville, Alabama, USA. Databases for markers using various panels are publicly available via the world wide web from the Stanford Genome Center and The Whitehead Institute for Biomedical Research/MIT Center for Genome Research. The statistical program RHMAP can be used to construct a map based on the data from radiation hybridization with a measure of the relative likelihood of one order versus another. RHMAP is available via the world wide web from the University of Michigan, Center for Statistical Genetics, Ann Arbor, Michigan. In addition, commercial programs are available for identifying regions of chromosomes commonly associated with disease, such as cancer.

Tissue Typing or Profiling. Expression of specific mRNA corresponding to the provided polynucleotides can vary in different cell types and can be tissue-specific. This variation of mRNA levels in different cell types can be exploited with nucleic acid probe assays to determine tissue types. For example, PCR, branched DNA probe assays, or blotting techniques utilizing nucleic acid probes substantially identical or complementary to polynucleotides listed in the Sequence Listing can determine the presence or absence of the corresponding cDNA or mRNA.

Tissue typing can be used to identify the developmental organ or tissue source of a metastatic lesion by identifying the expression of a particular marker of that organ or tissue. If a polynucleotide is expressed only in a specific tissue type, and a metastatic lesion is found to express that polynucleotide, then the developmental source of the lesion has been identified. Expression of a particular polynucleotide can be assayed by detection of either the corresponding mRNA or the protein product. As would be readily apparent to any forensic scientist, the sequences disclosed herein are useful in differentiating human tissue from non-human tissue. In particular, these sequences are useful to differentiate human tissue from bird, reptile, and amphibian tissue, for example.

Use of Polymorphisms. A polynucleotide of the invention can be used in forensics, genetic analysis, mapping, and diagnostic applications where the corresponding region of a gene is polymorphic in the human population. Any means for detecting a polymorphism in a gene can be used, including, but not limited to electrophoresis of protein polymorphic variants, differential sensitivity to restriction enzyme cleavage, and hybridization to allele-specific probes.

Antibody Production

Expression products of a polynucleotide of the invention, as well as the corresponding mRNA, cDNA, or complete gene, can be prepared and used for raising antibodies for experimental, diagnostic, and therapeutic purposes. For polynucleotides to which a corresponding gene has not been assigned, this provides an additional method of identifying the corresponding gene. The polynucleotide or related cDNA is expressed as described above, and antibodies are prepared. These antibodies are specific to an epitope on the polypeptide encoded by the polynucleotide, and can precipitate or bind to the corresponding native protein in a cell or tissue preparation or in a cell-free extract of an in vitro expression system.

Methods for production of antibodies that specifically bind a selected antigen are well known in the art. Immunogens for raising antibodies can be prepared by mixing a polypeptide encoded by a polynucleotide of the invention with an adjuvant, and/or by making fusion proteins with larger immunogenic proteins. Polypeptides can also be covalently linked to other larger immunogenic proteins, such as keyhole limpet hemocyanin. Immunogens are typically administered intradermally, subcutaneously, or intramuscularly to experimental animals such as rabbits, sheep,

and mice, to generate antibodies. Monoclonal antibodies can be generated by isolating spleen cells and fusing myeloma cells to form hybridomas. Alternatively, the selected polynucleotide is administered directly, such as by intramuscular injection, and expressed in vivo. The expressed protein generates a variety of protein-specific immune responses, including production of antibodies, comparable to administration of the protein.

Preparations of polyclonal and monoclonal antibodies specific for polypeptides encoded by a selected polynucleotide are made using standard methods known in the art. The antibodies specifically bind to epitopes present in the polypeptides encoded by polynucleotides disclosed in the Sequence Listing. Typically, at least 6, 8, 10, or 12 contiguous amino acids are required to form an epitope. Epitopes that involve non-contiguous amino acids may require a longer polypeptide, e.g., at least 15, 25, or 50 amino acids. Antibodies that specifically bind to human polypeptides encoded by the provided polypeptides should provide a detection signal at least 5-, 10-, or 20-fold higher than a detection signal provided with other proteins when used in Western blots or other immunochemical assays. Preferably, antibodies that specifically polypeptides of the invention do not bind to other proteins in immunochemical assays at detectable levels and can immunoprecipitate the specific polypeptide from solution.

The invention also contemplates naturally occurring antibodies specific for a polypeptide of the invention. For example, serum antibodies to a polypeptide of the invention in a human population can be purified by methods well known in the art, e.g., by passing antiserum over a column to which the corresponding selected polypeptide or fusion protein is bound. The bound antibodies can then be eluted from the column, for example using a buffer with a high salt concentration.

In addition to the antibodies discussed above, the invention also contemplates genetically engineered antibodies, antibody derivatives (e.g., single chain antibodies, antibody fragments (e.g., Fab, etc.)), according to methods well known in the art.

Polynucleotides or Arrays for Diagnostics

Polynucleotide arrays provide a high throughput technique that can assay a large number of polynucleotide sequences in a sample. This technology can be used as a diagnostic and as a tool to test for differential expression, e.g., to determine function of an encoded protein. Arrays can be created by spotting polynucleotide probes onto a substrate (e.g., glass, nitrocellulose, etc.) in a two-dimensional matrix or array having bound probes. The probes can be bound to the substrate by either covalent bonds or by non-specific interactions, such as hydrophobic interactions. Samples of polynucleotides can be detectably labeled (e.g., using radioactive or fluorescent labels) and then hybridized to the probes. Double stranded polynucleotides, comprising the labeled sample polynucleotides bound to probe polynucleotides, can be detected once the unbound portion of the

sample is washed away. Techniques for constructing arrays and methods of using these arrays are described in EP 799 897; WO 97/29212; WO 97/27317; EP 785 280; WO 97/02357; USPN 5,593,839; USPN 5,578,832; EP 728 520; USPN 5,599,695; EP 721 016; USPN 5,556,752; WO 95/22058; and USPN 5,631,734. Arrays can be used to, for example, examine differential

expression of genes and can be used to determine gene function. For example, arrays can be used to detect differential expression of a polynucleotide between a test cell and control cell (*e.g.*, cancer cells and normal cells). For example, high expression of a particular message in a cancer cell, which is not observed in a corresponding normal cell, can indicate a cancer specific gene product.

Exemplary uses of arrays are further described in, for example, Pappalarado *et al.*, *Sem. Radiation Oncol.* (1998) 8:217; and Ramsay *Nature Biotechnol.* (1998) 16:40.

Differential Expression in Diagnosis

The polynucleotides of the invention can also be used to detect differences in expression levels between two cells, *e.g.*, as a method to identify abnormal or diseased tissue in a human. For polynucleotides corresponding to profiles of protein families, the choice of tissue can be selected according to the putative biological function. In general, the expression of a gene corresponding to a specific polynucleotide is compared between a first tissue that is suspected of being diseased and a second, normal tissue of the human. The tissue suspected of being abnormal or diseased can be derived from a different tissue type of the human, but preferably it is derived from the same tissue type; for example an intestinal polyp or other abnormal growth should be compared with normal intestinal tissue. The normal tissue can be the same tissue as that of the test sample, or any normal tissue of the patient, especially those that express the polynucleotide-related gene of interest (*e.g.*, brain, thymus, testis, heart, prostate, placenta, spleen, small intestine, skeletal muscle, pancreas, and the mucosal lining of the colon). A difference between the polynucleotide-related gene, mRNA, or protein in the two tissues which are compared, for example in molecular weight, amino acid or nucleotide sequence, or relative abundance, indicates a change in the gene, or a gene which regulates it, in the tissue of the human that was suspected of being diseased. Examples of detection of differential expression and its use in diagnosis of cancer are described in USPNs 5,688,641 and 5,677,125.

A genetic predisposition to disease in a human can also be detected by comparing expression levels of an mRNA or protein corresponding to a polynucleotide of the invention in a fetal tissue with levels associated in normal fetal tissue. Fetal tissues that are used for this purpose include, but are not limited to, amniotic fluid, chorionic villi, blood, and the blastomere of an in vitro-fertilized embryo. The comparable normal polynucleotide-related gene is obtained from any tissue. The mRNA or protein is obtained from a normal tissue of a human in which the polynucleotide-related gene is expressed. Differences such as alterations in the nucleotide sequence

or size of the same product of the fetal polynucleotide-related gene or mRNA, or alterations in the molecular weight, amino acid sequence, or relative abundance of fetal protein, can indicate a germline mutation in the polynucleotide-related gene of the fetus, which indicates a genetic predisposition to disease. In general, diagnostic, prognostic, and other methods of the invention
5 based on differential expression involve detection of a level or amount of a gene product, particularly a differentially expressed gene product, in a test sample obtained from a patient suspected of having or being susceptible to a disease (*e.g.*, breast cancer, lung cancer, colon cancer and/or metastatic forms thereof), and comparing the detected levels to those levels found in normal cells (*e.g.*, cells substantially unaffected by cancer) and/or other control cells (*e.g.*, to differentiate a
10 cancerous cell from a cell affected by dysplasia). Furthermore, the severity of the disease can be assessed by comparing the detected levels of a differentially expressed gene product with those levels detected in samples representing the levels of differentially gene product associated with varying degrees of severity of disease. It should be noted that use of the term “diagnostic” herein is not necessarily meant to exclude “prognostic” or “prognosis,” but rather is used as a matter of
15 convenience.

The term “differentially expressed gene” is generally intended to encompass a polynucleotide that can, for example, include an open reading frame encoding a gene product (*e.g.*, a polypeptide), and/or introns of such genes and adjacent 5' and 3' non-coding nucleotide sequences involved in the regulation of expression, up to about 20 kb beyond the coding region, but possibly
20 further in either direction. The gene can be introduced into an appropriate vector for extrachromosomal maintenance or for integration into a host genome. In general, a difference in expression level associated with a decrease in expression level of at least about 25%, usually at least about 50% to 75%, more usually at least about 90% or more is indicative of a differentially expressed gene of interest, *i.e.*, a gene that is underexpressed or down-regulated in the test sample
25 relative to a control sample. Furthermore, a difference in expression level associated with an increase in expression of at least about 25%, usually at least about 50% to 75%, more usually at least about 90% and can be at least about 1 ½-fold, usually at least about 2-fold to about 10-fold, and can be about 100-fold to about 1,000-fold increase relative to a control sample is indicative of a differentially expressed gene of interest, *i.e.*, an overexpressed or up-regulated gene.

30 “Differentially expressed polynucleotide” as used herein means a nucleic acid molecule (RNA or DNA) comprising a sequence that represents a differentially expressed gene, *e.g.*, the differentially expressed polynucleotide comprises a sequence (*e.g.*, an open reading frame encoding a gene product) that uniquely identifies a differentially expressed gene so that detection of the differentially expressed polynucleotide in a sample is correlated with the presence of a differentially
35 expressed gene in a sample. “Differentially expressed polynucleotides” is also meant to encompass

fragments of the disclosed polynucleotides, *e.g.*, fragments retaining biological activity, as well as nucleic acids homologous, substantially similar, or substantially identical (*e.g.*, having about 90% sequence identity) to the disclosed polynucleotides.

"Diagnosis" as used herein generally includes determination of a subject's susceptibility to a disease or disorder, determination as to whether a subject is presently affected by a disease or disorder, as well as to the prognosis of a subject affected by a disease or disorder (*e.g.*, identification of pre-metastatic or metastatic cancerous states, stages of cancer, or responsiveness of cancer to therapy). The present invention particularly encompasses diagnosis of subjects in the context of breast cancer (*e.g.*, carcinoma in situ (*e.g.*, ductal carcinoma in situ), estrogen receptor (ER)-positive breast cancer, ER-negative breast cancer, or other forms and/or stages of breast cancer), lung cancer (*e.g.*, small cell carcinoma, non-small cell carcinoma, mesothelioma, and other forms and/or stages of lung cancer), and colon cancer (*e.g.*, adenomatous polyp, colorectal carcinoma, and other forms and/or stages of colon cancer).

"Sample" or "biological sample" as used throughout here are generally meant to refer to samples of biological fluids or tissues, particularly samples obtained from tissues, especially from cells of the type associated with the disease for which the diagnostic application is designed (*e.g.*, ductal adenocarcinoma), and the like. "Samples" is also meant to encompass derivatives and fractions of such samples (*e.g.*, cell lysates). Where the sample is solid tissue, the cells of the tissue can be dissociated or tissue sections can be analyzed.

Methods of the subject invention useful in diagnosis or prognosis typically involve comparison of the abundance of a selected differentially expressed gene product in a sample of interest with that of a control to determine any relative differences in the expression of the gene product, where the difference can be measured qualitatively and/or quantitatively. Quantitation can be accomplished, for example, by comparing the level of expression product detected in the sample with the amounts of product present in a standard curve. A comparison can be made visually; by using a technique such as densitometry, with or without computerized assistance; by preparing a representative library of cDNA clones of mRNA isolated from a test sample, sequencing the clones in the library to determine that number of cDNA clones corresponding to the same gene product, and analyzing the number of clones corresponding to that same gene product relative to the number of clones of the same gene product in a control sample; or by using an array to detect relative levels of hybridization to a selected sequence or set of sequences, and comparing the hybridization pattern to that of a control. The differences in expression are then correlated with the presence or absence of an abnormal expression pattern. A variety of different methods for determining the nucleic acid abundance in a sample are known to those of skill in the art (see, *e.g.*, WO 97/27317).

In general, diagnostic assays of the invention involve detection of a gene product of a the polynucleotide sequence (*e.g.*, mRNA or polypeptide) that corresponds to a sequence of SEQ ID NOS:1-2396 The patient from whom the sample is obtained can be apparently healthy, susceptible to disease (*e.g.*, as determined by family history or exposure to certain environmental factors), or can already be identified as having a condition in which altered expression of a gene product of the invention is implicated.

Diagnosis can be determined based on detected gene product expression levels of a gene product encoded by at least one, preferably at least two or more, at least 3 or more, or at least 4 or more of the polynucleotides having a sequence set forth in SEQ ID NOS:1-2396, and can involve detection of expression of genes corresponding to all of SEQ ID NOS:1-2396 and/or additional sequences that can serve as additional diagnostic markers and/or reference sequences. Where the diagnostic method is designed to detect the presence or susceptibility of a patient to cancer, the assay preferably involves detection of a gene product encoded by a gene corresponding to a polynucleotide that is differentially expressed in cancer. Examples of such differentially expressed polynucleotides are described in the Examples below. Given the provided polynucleotides and information regarding their relative expression levels provided herein, assays using such polynucleotides and detection of their expression levels in diagnosis and prognosis will be readily apparent to the ordinarily skilled artisan.

Any of a variety of detectable labels can be used in connection with the various embodiments of the diagnostic methods of the invention. Suitable detectable labels include fluorochromes, (*e.g.* fluorescein isothiocyanate (FITC), rhodamine, Texas Red, phycoerythrin, allophycocyanin, 6-carboxyfluorescein (6-FAM), 2',7'-dimethoxy-4',5'-dichloro-6-carboxyfluorescein, 6-carboxy-X-rhodamine (ROX), 6-carboxy-2',4',7',4,7-hexachlorofluorescein (HEX), 5-carboxyfluorescein (5-FAM) or N,N,N',N'-tetramethyl-6-carboxyrhodamine (TAMRA)), radioactive labels, (*e.g.* ^{32}P , ^{35}S , ^3H , *etc.*), and the like. The detectable label can involve a two stage systems (*e.g.*, biotin-avidin, hapten-anti-hapten antibody, *etc.*)

Reagents specific for the polynucleotides and polypeptides of the invention, such as antibodies and nucleotide probes, can be supplied in a kit for detecting the presence of an expression product in a biological sample. The kit can also contain buffers or labeling components, as well as instructions for using the reagents to detect and quantify expression products in the biological sample. Exemplary embodiments of the diagnostic methods of the invention are described below in more detail.

Polypeptide detection in diagnosis. In one embodiment, the test sample is assayed for the level of a differentially expressed polypeptide. Diagnosis can be accomplished using any of a number of methods to determine the absence or presence or altered amounts of the differentially

expressed polypeptide in the test sample. For example, detection can utilize staining of cells or histological sections with labeled antibodies, performed in accordance with conventional methods. Cells can be permeabilized to stain cytoplasmic molecules. In general, antibodies that specifically bind a differentially expressed polypeptide of the invention are added to a sample, and incubated for a period of time sufficient to allow binding to the epitope, usually at least about 10 minutes. The antibody can be detectably labeled for direct detection (e.g., using radioisotopes, enzymes, fluorescers, chemilumescers, and the like), or can be used in conjunction with a second stage antibody or reagent to detect binding (e.g., biotin with horseradish peroxidase-conjugated avidin, a secondary antibody conjugated to a fluorescent compound, e.g. fluorescein, rhodamine, Texas red, etc.). The absence or presence of antibody binding can be determined by various methods, including flow cytometry of dissociated cells, microscopy, radiography, scintillation counting, etc. Any suitable alternative methods can of qualitative or quantitative detection of levels or amounts of differentially expressed polypeptide can be used, for example ELISA, western blot, immunoprecipitation, radioimmunoassay, etc.

mRNA detection. The diagnostic methods of the invention can also or alternatively involve detection of mRNA encoded by a gene corresponding to a differentially expressed polynucleotides of the invention. Any suitable qualitative or quantitative methods known in the art for detecting specific mRNAs can be used. mRNA can be detected by, for example, *in situ* hybridization in tissue sections, by reverse transcriptase-PCR, or in Northern blots containing poly A+ mRNA. One of skill in the art can readily use these methods to determine differences in the size or amount of mRNA transcripts between two samples. mRNA expression levels in a sample can also be determined by generation of a library of expressed sequence tags (ESTs) from the sample, where the EST library is representative of sequences present in the sample (Adams, et al., (1991) *Science* 252:1651).

Enumeration of the relative representation of ESTs within the library can be used to approximate the relative representation of the gene transcript within the starting sample. The results of EST analysis of a test sample can then be compared to EST analysis of a reference sample to determine the relative expression levels of a selected polynucleotide, particularly a polynucleotide corresponding to one or more of the differentially expressed genes described herein. Alternatively, gene expression in a test sample can be performed using serial analysis of gene expression (SAGE) methodology (e.g., Velculescu et al., *Science* (1995) 270:484) or differential display (DD) methodology (see, e.g., U.S. 5,776,683; and U.S. 5,807,680).

Alternatively, gene expression can be analyzed using hybridization analysis.

Oligonucleotides or cDNA can be used to selectively identify or capture DNA or RNA of specific sequence composition, and the amount of RNA or cDNA hybridized to a known capture sequence determined qualitatively or quantitatively, to provide information about the relative representation of

a particular message within the pool of cellular messages in a sample. Hybridization analysis can be designed to allow for concurrent screening of the relative expression of hundreds to thousands of genes by using, for example, array-based technologies having high density formats, including filters, microscope slides, or microchips, or solution-based technologies that use spectroscopic analysis (e.g., mass spectrometry). One exemplary use of arrays in the diagnostic methods of the invention is described below in more detail.

Use of a single gene in diagnostic applications. The diagnostic methods of the invention can focus on the expression of a single differentially expressed gene. For example, the diagnostic method can involve detecting a differentially expressed gene, or a polymorphism of such a gene (e.g., a polymorphism in an coding region or control region), that is associated with disease. Disease-associated polymorphisms can include deletion or truncation of the gene, mutations that alter expression level and/or affect activity of the encoded protein, *etc.*

A number of methods are available for analyzing nucleic acids for the presence of a specific sequence, e.g. a disease associated polymorphism. Where large amounts of DNA are available, genomic DNA is used directly. Alternatively, the region of interest is cloned into a suitable vector and grown in sufficient quantity for analysis. Cells that express a differentially expressed gene can be used as a source of mRNA, which can be assayed directly or reverse transcribed into cDNA for analysis. The nucleic acid can be amplified by conventional techniques, such as the polymerase chain reaction (PCR), to provide sufficient amounts for analysis, and a detectable label can be included in the amplification reaction (e.g., using a detectably labeled primer or detectably labeled oligonucleotides) to facilitate detection. Alternatively, various methods are also known in the art that utilize oligonucleotide ligation as a means of detecting polymorphisms, see e.g., Riley *et al.*, *Nucl. Acids Res.* (1990) 18:2887; and Delahunty *et al.*, *Am. J. Hum. Genet.* (1996) 58:1239.

The amplified or cloned sample nucleic acid can be analyzed by one of a number of methods known in the art. The nucleic acid can be sequenced by dideoxy or other methods, and the sequence of bases compared to a selected sequence, e.g., to a wild-type sequence. Hybridization with the polymorphic or variant sequence can also be used to determine its presence in a sample (e.g., by Southern blot, dot blot, *etc.*). The hybridization pattern of a polymorphic or variant sequence and a control sequence to an array of oligonucleotide probes immobilized on a solid support, as described in US 5,445,934, or in WO 95/35505, can also be used as a means of identifying polymorphic or variant sequences associated with disease. Single strand conformational polymorphism (SSCP) analysis, denaturing gradient gel electrophoresis (DGGE), and heteroduplex analysis in gel matrices are used to detect conformational changes created by DNA sequence variation as alterations in electrophoretic mobility. Alternatively, where a polymorphism creates or destroys a recognition site for a restriction endonuclease, the sample is digested with that endonuclease, and the products size

fractionated to determine whether the fragment was digested. Fractionation is performed by gel or capillary electrophoresis, particularly acrylamide or agarose gels.

Screening for mutations in a gene can be based on the functional or antigenic characteristics of the protein. Protein truncation assays are useful in detecting deletions that can affect the biological activity of the protein. Various immunoassays designed to detect polymorphisms in proteins can be used in screening. Where many diverse genetic mutations lead to a particular disease phenotype, functional protein assays have proven to be effective screening tools. The activity of the encoded protein can be determined by comparison with the wild-type protein.

Pattern matching in diagnosis using arrays. In another embodiment, the diagnostic and/or prognostic methods of the invention involve detection of expression of a selected set of genes in a test sample to produce a test expression pattern (TEP). The TEP is compared to a reference expression pattern (REP), which is generated by detection of expression of the selected set of genes in a reference sample (e.g., a positive or negative control sample). The selected set of genes includes at least one of the genes of the invention, which genes correspond to the polynucleotide sequences of SEQ ID NOS:1-2396. Of particular interest is a selected set of genes that includes gene differentially expressed in the disease for which the test sample is to be screened.

"Reference sequences" or "reference polynucleotides" as used herein in the context of differential gene expression analysis and diagnosis/prognosis refers to a selected set of polynucleotides, which selected set includes at least one or more of the differentially expressed polynucleotides described herein. A plurality of reference sequences, preferably comprising positive and negative control sequences, can be included as reference sequences. Additional suitable reference sequences are found in GenBank, Unigene, and other nucleotide sequence databases (including, e.g., expressed sequence tag (EST), partial, and full-length sequences).

"Reference array" means an array having reference sequences for use in hybridization with a sample, where the reference sequences include all, at least one of, or any subset of the differentially expressed polynucleotides described herein. Usually such an array will include at least 3 different reference sequences, and can include any one or all of the provided differentially expressed sequences. Arrays of interest can further comprise sequences, including polymorphisms, of other genetic sequences, particularly other sequences of interest for screening for a disease or disorder (e.g., cancer, dysplasia, or other related or unrelated diseases, disorders, or conditions). The oligonucleotide sequence on the array will usually be at least about 12 nt in length, and can be of about the length of the provided sequences, or can extend into the flanking regions to generate fragments of 100 nt to 200 nt in length or more. Reference arrays can be produced according to any suitable methods known in the art. For example, methods of producing large arrays of oligonucleotides are described in U.S. 5,134,854, and U.S. 5,445,934 using light-directed synthesis

techniques. Using a computer controlled system, a heterogeneous array of monomers is converted, through simultaneous coupling at a number of reaction sites, into a heterogeneous array of polymers. Alternatively, microarrays are generated by deposition of pre-synthesized oligonucleotides onto a solid substrate, for example as described in PCT published application no. WO 95/35505.

5 A "reference expression pattern" or "REP" as used herein refers to the relative levels of expression of a selected set of genes, particularly of differentially expressed genes, that is associated with a selected cell type, *e.g.*, a normal cell, a cancerous cell, a cell exposed to an environmental stimulus, and the like. A "test expression pattern" or "TEP" refers to relative levels of expression of a selected set of genes, particularly of differentially expressed genes, in a test sample (*e.g.*, a cell of
10 unknown or suspected disease state, from which mRNA is isolated).

REPs can be generated in a variety of ways according to methods well known in the art. For example, REPs can be generated by hybridizing a control sample to an array having a selected set of polynucleotides (particularly a selected set of differentially expressed polynucleotides), acquiring the hybridization data from the array, and storing the data in a format that allows for ready comparison
15 of the REP with a TEP. Alternatively, all expressed sequences in a control sample can be isolated and sequenced, *e.g.*, by isolating mRNA from a control sample, converting the mRNA into cDNA, and sequencing the cDNA. The resulting sequence information roughly or precisely reflects the identity and relative number of expressed sequences in the sample. The sequence information can then be stored in a format (*e.g.*, a computer-readable format) that allows for ready comparison of the
20 REP with a TEP. The REP can be normalized prior to or after data storage, and/or can be processed to selectively remove sequences of expressed genes that are of less interest or that might complicate analysis (*e.g.*, some or all of the sequences associated with housekeeping genes can be eliminated from REP data).

TEPs can be generated in a manner similar to REPs, *e.g.*, by hybridizing a test sample to an
25 array having a selected set of polynucleotides, particularly a selected set of differentially expressed polynucleotides, acquiring the hybridization data from the array, and storing the data in a format that allows for ready comparison of the TEP with a REP. The REP and TEP to be used in a comparison can be generated simultaneously, or the TEP can be compared to previously generated and stored REPs.

30 In one embodiment of the invention, comparison of a TEP with a REP involves hybridizing a test sample with a reference array, where the reference array has one or more reference sequences for use in hybridization with a sample. The reference sequences include all, at least one of, or any subset of the differentially expressed polynucleotides described herein. Hybridization data for the test sample is acquired, the data normalized, and the produced TEP compared with a REP generated
35 using an array having the same or similar selected set of differentially expressed polynucleotides.

Probes that correspond to sequences differentially expressed between the two samples will show decreased or increased hybridization efficiency for one of the samples relative to the other.

Methods for collection of data from hybridization of samples with a reference arrays are well known in the art. For example, the polynucleotides of the reference and test samples can be generated using a detectable fluorescent label, and hybridization of the polynucleotides in the samples detected by scanning the microarrays for the presence of the detectable label using, for example, a microscope and light source for directing light at a substrate. A photon counter detects fluorescence from the substrate, while an x-y translation stage varies the location of the substrate. A confocal detection device that can be used in the subject methods is described in USPN 5,631,734.

A scanning laser microscope is described in Shalon et al., *Genome Res.* (1996) 6:639. A scan, using the appropriate excitation line, is performed for each fluorophore used. The digital images generated from the scan are then combined for subsequent analysis. For any particular array element, the ratio of the fluorescent signal from one sample (e.g., a test sample) is compared to the fluorescent signal from another sample (e.g., a reference sample), and the relative signal intensity determined.

Methods for analyzing the data collected from hybridization to arrays are well known in the art. For example, where detection of hybridization involves a fluorescent label, data analysis can include the steps of determining fluorescent intensity as a function of substrate position from the data collected, removing outliers, i.e. data deviating from a predetermined statistical distribution, and calculating the relative binding affinity of the targets from the remaining data. The resulting data can be displayed as an image with the intensity in each region varying according to the binding affinity between targets and probes.

In general, the test sample is classified as having a gene expression profile corresponding to that associated with a disease or non-disease state by comparing the TEP generated from the test sample to one or more REPs generated from reference samples (e.g., from samples associated with cancer or specific stages of cancer, dysplasia, samples affected by a disease other than cancer, normal samples, etc.). The criteria for a match or a substantial match between a TEP and a REP include expression of the same or substantially the same set of reference genes, as well as expression of these reference genes at substantially the same levels (e.g., no significant difference between the samples for a signal associated with a selected reference sequence after normalization of the samples, or at least no greater than about 25% to about 40% difference in signal strength for a given reference sequence. In general, a pattern match between a TEP and a REP includes a match in expression, preferably a match in qualitative or quantitative expression level, of at least one of, all or any subset of the differentially expressed genes of the invention.

Pattern matching can be performed manually, or can be performed using a computer program. Methods for preparation of substrate matrices (e.g., arrays), design of oligonucleotides for

use with such matrices, labeling of probes, hybridization conditions, scanning of hybridized matrices, and analysis of patterns generated, including comparison analysis, are described in, for example, U.S. 5,800,992.

Targets for inhibition of tumor growth. The polynucleotides of the invention can correspond to therapeutic targets, and modulation of expression and/or activity of these targets can provide for inhibition of tumor growth. For example, where overexpression of a gene is associated with tumor growth or metastasis, the gene product is a suitable target for inhibition of its expression and/or activity to facilitate inhibition of tumor growth or metastasis. The polynucleotides of the invention can correspond to such genes, and thus in some embodiments the antisense of these polynucleotides can be used to inhibit the expression of the gene and its corresponding gene product.

Diagnosis, Prognosis and Management of Cancer

The polynucleotides of the invention and their gene products are of particular interest as genetic or biochemical markers (e.g., in blood or tissues) that will detect the earliest changes along the carcinogenesis pathway and/or to monitor the efficacy of various therapies and preventive interventions. For example, the level of expression of certain polynucleotides can be indicative of a poorer prognosis, and therefore warrant more aggressive chemo- or radio-therapy for a patient or vice versa. The correlation of novel surrogate tumor specific features with response to treatment and outcome in patients can define prognostic indicators that allow the design of tailored therapy based on the molecular profile of the tumor. These therapies include antibody targeting and gene therapy. Determining expression of certain polynucleotides and comparison of a patient's profile with known expression in normal tissue and variants of the disease allows a determination of the best possible treatment for a patient, both in terms of specificity of treatment and in terms of comfort level of the patient. Surrogate tumor markers, such as polynucleotide expression, can also be used to better classify, and thus diagnose and treat, different forms and disease states of cancer. Two classifications widely used in oncology that can benefit from identification of the expression levels of the polynucleotides of the invention are staging of the cancerous disorder, and grading the nature of the cancerous tissue.

The polynucleotides of the invention can be useful to monitor patients having or susceptible to cancer to detect potentially malignant events at a molecular level before they are detectable at a gross morphological level. Furthermore, a polynucleotide of the invention identified as important for one type of cancer can also have implications for development or risk of development of other types of cancer, e.g., where a polynucleotide is differentially expressed across various cancer types. Thus, for example, expression of a polynucleotide that has clinical implications for metastatic colon cancer can also have clinical implications for stomach cancer or endometrial cancer.

Staging. Staging is a process used by physicians to describe how advanced the cancerous state is in a patient. Staging assists the physician in determining a prognosis, planning treatment and evaluating the results of such treatment. Staging systems vary with the types of cancer, but generally involve the following “TNM” system: the type of tumor, indicated by T; whether the cancer has metastasized to nearby lymph nodes, indicated by N; and whether the cancer has metastasized to more distant parts of the body, indicated by M. Generally, if a cancer is only detectable in the area of the primary lesion without having spread to any lymph nodes it is called Stage I. If it has spread only to the closest lymph nodes, it is called Stage II. In Stage III, the cancer has generally spread to the lymph nodes in near proximity to the site of the primary lesion. Cancers that have spread to a distant part of the body, such as the liver, bone, brain or other site, are Stage IV, the most advanced stage.

The polynucleotides of the invention can facilitate fine-tuning of the staging process by identifying markers for the aggressivity of a cancer, *e.g.* the metastatic potential, as well as the presence in different areas of the body. Thus, a Stage II cancer with a polynucleotide signifying a high metastatic potential cancer can be used to change a borderline Stage II tumor to a Stage III tumor, justifying more aggressive therapy. Conversely, the presence of a polynucleotide signifying a lower metastatic potential allows more conservative staging of a tumor.

Grading of cancers. Grade is a term used to describe how closely a tumor resembles normal tissue of its same type. The microscopic appearance of a tumor is used to identify tumor grade based on parameters such as cell morphology, cellular organization, and other markers of differentiation. As a general rule, the grade of a tumor corresponds to its rate of growth or aggressiveness, with undifferentiated or high-grade tumors being more aggressive than well differentiated or low-grade tumors. The following guidelines are generally used for grading tumors: 1) GX Grade cannot be assessed; 2) G1 Well differentiated; G2 Moderately well differentiated; 3) G3 Poorly differentiated; 4) G4 Undifferentiated. The polynucleotides of the invention can be especially valuable in determining the grade of the tumor, as they not only can aid in determining the differentiation status of the cells of a tumor, they can also identify factors other than differentiation that are valuable in determining the aggressiveness of a tumor, such as metastatic potential.

Detection of lung cancer. The polynucleotides of the invention can be used to detect lung cancer in a subject. Although there are more than a dozen different kinds of lung cancer, the two main types of lung cancer are small cell and nonsmall cell, which encompass about 90% of all lung cancer cases. Small cell carcinoma (also called oat cell carcinoma) usually starts in one of the larger bronchial tubes, grows fairly rapidly, and is likely to be large by the time of diagnosis. Nonsmall cell lung cancer (NSCLC) is made up of three general subtypes of lung cancer. Epidermoid carcinoma (also called squamous cell carcinoma) usually starts in one of the larger bronchial tubes

and grows relatively slowly. The size of these tumors can range from very small to quite large. Adenocarcinoma starts growing near the outside surface of the lung and can vary in both size and growth rate. Some slowly growing adenocarcinomas are described as alveolar cell cancer. Large cell carcinoma starts near the surface of the lung, grows rapidly, and the growth is usually fairly large when diagnosed. Other less common forms of lung cancer are carcinoid, cylindroma, mucoepidermoid, and malignant mesothelioma.

The polynucleotides of the invention, e.g., polynucleotides differentially expressed in normal cells versus cancerous lung cells (e.g., tumor cells of high or low metastatic potential) or between types of cancerous lung cells (e.g., high metastatic versus low metastatic), can be used to distinguish types of lung cancer as well as identifying traits specific to a certain patient's cancer and selecting an appropriate therapy. For example, if the patient's biopsy expresses a polynucleotide that is associated with a low metastatic potential, it may justify leaving a larger portion of the patient's lung in surgery to remove the lesion. Alternatively, a smaller lesion with expression of a polynucleotide that is associated with high metastatic potential may justify a more radical removal of lung tissue and/or the surrounding lymph nodes, even if no metastasis can be identified through pathological examination.

Detection of breast cancer. The majority of breast cancers are adenocarcinomas subtypes, which can be summarized as follows: 1) ductal carcinoma in situ (DCIS), including comedocarcinoma; 2) infiltrating (or invasive) ductal carcinoma (IDC); 3) lobular carcinoma in situ (LCIS); 4) infiltrating (or invasive) lobular carcinoma (ILC); 5) inflammatory breast cancer; 6) medullary carcinoma; 7) mucinous carcinoma; 8) Paget's disease of the nipple; 9) Phyllodes tumor; and 10) tubular carcinoma;

The expression of polynucleotides of the invention can be used in the diagnosis and management of breast cancer, as well as to distinguish between types of breast cancer. Detection of breast cancer can be determined using expression levels of any of the appropriate polynucleotides of the invention, either alone or in combination. Determination of the aggressive nature and/or the metastatic potential of a breast cancer can also be determined by comparing levels of one or more polynucleotides of the invention and comparing levels of another sequence known to vary in cancerous tissue, e.g. ER expression. In addition, development of breast cancer can be detected by examining the ratio of expression of a differentially expressed polynucleotide to the levels of steroid hormones (e.g., testosterone or estrogen) or to other hormones (e.g., growth hormone, insulin). Thus expression of specific marker polynucleotides can be used to discriminate between normal and cancerous breast tissue, to discriminate between breast cancers with different cells of origin, to discriminate between breast cancers with different potential metastatic rates, etc.

Detection of colon cancer. The polynucleotides of the invention exhibiting the appropriate expression pattern can be used to detect colon cancer in a subject. Colorectal cancer is one of the most common neoplasms in humans and perhaps the most frequent form of hereditary neoplasia. Prevention and early detection are key factors in controlling and curing colorectal cancer. Colorectal cancer begins as polyps, which are small, benign growths of cells that form on the inner lining of the colon. Over a period of several years, some of these polyps accumulate additional mutations and become cancerous. Multiple familial colorectal cancer disorders have been identified, which are summarized as follows: 1) Familial adenomatous polyposis (FAP); 2) Gardner's syndrome; 3) Hereditary nonpolyposis colon cancer (HNPCC); and 4) Familial colorectal cancer in Ashkenazi Jews. The expression of appropriate polynucleotides of the invention can be used in the diagnosis, prognosis and management of colorectal cancer. Detection of colon cancer can be determined using expression levels of any of these sequences alone or in combination with the levels of expression. Determination of the aggressive nature and/or the metastatic potential of a colon cancer can be determined by comparing levels of one or more polynucleotides of the invention and comparing total levels of another sequence known to vary in cancerous tissue, *e.g.*, expression of p53, DCC ras, for FAP (see, *e.g.*, Fearon ER, *et al.*, *Cell* (1990) 61(5):759; Hamilton SR *et al.*, *Cancer* (1993) 72:957; Bodmer W, *et al.*, *Nat Genet.* (1994) 4(3):217; Fearon ER, *Ann N Y Acad Sci.* (1995) 768:101). For example, development of colon cancer can be detected by examining the ratio of any of the polynucleotides of the invention to the levels of oncogenes (*e.g.* ras) or tumor suppressor genes (*e.g.* FAP or p53). Thus expression of specific marker polynucleotides can be used to discriminate between normal and cancerous colon tissue, to discriminate between colon cancers with different cells of origin, to discriminate between colon cancers with different potential metastatic rates, etc.

Detection of prostate cancer. The polynucleotides and their corresponding genes and gene products exhibiting the appropriate differential expression pattern can be used to detect prostate cancer in a subject. Over 95% of primary prostate cancers are adenocarcinomas. Signs and symptoms may include: frequent urination, especially at night, inability to urinate, trouble starting or holding back urination, a weak or interrupted urine flow and frequent pain or stiffness in the lower back, hips or upper thighs.

Many of the signs and symptoms of prostate cancer can be caused by a variety of other non-cancerous conditions. For example, one common cause of many of these signs and symptoms is a condition called benign prostatic hypertrophy, or BPH. In BPH, the prostate gets bigger and may block the flow of urine or interfere with sexual function. The methods and compositions of the invention can be used to distinguish between prostate cancer and such non-cancerous conditions. The methods of the invention can be used in conjunction with conventional methods of diagnosis,

e.g., digital rectal exam and/or detection of the level of prostate specific antigen (PSA), a substance produced and secreted by the prostate.

Use of Polynucleotides to Screen for Peptide Analogs and Antagonists

Polypeptides encoded by the instant polynucleotides and corresponding full length genes can be used to screen peptide libraries to identify binding partners, such as receptors, from among the encoded polypeptides. Peptide libraries can be synthesized according to methods known in the art (see, e.g., USPN 5,010,175 , and WO 91/17823). Agonists or antagonists of the polypeptides of the invention can be screened using any available method known in the art, such as signal transduction, antibody binding, receptor binding, mitogenic assays, chemotaxis assays, etc. The assay conditions ideally should resemble the conditions under which the native activity is exhibited *in vivo*, that is, under physiologic pH, temperature, and ionic strength. Suitable agonists or antagonists will exhibit strong inhibition or enhancement of the native activity at concentrations that do not cause toxic side effects in the subject. Agonists or antagonists that compete for binding to the native polypeptide can require concentrations equal to or greater than the native concentration, while inhibitors capable of binding irreversibly to the polypeptide can be added in concentrations on the order of the native concentration.

Such screening and experimentation can lead to identification of a novel polypeptide binding partner, such as a receptor, encoded by a gene or a cDNA corresponding to a polynucleotide of the invention, and at least one peptide agonist or antagonist of the novel binding partner. Such agonists and antagonists can be used to modulate, enhance, or inhibit receptor function in cells to which the receptor is native, or in cells that possess the receptor as a result of genetic engineering. Further, if the novel receptor shares biologically important characteristics with a known receptor, information about agonist/antagonist binding can facilitate development of improved agonists/antagonists of the known receptor.

Pharmaceutical Compositions and Therapeutic Uses

Pharmaceutical compositions of the invention can comprise polypeptides, antibodies, or polynucleotides (including antisense nucleotides and ribozymes) of the claimed invention in a therapeutically effective amount. The term "therapeutically effective amount" as used herein refers to an amount of a therapeutic agent to treat, ameliorate, or prevent a desired disease or condition, or to exhibit a detectable therapeutic or preventative effect. The effect can be detected by, for example, chemical markers or antigen levels. Therapeutic effects also include reduction in physical symptoms, such as decreased body temperature. The precise effective amount for a subject will depend upon the subject's size and health, the nature and extent of the condition, and the therapeutics or combination of therapeutics selected for administration. Thus, it is not useful to specify an exact effective amount in advance. However, the effective amount for a given situation is

determined by routine experimentation and is within the judgment of the clinician. For purposes of the present invention, an effective dose will generally be from about 0.01 mg/ kg to 50 mg/kg or 0.05 mg/kg to about 10 mg/kg of the DNA constructs in the individual to which it is administered.

A pharmaceutical composition can also contain a pharmaceutically acceptable carrier. The term “pharmaceutically acceptable carrier” refers to a carrier for administration of a therapeutic agent, such as antibodies or a polypeptide, genes, and other therapeutic agents. The term refers to any pharmaceutical carrier that does not itself induce the production of antibodies harmful to the individual receiving the composition, and which can be administered without undue toxicity.

Suitable carriers can be large, slowly metabolized macromolecules such as proteins, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids, amino acid copolymers, and inactive virus particles. Such carriers are well known to those of ordinary skill in the art. Pharmaceutically acceptable carriers in therapeutic compositions can include liquids such as water, saline, glycerol and ethanol. Auxiliary substances, such as wetting or emulsifying agents, pH buffering substances, and the like, can also be present in such vehicles. Typically, the therapeutic compositions are prepared as injectables, either as liquid solutions or suspensions; solid forms suitable for solution in, or suspension in, liquid vehicles prior to injection can also be prepared. Liposomes are included within the definition of a pharmaceutically acceptable carrier. Pharmaceutically acceptable salts can also be present in the pharmaceutical composition, e.g., mineral acid salts such as hydrochlorides, hydrobromides, phosphates, sulfates, and the like; and the salts of organic acids such as acetates, propionates, malonates, benzoates, and the like. A thorough discussion of pharmaceutically acceptable excipients is available in *Remington's Pharmaceutical Sciences* (Mack Pub. Co., N.J. 1991).

Delivery Methods. Once formulated, the compositions of the invention can be (1) administered directly to the subject (e.g., as polynucleotide or polypeptides); or (2) delivered ex vivo, to cells derived from the subject (e.g., as in *ex vivo* gene therapy). Direct delivery of the compositions will generally be accomplished by parenteral injection, e.g., subcutaneously, intraperitoneally, intravenously or intramuscularly, intratumoral or to the interstitial space of a tissue. Other modes of administration include oral and pulmonary administration, suppositories, and transdermal applications, needles, and gene guns or hyposprays. Dosage treatment can be a single dose schedule or a multiple dose schedule.

Methods for the *ex vivo* delivery and reimplantation of transformed cells into a subject are known in the art and described in e.g., International Publication No. WO 93/14778. Examples of cells useful in *ex vivo* applications include, for example, stem cells, particularly hematopoietic, lymph cells, macrophages, dendritic cells, or tumor cells. Generally, delivery of nucleic acids for both *ex vivo* and *in vitro* applications can be accomplished by, for example, dextran-mediated

transfection, calcium phosphate precipitation, polybrene mediated transfection, protoplast fusion, electroporation, encapsulation of the polynucleotide(s) in liposomes, and direct microinjection of the DNA into nuclei, all well known in the art.

Once a gene corresponding to a polynucleotide of the invention has been found to correlate with a proliferative disorder, such as neoplasia, dysplasia, and hyperplasia, the disorder can be amenable to treatment by administration of a therapeutic agent based on the provided polynucleotide, corresponding polypeptide or other corresponding molecule (e.g., antisense, ribozyme, etc.).

The dose and the means of administration of the inventive pharmaceutical compositions are determined based on the specific qualities of the therapeutic composition, the condition, age, and weight of the patient, the progression of the disease, and other relevant factors. For example, administration of polynucleotide therapeutic compositions agents of the invention includes local or systemic administration, including injection, oral administration, particle gun or catheterized administration, and topical administration. Preferably, the therapeutic polynucleotide composition contains an expression construct comprising a promoter operably linked to a polynucleotide of at least 12, 22, 25, 30, or 35 contiguous nt of the polynucleotide disclosed herein. Various methods can be used to administer the therapeutic composition directly to a specific site in the body. For example, a small metastatic lesion is located and the therapeutic composition injected several times in several different locations within the body of tumor. Alternatively, arteries which serve a tumor are identified, and the therapeutic composition injected into such an artery, in order to deliver the composition directly into the tumor. A tumor that has a necrotic center is aspirated and the composition injected directly into the now empty center of the tumor. The antisense composition is directly administered to the surface of the tumor, for example, by topical application of the composition. X-ray imaging is used to assist in certain of the above delivery methods.

Receptor-mediated targeted delivery of therapeutic compositions containing an antisense polynucleotide, subgenomic polynucleotides, or antibodies to specific tissues can also be used. Receptor-mediated DNA delivery techniques are described in, for example, Findeis *et al.*, *Trends Biotechnol.* (1993) 11:202; Chiou *et al.*, *Gene Therapeutics: Methods And Applications Of Direct Gene Transfer* (J.A. Wolff, ed.) (1994); Wu *et al.*, *J. Biol. Chem.* (1988) 263:621; Wu *et al.*, *J. Biol. Chem.* (1994) 269:542; Zenke *et al.*, *Proc. Natl. Acad. Sci. (USA)* (1990) 87:3655; Wu *et al.*, *J. Biol. Chem.* (1991) 266:338. Therapeutic compositions containing a polynucleotide are administered in a range of about 100 ng to about 200 mg of DNA for local administration in a gene therapy protocol. Concentration ranges of about 500 ng to about 50 mg, about 1 µg to about 2 mg, about 5 µg to about 500 µg, and about 20 µg to about 100 µg of DNA can also be used during a gene therapy protocol. Factors such as method of action (e.g., for enhancing or inhibiting levels of the

encoded gene product) and efficacy of transformation and expression are considerations which will affect the dosage required for ultimate efficacy of the antisense subgenomic polynucleotides. Where greater expression is desired over a larger area of tissue, larger amounts of antisense subgenomic polynucleotides or the same amounts readministered in a successive protocol of administrations, or several administrations to different adjacent or close tissue portions of, for example, a tumor site, may be required to effect a positive therapeutic outcome. In all cases, routine experimentation in clinical trials will determine specific ranges for optimal therapeutic effect. For polynucleotide related genes encoding polypeptides or proteins with anti-inflammatory activity, suitable use, doses, and administration are described in USPN 5,654,173.

The therapeutic polynucleotides and polypeptides of the present invention can be delivered using gene delivery vehicles. The gene delivery vehicle can be of viral or non-viral origin (see generally, Jolly, *Cancer Gene Therapy* (1994) 1:51; Kimura, *Human Gene Therapy* (1994) 5:845; Connelly, *Human Gene Therapy* (1995) 1:185; and Kaplitt, *Nature Genetics* (1994) 6:148). Expression of such coding sequences can be induced using endogenous mammalian or heterologous promoters. Expression of the coding sequence can be either constitutive or regulated.

Viral-based vectors for delivery of a desired polynucleotide and expression in a desired cell are well known in the art. Exemplary viral-based vehicles include, but are not limited to, recombinant retroviruses (see, e.g., WO 90/07936; WO 94/03622; WO 93/25698; WO 93/25234; USPN 5, 219,740; WO 93/11230; WO 93/10218; USPN 4,777,127; GB Patent No. 2,200,651; EP 0 345 242; and WO 91/02805), alphavirus-based vectors (e.g., Sindbis virus vectors, Semliki forest virus (ATCC VR-67; ATCC VR-1247), Ross River virus (ATCC VR-373; ATCC VR-1246) and Venezuelan equine encephalitis virus (ATCC VR-923; ATCC VR-1250; ATCC VR 1249; ATCC VR-532), and adeno-associated virus (AAV) vectors (see, e.g., WO 94/12649, WO 93/03769; WO 93/19191; WO 94/28938; WO 95/11984 and WO 95/00655). Administration of DNA linked to killed adenovirus as described in Curiel, *Hum. Gene Ther.* (1992) 3:147 can also be employed.

Non-viral delivery vehicles and methods can also be employed, including, but not limited to, polycationic condensed DNA linked or unlinked to killed adenovirus alone (see, e.g., Curiel, *Hum. Gene Ther.* (1992) 3:147); ligand-linked DNA (see, e.g., Wu, *J. Biol. Chem.* (1989) 264:16985); eukaryotic cell delivery vehicles (see, e.g., USPN 5,814,482; WO 95/07994; WO 96/17072; WO 95/30763; and WO 97/42338) and nucleic charge neutralization or fusion with cell membranes. Naked DNA can also be employed. Exemplary naked DNA introduction methods are described in WO 90/11092 and USPN 5,580,859. Liposomes that can act as gene delivery vehicles are described in USPN 5,422,120; WO 95/13796; WO 94/23697; WO 91/14445; and EP 0524968. Additional approaches are described in Philip, *Mol. Cell Biol.* (1994) 14:2411, and in Woffendin, *Proc. Natl. Acad. Sci.* (1994) 91:1581

Further non-viral delivery suitable for use includes mechanical delivery systems such as the approach described in Woffendin *et al.*, *Proc. Natl. Acad. Sci. USA* (1994) 91(24):11581.

Moreover, the coding sequence and the product of expression of such can be delivered through deposition of photopolymerized hydrogel materials or use of ionizing radiation (see, e.g., USPN 5,206,152 and WO 92/11033). Other conventional methods for gene delivery that can be used for delivery of the coding sequence include, for example, use of hand-held gene transfer particle gun (see, e.g., USPN 5,149,655); use of ionizing radiation for activating transferred gene (see, e.g., USPN 5,206,152 and WO 92/11033).

The present invention will now be illustrated by reference to the following examples which set forth particularly advantageous embodiments. However, it should be noted that these embodiments are illustrative and are not to be construed as restricting the invention in any way.

EXAMPLES

The following examples are offered primarily for purposes of illustration. It will be readily apparent to those skilled in the art that the formulations, dosages, methods of administration, and other parameters of this invention may be further modified or substituted in various ways without departing from the spirit and scope of the invention.

Example 1: Source of Biological Materials and Overview of Novel Polynucleotides Expressed by the Biological Materials

cDNA libraries were constructed from mRNA isolated from the cell lines indicated in Table 4. The specific library from which any polynucleotide was isolated is indicated in Table 1, with the number of the entry under the "LIBRARY" column correlating to the library number in Table 4. Polynucleotides expressed by the selected cell lines were isolated and analyzed; the sequences of these polynucleotides were about 275-300 nucleotides in length.

The sequences of the isolated polynucleotides were first masked to eliminate low complexity sequences using the XBLAST masking program (Claverie "Effective Large-Scale Sequence Similarity Searches," In: Computer Methods for Macromolecular Sequence Analysis, Doolittle, ed., *Meth. Enzymol.* 266:212-227 Academic Press, NY, NY (1996); see particularly Claverie, in "Automated DNA Sequencing and Analysis Techniques" Adams *et al.*, eds., Chap. 36, p. 267 Academic Press, San Diego, 1994 and Claverie *et al. Comput. Chem.* (1993) 17:191). Generally, masking does not influence the final search results, except to eliminate sequences of relative little interest due to their low complexity, and to eliminate multiple "hits" based on similarity to repetitive regions common to multiple sequences, e.g., Alu repeats. The remaining sequences were then used in a BLASTN vs. GenBank search; sequences that exhibited greater than 70% overlap, 99% identity,

and a p value of less than 1×10^{-40} were discarded. Sequences from this search also were discarded if the inclusive parameters were met, but the sequence was ribosomal or vector-derived.

The resulting sequences from the previous search were classified into three groups (1, 2 and 3 below) and searched in a BLASTX vs. NRP (non-redundant proteins) database search: (1) unknown (no hits in the GenBank search), (2) weak similarity (greater than 45% identity and p value of less than 1×10^{-5}), and (3) high similarity (greater than 60% overlap, greater than 80% identity, and p value less than 1×10^{-5}). Sequences having greater than 70% overlap, greater than 99% identity, and p value of less than 1×10^{-40} were discarded.

The remaining sequences were classified as unknown (no hits), weak similarity, and high similarity (parameters as above). Two searches were performed on these sequences. First, a BLAST vs. EST database search was performed and sequences with greater than 99% overlap, greater than 99% similarity and a p value of less than 1×10^{-40} were discarded. Sequences with a p value of less than 1×10^{-65} when compared to a database sequence of human origin were also excluded. Second, a BLASTN vs. Patent GeneSeq database was performed and sequences having greater than 99% identity, p value less than 1×10^{-40} , and greater than 99% overlap were discarded.

The remaining sequences were subjected to screening using other rules and redundancies in the dataset. Sequences with a p value of less than 1×10^{-111} in relation to a database sequence of human origin were specifically excluded. The final result provided the 2396 sequences listed as SEQ ID NOS:1-2396 in the accompanying Sequence Listing and summarized in Table 1 (inserted prior to claims). Each identified polynucleotide represents sequence from at least a partial mRNA transcript.

Table 1 provides: 1) the SEQ ID NO assigned to each sequence for use in the present specification; 2) the cluster to which the sequence is assigned; 3) the sequence name used as an internal identifier of the sequence; 4) the orientation of the insert in the clone (F=forward; R=reverse); 5) the name assigned to the clone from which the sequence was isolated; and 6) the library from which the sequence was originally isolated. Because the provided polynucleotides represent partial mRNA transcripts, two or more polynucleotides of the invention may represent different regions of the same mRNA transcript and the same gene. Thus, if two or more SEQ ID NOS: are identified as belonging to the same clone, then either sequence can be used to obtain the full-length mRNA or gene.

Example 2: Results of Public Database Search to Identify Function of Gene Products

SEQ ID NOS:1-2396 were translated in all three reading frames, and the nucleotide sequences and translated amino acid sequences used as query sequences to search for homologous sequences in either the GenBank (nucleotide sequences) or Non-Redundant Protein (amino acid sequences) databases. Query and individual sequences were aligned using the BLAST 2.0 programs (National Center for Biotechnology Information, Bethesda, Maryland; see also Altschul, et al. *Nucleic Acids Res.* (1997) 25:3389-3402). The sequences were masked to various extents to prevent searching of repetitive sequences or poly-A sequences, using the XBLAST program for masking low complexity as described above in Example 1.

Tables 2A and 2B (inserted before the claims) provide the alignment summaries having a p value of 1×10^{-2} or less indicating substantial homology between the sequences of the present invention and those of the indicated public databases. Table 2A provides the SEQ ID NO of the query sequence, the accession number of the GenBank database entry of the homologous sequence, and the p value of the alignment. Table 2B provides the SEQ ID NO of the query sequence, the accession number of the Non-Redundant Protein database entry of the homologous sequence, and the p value of the alignment. The alignments provided in Tables 2A and 2B are the best available alignment to a DNA or amino acid sequence at a time just prior to filing of the present specification.

The activity of the polypeptide encoded by the SEQ ID NOS listed in Tables 2A and 2B can be extrapolated to be substantially the same or substantially similar to the activity of the reported nearest neighbor or closely related sequence. The accession number of the nearest neighbor is reported, providing a publicly available reference to the activities and functions exhibited by the nearest neighbor. The public information regarding the activities and functions of each of the nearest neighbor sequences is incorporated by reference in this application. Also incorporated by reference is all publicly available information regarding the sequence, as well as the putative and actual activities and functions of the nearest neighbor sequences listed in Table 2B and their related sequences. The search program and database used for the alignment, as well as the calculation of the p value are also indicated.

Full length sequences or fragments of the polynucleotide sequences of the nearest neighbors can be used as probes and primers to identify and isolate the full length sequence of the corresponding polynucleotide. The nearest neighbors can indicate a tissue or cell type to be used to construct a library for the full-length sequences of the corresponding polynucleotides.

Example 3: Members of Protein Families

SEQ ID NOS:1-2396 were used to conduct a profile search as described in the specification above. Several of the polynucleotides of the invention were found to encode polypeptides having

characteristics of a polypeptide belonging to a known protein family (and thus represent members of these protein families) and/or comprising a known functional domain. Table provides the SEQ ID NO: of the query sequence, the profile name, and a brief description of the profile hit.

Table 3		
SEQ ID	Profilename	Description
410	ATPases	ATPases Associated with Various Cellular Activities
537	ATPases	ATPases Associated with Various Cellular Activities
539	ATPases	ATPases Associated with Various Cellular Activities
540	ATPases	ATPases Associated with Various Cellular Activities
662	rrm	RNA recognition motif. (aka RRM, RBD, or RNP domain)
683	rrm	RNA recognition motif. (aka RRM, RBD, or RNP domain)
707	dualspecphosphatase	Dual specificity phosphatase, catalytic domain
708	rrm	RNA recognition motif. (aka RRM, RBD, or RNP domain)
719	EFhand	EF-hand
738	ATPases	ATPases Associated with Various Cellular Activities
779	Zincfing_C2H2	Zinc finger, C2H2 type
781	rrm	RNA recognition motif. (aka RRM, RBD, or RNP domain)
783	rrm	RNA recognition motif. (aka RRM, RBD, or RNP domain)
1110	WD_domain	WD domain, G-beta repeats
1415	Dead_box_helic	DEAD and DEAH box helicases
1533	C2	C2 domain (prot. kinase C like)
1633	dualspecphosphatase	Dual specificity phosphatase, catalytic domain
1637	Dead_box_helic	DEAD and DEAH box helicases
1638	Dead_box_helic	DEAD and DEAH box helicases
1744	WD_domain	WD domain, G-beta repeats
1759	BZIP	Basic region plus leucine zipper transcription factors
1993	WD_domain	WD domain, G-beta repeats
2083	WD_domain	WD domain, G-beta repeats
2209	ATPases	ATPases Associated with Various Cellular Activities
2228	ras	Ras family
2287	ras	Ras family
2300	neur_chan	Neurotransmitter-gated ion-channel
2302	tor_domain2	kinase domain of tors (Christoph Reinhard)
2306	homeobox	Homeobox Domain
2318	Metallothion	Metallothioneins
2327	asp	Eukaryotic aspartyl proteases

Some polynucleotides exhibited multiple profile hits where the query sequence contains overlapping profile regions, and/or where the sequence contains two different functional domains. Each of the profile hits of Table 3 are described in more detail below. The acronyms for the profiles (provided in parentheses) are those used to identify the profile in the Pfam and Prosite databases.

The Pfam database can be accessed through web sites supported by the Washington University, St. Louis (Missouri), The Sanger Centre (United Kingdom); and The Karolinska Institute Center for Genomics Research. The Prosite database is publically available through the ExPASy Molecular Biology Server. The public information available on the Pfam and Prosite databases regarding the various profiles, including but not limited to the activities, function, and consensus sequences of various proteins families and protein domains, is incorporated herein by reference.

Eukaryotic Aspartyl Proteases (asp; Pfam Accession No. PF00026). SEQ ID NO:2327 corresponds to a gene encoding a novel eukaryotic aspartyl protease. Aspartyl proteases, known as acid proteases, (EC 3.4.23.-) are a widely distributed family of proteolytic enzymes (Foltmann B., *Essays Biochem.* (1981) 17:52; Davies D.R., *Annu. Rev. Biophys. Chem.* (1990) 19:189; Rao J.K.M., *et al.*, *Biochemistry* (1991) 30:4663) known to exist in vertebrates, fungi, plants, retroviruses and some plant viruses. Aspartate proteases of eukaryotes are monomeric enzymes which consist of two domains. Each domain contains an active site centered on a catalytic aspartyl residue. The consensus pattern to identify eukaryotic aspartyl protease is: [LIVMFGAC]-[LIVMTADN]-[LIVFSA]-D-[ST]-G-[STAV]-[STAPDENQ]-x-[LIVMFSTNC]-x-[LIVMFGTA], where D is the active site residue.

ATPases Associated with Various Cellular Activities (ATPases; Pfam Accession No. PF00004). SEQ ID NOS:410, 537, 539, 540, 738, and 2209 correspond to a sequence that encodes a member of a family of ATPases Associated with diverse cellular Activities (AAA). The AAA protein family is composed of a large number of ATPases that share a conserved region of about 220 amino acids containing an ATP-binding site (Froehlich *et al.*, *J. Cell Biol.* (1991) 114:443; Erdmann *et al.* *Cell* (1991) 64:499; Peters *et al.*, *EMBO J.* (1990) 9:1757; Kunau *et al.*, *Biochimie* (1993) 75:209-224; Confalonieri *et al.*, *BioEssays* (1995) 17:639; see also the AAA Server Homepage). The AAA domain, which can be present in one or two copies, acts as an ATP-dependent protein clamp (Confalonieri *et al.* (1995) *BioEssays* 17:639) and contains a highly conserved region located in the central part of the domain. The consensus pattern is: [LIVMT]-x-[LIVMT]-[LIVMF]-x-[GATMC]-[ST]-[NS]-x(4)-[LIVM]-D-x-A-[LIFA]-x-R.

Basic Region Plus Leucine Zipper Transcription Factors (BZIP; Pfam Accession No. PF00170). SEQ ID NO:1759 represents a polynucleotide encoding a novel member of the family of basic region plus leucine zipper transcription factors. The bZIP superfamily (Hurst, *Protein Prof.* (1995) 2:105; and Ellenberger, *Curr. Opin. Struct. Biol.* (1994) 4:12) of eukaryotic

DNA-binding transcription factors encompasses proteins that contain a basic region mediating sequence-specific DNA-binding followed by a leucine zipper required for dimerization. The consensus pattern for this protein family is: [KR]-x(1,3)-[RKSAQ]-N-x(2)-[SAQ](2)-x-[RKTAENQ]-x-R-x-[RK].

5 C2 domain (C2; Pfam Accession No. PF00168). SEQ ID NO:1533 corresponds to a sequence encoding a C2 domain, which is involved in calcium-dependent phospholipid binding (Davletov *J. Biol. Chem.* (1993) 268:26386-26390) or, in proteins that do not bind calcium, the domain may facilitate binding to inositol-1,3,4,5-tetraphosphate (Fukuda et al. *J. Biol. Chem.* (1994) 269:29206-29211; Sutton et al. *Cell* (1995) 80:929-938). The consensus sequence is: [ACG]-x(2)-
10 L-x(2,3)-D-x(1,2)-[NGSTLIF]-[GTMR]-x-[STAP]-D- [PA]-[FY].

DEAD and DEAH box families ATP-dependent helicases (Dead box helic; Pfam Accession No. PF00270). SEQ ID NOS:1415, 1637, and 1638 represent polynucleotides encoding a novel member of the DEAD and DEAH box families (Schmid et al., *Mol. Microbiol.* (1992) 6:283; Linder et al., *Nature* (1989) 337:121; Wassarman, et al., *Nature* (1991) 349:463). All members of these families are involved in ATP-dependent, nucleic-acid unwinding. All DEAD box family members share a number of conserved sequence motifs, some of which are specific to the DEAD family, with others shared by other ATP-binding proteins or by proteins belonging to the helicases 'superfamily' (Hodgman *Nature* (1988) 333:22 and *Nature* (1988) 333:578 (Errata)). One of these motifs, called the 'D-E-A-D-box', represents a special version of the B motif of ATP-binding proteins. Proteins that have His instead of the second Asp and are 'D-E-A-H-box' proteins (Wassarman et al., *Nature* (1991) 349:463; Harosh, et al., *Nucleic Acids Res.* (1991) 19:6331; Koonin, et al., *J. Gen. Virol.* (1992) 73:989). The following signature patterns are used to identify member for both subfamilies: 1) [LIVMF](2)-D-E-A-D-[RKEN]-x-[LIVMFYGSTN]; and 2) [GSAH]-x-[LIVMF](3)-D-E-[ALIV]-H-[NECR].

25 Dual specificity phosphatase (DSPc; Pfam Accession No. PF00782). SEQ ID NOS:707 and 1633 correspond to sequences that encode members of a family of dual specificity phosphatases (DSPs). DSPs are Ser/Thr and Tyr protein phosphatases that comprise a tertiary fold highly similar to that of tyrosine-specific phosphatases, except for a "recognition" region connecting helix alpha1 to strand beta1. This tertiary fold may determine differences in substrate specific between VH-1
30 related dual specificity phosphatase (VHR), the protein tyrosine phosphatases (PTPs), and other DSPs. Phosphatases are important in the control of cell growth, proliferation, differentiation and transformation.

EF Hand (Efhand; Pfam Accession No. PF00036). SEQ ID NO:719 corresponds to a polynucleotide encoding a member of the EF-hand protein family, a calcium binding domain shared
35 by many calcium-binding proteins belonging to the same evolutionary family (Kawasaki *et al.*,

Protein. Prof. (1995) 2:305-490). The domain is a twelve residue loop flanked on both sides by a twelve residue alpha-helical domain, with a calcium ion coordinated in a pentagonal bipyramidal configuration. The six residues involved in the binding are in positions 1, 3, 5, 7, 9 and 12; these residues are denoted by X, Y, Z, -Y, -X and -Z. The invariant Glu or Asp at position 12 provides two oxygens for liganding Ca (bidentate ligand). The consensus pattern includes the complete EF-hand loop as well as the first residue which follows the loop and which seem to always be hydrophobic: D-x-[DNS]-{ILVFYW}-[DENSTG]-[DNQGHRK]-{GP}-[LIVMC]-[DENQSTAGC]-x(2)-[DE]-[LIVMFYW].

Homeobox domain (homeobox; Pfam Accession No. PF00046). SEQ ID NO:2306 represents a polynucleotide encoding a protein having a homeobox domain. The 'homeobox' is a protein domain of 60 amino acids (Gehring In: Guidebook to the Homeobox Genes, Duboule D., Ed., pp1-10, Oxford University Press, Oxford, (1994); Buerklin In: Guidebook to the Homeobox Genes, pp25-72, Oxford University Press, Oxford, (1994); Gehring *Trends Biochem. Sci.* (1992) 17:277-280; Gehring *et al Annu. Rev. Genet.* (1986) 20:147-173; Schofield *Trends Neurosci.* (1987) 10:3-6) first identified in number of Drosophila homeotic and segmentation proteins. It is extremely well conserved in many other animals, including vertebrates. This domain binds DNA through a helix-turn-helix type of structure. Several proteins that contain a homeobox domain play an important role in development. Most of these proteins are sequence-specific DNA-binding transcription factors. The homeobox domain is also very similar to a region of the yeast mating type proteins. These are sequence-specific DNA-binding proteins that act as master switches in yeast differentiation by controlling gene expression in a cell type-specific fashion.

A schematic representation of the homeobox domain is shown below. The helix-turn-helix region is shown by the symbols 'H' (for helix), and 't' (for turn).

xxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxxHHHHHHHHtttHHHHHHHHHHxxxxxxxxxxxx

The pattern detects homeobox sequences 24 residues long and spans positions 34 to 57 of the homeobox domain. The consensus pattern is as follows: [LIVMFYGG]-[ASLVR]-x(2)-[LIVMSTACN]-x-[LIVM]-x(4)-[LIV]-[RKNQESTAIY]-[LIVFSTNKH]-W-[FYVC]-x-[NDQTAH]-x(5)-[RKNAIMW].

Metallothioneins (metalthio; Pfam Accession No. PF00131). SEQ ID NO:2318 corresponds to a polynucleotide encoding a member of the metallothionein (MT) protein family (Hamer *Annu. Rev. Biochem.* (1986) 55:913-951; and Kagi *et al. Biochemistry* (1988) 27:8509-8515), small proteins which bind heavy metals such as zinc, copper, cadmium, nickel, *etc.*, through clusters of thiolate bonds. MT's occur throughout the animal kingdom and are also found in higher plants, fungi and some prokaryotes. On the basis of structural relationships MT's have been subdivided into

three classes. Class I includes mammalian MT's as well as MT's from crustacean and molluscs, but with clearly related primary structure. Class II groups together MT's from various species such as sea urchins, fungi, insects and cyanobacteria which display none or only very distant correspondence to class I MT's. Class III MT's are atypical polypeptides containing gamma-glutamylcysteinyl units. The consensus pattern for this protein family is: C-x-C-[GSTAP]-x(2)-C-x-C-x(2)-C-x-C-x(2)-C-x-K.

Neurotransmitter-Gated Ion-Channel (neur_chan; Pfam Accession No. PF00065). SEQ ID NO:2300 corresponds to a sequence encoding a neurotransmitter-gated ion channel.

Neurotransmitter-gated ion-channels, which provide the molecular basis for rapid signal transmission at chemical synapses, are post-synaptic oligomeric transmembrane complexes that transiently form a ionic channel upon the binding of a specific neurotransmitter. Five types of neurotransmitter-gated receptors are known: 1) nicotinic acetylcholine receptor (AChR); 2) glycine receptor; 3) gamma-aminobutyric-acid (GABA) receptor; 4) serotonin 5HT3 receptor; and 5) glutamate receptor. All known sequences of subunits from neurotransmitter-gated ion-channels are structurally related, and are composed of a large extracellular glycosylated N-terminal ligand-binding domain, followed by three hydrophobic transmembrane regions that form the ionic channel, followed by an intracellular region of variable length. A fourth hydrophobic region is found at the C-terminal of the sequence. The consensus pattern is: C-x-[LIVMFQ]-x-[LIVMF]-x(2)-[FY]-P-x-D-x(3)-C, where the two C's are linked by a disulfide bond.

Ras family proteins (ras; Pfam Accession No. PF00071). SEQ ID NOS:2228 and 2287 represent polynucleotides encoding the ras family of small GTP/GDP-binding proteins (Valencia et al., 1991, Biochemistry 30:4637-4648). Ras family members generally require a specific guanine nucleotide exchange factor (GEF) and a specific GTPase activating protein (GAP) as stimulators of overall GTPase activity. Among ras-related proteins, the highest degree of sequence conservation is found in four regions that are directly involved in guanine nucleotide binding. The first two constitute most of the phosphate and Mg²⁺ binding site (PM site) and are located in the first half of the G-domain. The other two regions are involved in guanosine binding and are located in the C-terminal half of the molecule. Motifs and conserved structural features of the ras-related proteins are described in Valencia et al., 1991, Biochemistry 30:4637-4648. A major consensus pattern of ras proteins is: D-T-A-G-Q-E-K-[LF]-G-G-L-R-[DE]-G-Y-Y.

RNA Recognition Motif (rrm; Pfam Accession No. PF00076). SEQ ID NOS:662, 683, 708, 781, and 783 correspond to sequence encoding an RNA recognition motif, also known as an RRM, RBD, or RNP domain. This domain, which is about 90 amino acids long, is contained in eukaryotic proteins that bind single-stranded RNA (Bandziulis et al. *Genes Dev.* (1989) 3:431-437; Dreyfuss et al. *Trends Biochem. Sci.* (1988) 13:86-91). Two regions within the RNA-binding domain are highly

conserved: the first is a hydrophobic segment of six residues (which is called the RNP-2 motif), the second is an octapeptide motif (which is called RNP-1 or RNP-CS). The consensus pattern is: [RK]-G-{EDRKHPCG}-[AGSCI]-[FY]-[LIVA]-x-[FYLM].

5 Kinase Domain of Tors (tor_domain2). SEQ ID NO:2302 corresponds to a member of the TOR lipid kinase protein family. This family is composed of large proteins with a lipid and protein kinase domain and characterized through their sensitivity to rapamycin (an antifungal compound). TOR proteins are involved in signal transduction downstream of PI3 kinase and many other signals. TOR (also called FRAP, RAFT) plays a role in regulating protein synthesis and cell growth., and in yeast controls translation initiation and early G1 progression. See, *e.g.*, Barbet *et al. Mol Biol Cell.*
10 (1996) 7(1):25-42; Helliwell *et al. Genetics* (1998) 148:99-112.

WD Domain, G-Beta Repeats (WD_domain; Pfam Accession No. PF00400). SEQ ID NOS:1110, 1744, 1993, and 2083 represent novel members of the WD domain/G-beta repeat family. Beta-transducin (G-beta) is one of the three subunits (alpha, beta, and gamma) of the guanine nucleotide-binding proteins (G proteins) which act as intermediaries in the transduction of signals generated by transmembrane receptors (Gilman, *Annu. Rev. Biochem.* (1987) 56:615). The alpha subunit binds to and hydrolyzes GTP; the functions of the beta and gamma subunits are less clear but they seem to be required for the replacement of GDP by GTP as well as for membrane anchoring and receptor recognition. In higher eukaryotes, G-beta exists as a small multigene family of highly conserved proteins of about 340 amino acid residues. Structurally, G-beta consists of eight tandem
20 repeats of about 40 residues, each containing a central Trp-Asp motif (this type of repeat is sometimes called a WD-40 repeat). The consensus pattern for the WD domain/G-Beta repeat family is: [LIVMSTAC]-[LIVMFYWSTAGC]-[LIMSTAG]-[LIVMSTAGC]-x(2)-[DN]-x(2)-[LIVMWSTAC]-x-[LIVMFSTAG]-W-[DEN]-[LIVMFSTAGCN].

Zinc Finger, C2H2 Type (Zincfing_C2H2; Pfam Accession No. PF00096). SEQ ID NO:779 corresponds to a polynucleotid encoding a member of the C2H2 type zinc finger protein family, which contain zinc finger domains that facilitate nucleic acid binding (Klug *et al., Trends Biochem. Sci.* (1987) 12:464; Evans *et al., Cell* (1988) 52:1; Payre *et al., FEBS Lett.* (1988) 234:245; Miller *et al., EMBO J.* (1985) 4:1609; and Berg, *Proc. Natl. Acad. Sci. USA* (1988) 85:99).

30 In addition to the conserved zinc ligand residues, a number of other positions are also important for the structural integrity of the C2H2 zinc fingers. (Rosenfeld *et al., J. Biomol. Struct. Dyn.* (1993) 11:557) The best conserved position, which is generally an aromatic or aliphatic residue, is located four residues after the second cysteine. The consensus pattern for C2H2 zinc fingers is: C-x(2,4)-C-x(3)-[LIVMFYWC]-x(8)-H-x(3,5)-H. The two C's and two H's are zinc
35 ligands.

Example 4: Differential Expression of Polynucleotides of the Invention: Description of Libraries and Detection of Differential Expression

The relative expression levels of the polynucleotides of the invention was assessed in several libraries prepared from various sources, including cell lines and patient tissue samples. Table 4 provides a summary of these libraries, including the shortened library name (used hereafter), the mRNA source used to prepared the cDNA library, and the approximate number of clones in the library.

Table 4. Description of cDNA Libraries

Library (Lib#)	Description	Number of Clones in Library
1	Human Colon Cell Line Km12 L4: High Metastatic Potential (derived from Km12C)	308731
2	Human Colon Cell Line Km12C: Low Metastatic Potential	284771
3	Human Breast Cancer Cell Line MDA-MB-231: High Metastatic Potential; micro-mets in lung	326937
4	Human Breast Cancer Cell Line MCF7: Non Metastatic	318979
8	Human Lung Cancer Cell Line MV-522: High Metastatic Potential	223620
9	Human Lung Cancer Cell Line UCP-3: Low Metastatic Potential	312503
12	Human microvascular endothelial cells (HMVEC) - UNTREATED (PCR (OligodT) cDNA library)	41938
13	Human microvascular endothelial cells (HMVEC) - bFGF TREATED (PCR (OligodT) cDNA library)	42100
14	Human microvascular endothelial cells (HMVEC) - VEGF TREATED (PCR (OligodT) cDNA library)	42825
15	Normal Colon - UC#2 Patient (MICRODISSECTED PCR (OligodT) cDNA library)	282722
16	Colon Tumor - UC#2 Patient (MICRODISSECTED PCR (OligodT) cDNA library)	298831
17	Liver Metastasis from Colon Tumor of UC#2 Patient (MICRODISSECTED PCR (OligodT) cDNA library)	303467
18	Normal Colon - UC#3 Patient (MICRODISSECTED PCR (OligodT) cDNA library)	36216
19	Colon Tumor - UC#3 Patient (MICRODISSECTED PCR (OligodT) cDNA library)	41388
20	Liver Metastasis from Colon Tumor of UC#3 Patient (MICRODISSECTED PCR (OligodT) cDNA library)	30956
21	GRRpz Cells derived from normal prostate epithelium	164801
22	WOca Cells derived from Gleason Grade 4 prostate cancer epithelium	162088
23	Normal Lung Epithelium of Patient #1006 (MICRODISSECTED PCR (OligodT) cDNA library)	306198
24	Primary tumor, Large Cell Carcinoma of Patient #1006	309349

Library (Lib#)	Description	Number of Clones in Library
	(MICRODISSECTED PCR (OligodT) cDNA library)	

The KM12L4 cell line (Morikawa, et al., *Cancer Research* (1988) 48:6863) is derived from the KM12C cell line (Morikawa et al. *Cancer Res.* (1988) 48:1943-1948). The KM12C cell line, which is poorly metastatic (low metastatic) was established in culture from a Dukes' stage B₂ surgical specimen (Morikawa et al. *Cancer Res.* (1988) 48:6863). The KM12L4-A is a highly metastatic subline derived from KM12C (Yeatman et al. *Nucl. Acids. Res.* (1995) 23:4007; Bao-Ling et al. *Proc. Annu. Meet. Am. Assoc. Cancer. Res.* (1995) 21:3269). The KM12C and KM12C-derived cell lines (e.g., KM12L4, KM12L4-A, etc.) are well-recognized in the art as a model cell line for the study of colon cancer (see, e.g., Moriakawa et al., *supra*; Radinsky et al. *Clin. Cancer Res.* (1995) 1:19; Yeatman et al., (1995) *supra*; Yeatman et al. *Clin. Exp. Metastasis* (1996) 14:246). The MDA-MB-231 cell line was originally isolated from pleural effusions (Cailleau, J. *Natl. Cancer. Inst.* (1974) 53:661), is of high metastatic potential, and forms poorly differentiated adenocarcinoma grade II in nude mice consistent with breast carcinoma. The MCF7 cell line was derived from a pleural effusion of a breast adenocarcinoma and is non-metastatic. The MDA-MB-231 and MCF-7 cell lines are well-recognized in the art as a models for the study of human breast cancer (see, e.g., Chandrasekaran et al., *Cancer Res.* (1979) 39:870; Gastpar et al., *J Med Chem* (1998) 41:4965; Ranson et al., *Br J Cancer* (1998) 77:1586; and Kuang et al., *Nucleic Acids Res* (1998) 26:1116).

The MV-522 cell line is derived from a human lung carcinoma and is of high metastatic potential. The UCP-3 cell line is a low metastatic human lung carcinoma cell line; the MV-522 is a high metastatic variant of UCP-3. These cell lines are well-recognized in the art as models for the study of human lung cancer (see, e.g., Varki et al., *Int J Cancer* (1987) 40:46 (UCP-3); Varki et al., *Tumour Biol.* (1990) 11:327; (MV-522 and UCP-3); Varki et al., *Anticancer Res.* (1990) 10:637; (MV-522); Kelner et al., *Anticancer Res* (1995) 15:867 (MV-522); and Zhang et al., *Anticancer Drugs* (1997) 8:696 (MV522)). The samples of libraries 15-20 are derived from two different patients (UC#2, and UC#3). The bFGF-treated HMVEC were prepared by incubation with bFGF at 10ng/ml for 2 hrs; the VEGF-treated HMVEC were prepared by incubation with 20ng/ml VEGF for 2 hrs. Following incubation with the respective growth factor, the cells were washed and lysis buffer added for RNA preparation. The GRRpz and WOca cell lines were provided by Dr. Donna M. Peehl, Department of Medicine, Stanford University School of Medicine. GRRpz was derived from normal prostate epithelium. The WOca cell line is a Gleason Grade 4 cell line.

Each of the libraries is composed of a collection of cDNA clones that in turn are representative of the mRNAs expressed in the indicated mRNA source. In order to facilitate the

analysis of the millions of sequences in each library, the sequences were assigned to clusters. The concept of "cluster of clones" is derived from a sorting/grouping of cDNA clones based on their hybridization pattern to a panel of roughly 300 7bp oligonucleotide probes (see Drmanac *et al.*, *Genomics* (1996) 37(1):29). Random cDNA clones from a tissue library are hybridized at moderate stringency to 300 7bp oligonucleotides. Each oligonucleotide has some measure of specific hybridization to that specific clone. The combination of 300 of these measures of hybridization for 300 probes equals the "hybridization signature" for a specific clone. Clones with similar sequence will have similar hybridization signatures. By developing a sorting/grouping algorithm to analyze these signatures, groups of clones in a library can be identified and brought together computationally. These groups of clones are termed "clusters". Depending on the stringency of the selection in the algorithm (similar to the stringency of hybridization in a classic library cDNA screening protocol), the "purity" of each cluster can be controlled. For example, artifacts of clustering may occur in computational clustering just as artifacts can occur in "wet-lab" screening of a cDNA library with 400 bp cDNA fragments, at even the highest stringency. The stringency used in the implementation of cluster herein provides groups of clones that are in general from the same cDNA or closely related cDNAs. Closely related clones can be a result of different length clones of the same cDNA, closely related clones from highly related gene families, or splice variants of the same cDNA.

Differential expression for a selected cluster was assessed by first determining the number of cDNA clones corresponding to the selected cluster in the first library (Clones in 1st), and the determining the number of cDNA clones corresponding to the selected cluster in the second library (Clones in 2nd). Differential expression of the selected cluster in the first library relative to the second library is expressed as a "ratio" of percent expression between the two libraries. In general, the "ratio" is calculated by: 1) calculating the percent expression of the selected cluster in the first library by dividing the number of clones corresponding to a selected cluster in the first library by the total number of clones analyzed from the first library; 2) calculating the percent expression of the selected cluster in the second library by dividing the number of clones corresponding to a selected cluster in a second library by the total number of clones analyzed from the second library; 3) dividing the calculated percent expression from the first library by the calculated percent expression from the second library. If the "number of clones" corresponding to a selected cluster in a library is zero, the value is set at 1 to aid in calculation. The formula used in calculating the ratio takes into account the "depth" of each of the libraries being compared, *i.e.*, the total number of clones analyzed in each library.

In general, a polynucleotide is said to be significantly differentially expressed between two samples when the ratio value is greater than at least about 2, preferably greater than at least about 3,

more preferably greater than at least about 5, where the ratio value is calculated using the method described above. The significance of differential expression is determined using a z score test (Zar, Biostatistical Analysis, Prentice Hall, Inc., USA, "Differences between Proportions," pp 296-298 (1974).

5

Example 5: Differential Expression of Genes Corresponding to Polynucleotides of the Invention

A number of polynucleotide sequences have been identified that are differentially expressed between, for example, cells derived from high metastatic potential cancer tissue and low metastatic cancer cells, and between cells derived from metastatic cancer tissue and normal tissue. Evaluation of the levels of expression of the genes corresponding to these sequences can be valuable in diagnosis, prognosis, and/or treatment (*e.g.*, to facilitate rationale design of therapy, monitoring during and after therapy, *etc.*). Moreover, the genes corresponding to differentially expressed sequences described herein can be therapeutic targets due to their involvement in regulation (*e.g.*, inhibition or promotion) of development of, for example, the metastatic phenotype. For example, sequences that correspond to genes that are increased in expression in high metastatic potential cells relative to normal or non-metastatic tumor cells may encode genes or regulatory sequences involved in processes such as angiogenesis, differentiation, cell replication, and metastasis.

Detection of the relative expression levels of differentially expressed polynucleotides described herein can provide valuable information to guide the clinician in the choice of therapy. For example, a patient sample exhibiting an expression level of one or more of these polynucleotides that corresponds to a gene that is increased in expression in metastatic or high metastatic potential cells may warrant more aggressive treatment for the patient. In contrast, detection of expression levels of a polynucleotide sequence that corresponds to expression levels associated with that of low metastatic potential cells may warrant a more positive prognosis than the gross pathology would suggest.

The differential expression of the polynucleotides described herein can thus be used as, for example, diagnostic markers, prognostic markers, for risk assessment, patient treatment and the like.

These polynucleotide sequences can also be used in combination with other known molecular and/or biochemical markers. The following examples provide relative expression levels of polynucleotides from specified cell lines and patient tissue samples.

The differential expression data for polynucleotides of the invention that have been identified as being differentially expressed across various combinations of the libraries described above is summarized in Table 5 (inserted prior to the claims). Table 5 provides: 1) the Sequence Identification Number ("SEQ") assigned to the polynucleotide; 2) the cluster ("CLST") to which the polynucleotide has been assigned as described above; 3) the library comparisons that resulted in

identification of the polynucleotide as being differentially expressed ("Library Pair A,B"), with shorthand names of the compared libraries provided in parentheses following the library numbers; 4) the number of clones corresponding to the polynucleotide in the first library listed ("A"); 5) the number of clones corresponding to the polynucleotide in the second library listed ("B"); 6) the "A/B" where the comparison resulted in a finding that the number of clones in library A is greater than the number of clones in library B; and 7) the "B/A" where the comparison resulted in a finding that the number of clones in library B is greater than the number of clones in library A.

Example 6: Source of Biological Materials for Microarray-Based Experiments

The biological materials used in the experiments described in the subsequent examples relating to microarray data are described below.

Source of patient tissue samples

Normal and cancerous tissues were collected from patients using laser capture microdissection (LCM) techniques, which techniques are well known in the art (see, e.g., Ohyama *et al.* (2000) *Biotechniques* 29:530-6; Curran *et al.* (2000) *Mol. Pathol.* 53:64-8; Suarez-Quian *et al.* (1999) *Biotechniques* 26:328-35; Simone *et al.* (1998) *Trends Genet* 14:272-6; Conia *et al.* (1997) *J. Clin. Lab. Anal.* 11:28-38; Emmert-Buck *et al.* (1996) *Science* 274:998-1001). Table 9 (inserted following the last page of the Examples) provides information about each patient from which the samples were isolated, including: the Patient ID and Path ReportID, numbers assigned to the patient and the pathology reports for identification purposes; the anatomical location of the tumor (AnatomicalLoc); The Primary Tumor Size; the Primary Tumor Grade; the Histopathologic Grade; a description of local sites to which the tumor had invaded (Local Invasion); the presence of lymph node metastases (Lymph Node Metastasis); incidence of lymph node metastases (provided as number of lymph nodes positive for metastasis over the number of lymph nodes examined) (Incidence Lymphnode Metastasis); the Regional Lymphnode Grade; the identification or detection of metastases to sites distant to the tumor and their location (Distant Met & Loc); a description of the distant metastases (Description Distant Met); the grade of distant metastasis (Distant Met Grade); and general comments about the patient or the tumor (Comments). Adenoma was not described in any of the patients. ; adenoma dysplasia (described as hyperplasia by the pathologist) was described in Patient ID No. 695. Extranodal extensions were described in two patients, Patient ID Nos. 784 and 791. Lymphovascular invasion was described in seven patients, Patient ID Nos. 128, 278, 517,

534, 784, 786, and 791.. Crohn's-like infiltrates were described in seven patients, Patient ID Nos. 52, 264, 268, 392, 393, 784, and 791.

Polynucleotides on arrays

Polynucleotides spotted on the arrays were generated by PCR amplification of clones derived from cDNA libraries. The clones used for amplification were either the clones from which the sequences described herein (SEQ ID NOS:1-2396) were derived, or are clones having inserts with significant polynucleotide sequence overlap with the sequences described herein (SEQ ID NO:1-2396) as determined by BLAST2 homology searching.

Example 7: Microarray Design

Each array used in the examples below had an identical spatial layout and control spot set. Each microarray was divided into two areas, each area having an array with, on each half, twelve groupings of 32 x 12 spots for a total of about 9,216 spots on each array. The two areas are spotted identically which provide for at least two duplicates of each clone per array. Spotting was accomplished using PCR amplified products from 0.5kb to 2.0 kb and spotted using a Molecular Dynamics Gen III spotter according to the manufacturer's recommendations. The first row of each of the 24 regions on the array had about 32 control spots, including 4 negative control spots and 8 test polynucleotides.

The test polynucleotides were spiked into each sample before the labeling reaction with a range of concentrations from 2-600 pg/slide and ratios of 1:1 . For each array design, two slides were hybridized with the test samples reverse-labeled in the labeling reaction. This provided for about 4 duplicate measurements for each clone, two of one color and two of the other, for each sample.

Example 8: Identification Of Differentially Expressed Genes

cDNA probes were prepared from total RNA isolated from the patient cells described in Example 6. Since LCM provides for the isolation of specific cell types to provide a substantially homogenous cell sample, this provided for a similarly pure RNA sample.

Total RNA was first reverse transcribed into cDNA using a primer containing a T7 RNA polymerase promoter, followed by second strand DNA synthesis. cDNA was then

transcribed *in vitro* to produce antisense RNA using the T7 promoter-mediated expression (see, e.g., Luo *et al.* (1999) *Nature Med* 5:117-122), and the antisense RNA was then converted into cDNA. The second set of cDNAs were again transcribed *in vitro*, using the T7 promoter, to provide antisense RNA. Optionally, the RNA was again converted into cDNA, allowing for up to a third round of T7-mediated amplification to produce more antisense RNA. Thus the procedure provided for two or three rounds of *in vitro* transcription to produce the final RNA used for fluorescent labeling. Fluorescent probes were generated by first adding control RNA to the antisense RNA mix, and producing fluorescently labeled cDNA from the RNA starting material. Fluorescently labeled cDNAs prepared from the tumor RNA sample were compared to fluorescently labeled cDNAs prepared from normal cell RNA sample. For example, the cDNA probes from the normal cells were labeled with Cy3 fluorescent dye (green) and the cDNA probes prepared from the tumor cells were labeled with Cy5 fluorescent dye (red).

The differential expression assay was performed by mixing equal amounts of probes from tumor cells and normal cells of the same patient. The arrays were prehybridized by incubation for about 2 hrs at 60°C in 5X SSC/0.2% SDS/1 mM EDTA, and then washed three times in water and twice in isopropanol. Following prehybridization of the array, the probe mixture was then hybridized to the array under conditions of high stringency (overnight at 42°C in 50% formamide, 5X SSC, and 0.2% SDS. After hybridization, the array was washed at 55°C three times as follows: 1) first wash in 1X SSC/0.2% SDS; 2) second wash in 0.1X SSC/0.2% SDS; and 3) third wash in 0.1X SSC.

The arrays were then scanned for green and red fluorescence using a Molecular Dynamics Generation III dual color laser-scanner/detector. The images were processed using BioDiscovery Autogene software, and the data from each scan set normalized to provide for a ratio of expression relative to normal. Data from the microarray experiments was analyzed according to the algorithms described in U.S. application serial no. 60/252,358, filed November 20, 2000, by E.J. Moler, M.A. Boyle, and F.M. Randazzo, and entitled "Precision and accuracy in cDNA microarray data," which application is specifically incorporated herein by reference.

The experiment was repeated, this time labeling the two probes with the opposite color in order to perform the assay in both "color directions." Each experiment was sometimes repeated with two more slides (one in each color direction). The level

fluorescence for each sequence on the array expressed as a ratio of the geometric mean of 8 replicate spots/genes from the four arrays or 4 replicate spots/gene from 2 arrays or some other permutation. The data were normalized using the spiked positive controls present in each duplicated area, and the precision of this normalization was included in the final determination of the significance of each differential. The fluorescent intensity of each spot was also compared to the negative controls in each duplicated area to determine which spots have detected significant expression levels in each sample.

A statistical analysis of the fluorescent intensities was applied to each set of duplicate spots to assess the precision and significance of each differential measurement, resulting in a p-value testing the null hypothesis that there is no differential in the expression level between the tumor and normal samples of each patient. During initial analysis of the microarrays, the hypothesis was accepted if $p > 10^{-3}$, and the differential ratio was set to 1.000 for those spots. All other spots have a significant difference in expression between the tumor and normal sample. If the tumor sample has detectable expression and the normal does not, the ratio is truncated at 1000 since the value for expression in the normal sample would be zero, and the ratio would not be a mathematically useful value (e.g., infinity). If the normal sample has detectable expression and the tumor does not, the ratio is truncated to 0.001, since the value for expression in the tumor sample would be zero and the ratio would not be a mathematically useful value. These latter two situations are referred to herein as "on/off." Database tables were populated using a 95% confidence level ($p > 0.05$).

Tables 10-14:clf summarizes the results of the differential expression analysis, where the difference in the expression level in the colon tumor cell relative to the matched normal colon cells is greater than or equal to 2 fold (" $\geq 2x$ "), 2.5 fold (" $\geq 2.5x$ "), or 5 fold (" $\geq 5x$ ") in at least 20% or more of the patients analyzed. Each table provides: the SEQ ID NO; the percentage of patients tested having a colon tumor that exhibited at least 2 fold (" $\geq 2x$ "), 2.5 fold (" $\geq 2.5x$ "), or 5 fold (" $\geq 5x$ ") increase in expression levels of the indicated gene relative to matched normal colon tissue; and the ratio data for each patient sample tested (columns headed by "P#," indicating the Patient Identification Number, e.g., "P15" indicates the ratio data for patient 15).

In general, a polynucleotide is said to represent a significantly differentially expressed gene between two samples when there is detectable levels of expression in at

least one sample and the ratio value is greater than at least about 1.2 fold, preferably greater than at least about 1.5 fold, more preferably greater than at least about 2 fold, where the ratio value is calculated using the method described above.

A differential expression ratio of 1 indicates that the expression level of the gene in the tumor cell was not statistically different from expression of that gene in normal colon cells of the same patient. A differential expression ratio significantly greater than 1 in cancerous colon cells relative to normal colon cells indicates that the gene is increased in expression in cancerous cells relative to normal cells, indicating that the gene plays a role in the development of the cancerous phenotype, and may be involved in promoting metastasis of the cell. Detection of gene products from such genes can provide an indicator that the cell is cancerous, and may provide a therapeutic and/or diagnostic target.

Likewise, a differential expression ratio significantly less than 1 in cancerous colon cells relative to normal colon cells indicates that, for example, the gene is involved in suppression of the cancerous phenotype. Increasing activity of the gene product encoded by such a gene, or replacing such activity, can provide the basis for chemotherapy. Such gene can also serve as markers of cancerous cells, *e.g.*, the absence or decreased presence of the gene product in a colon cell relative to a normal colon cell indicates that the cell may be cancerous.

Example 9: Functional Analysis Of Gene Products Differentially Expressed In Cancer In Patients

The gene products of genes differentially expressed in cancerous cells are further analyzed to confirm the role and function of the gene product in tumorigenesis, *e.g.*, in promoting or inhibiting development of a metastatic phenotype.

Blocking expression of gene products using antisense

The effect of single genes upon development of cancer is assessed through use of antisense oligonucleotides specific for sequences corresponding to a selected sequence. Antisense oligonucleotides are prepared based upon a selected sequence that corresponds to a gene of interest. The antisense oligonucleotide is introduced into a test cell and the effect upon expression of the corresponding gene, as well as the effect upon a phenotype of interest assessed (*e.g.*, a normal cell is examined for induction of the cancerous phenotype,

or a cancerous cell is examined for suppression of a cancerous phenotype (*e.g.*, suppression of metastasis)).

Blocking function of gene products using gene product-specific antibodies and/or small molecule inhibitors

5 The function of gene products corresponding to genes/clusters identified herein can be assessed by blocking function of the gene products in the cell. For example, where the gene product is secreted, blocking antibodies can be generated and added to cells to examine the effect upon the cell phenotype in the context of, for example, the transformation of the cell to a cancerous, particularly a metastatic, phenotype. In order to generate antibodies, a
10 clone corresponding to a selected gene product/cluster is selected, and a sequence that represents a partial or complete coding sequence is obtained. The resulting clone is then expressed, the polypeptide produced isolated, and antibodies generated. The antibodies are then combined with cells and the effect upon tumorigenesis assessed.

15 Where the gene product of the gene/clusters identified herein exhibits sequence homology to a protein of known function (*e.g.*, to a specific kinase or protease) and/or to a protein family of known function (*e.g.*, contains a domain or other consensus sequence present in a protease family or in a kinase family), then the role of the gene product in tumorigenesis, as well as the activity of the gene product, can be examined using small molecule that inhibit or enhance function of the corresponding protein or protein family.

20 Those skilled in the art will recognize, or be able to ascertain, using not more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such specific embodiments and equivalents are intended to be encompassed by the following claims.

25 All publications and patent applications cited in this specification are herein incorporated by reference as if each individual publication or patent application were specifically and individually indicated to be incorporated by reference. The citation of any publication is for its disclosure prior to the filing date and should not be construed as an admission that the present invention is not entitled to antedate such publication by virtue of prior invention.

30 Although the foregoing invention has been described in some detail by way of illustration and example for purposes of clarity of understanding, it is readily apparent to those of ordinary skill in the art in light of the teachings of this invention that certain changes and modifications may be made thereto without departing from the spirit or scope of the appended claims.

Deposit Information. The following materials were deposited with the American Type Culture Collection (CMCC = Chiron Master Culture Collection).

Table 6. Cell Lines Deposited with ATCC

Cell Line	Deposit Date	ATCC Accession No.	CMCC Accession No.
KM12L4	March 19, 1998	CRL-12496	11606
Km12C	May 15, 1998	CRL-12533	11611
MDA-MB-231	May 15, 1998	CRL-12532	10583
MCF-7	October 9, 1998	CRL-12584	10377

5

In addition, pools of selected clones, as well as libraries containing specific clones, were assigned an "ES" number (internal reference) and deposited with the ATCC. Table 7 (inserted before the claims) provides the ATCC Accession Nos. and internal references (CMCC Nos.) of the ES deposits, all of which were deposited on or before the filing date of the present application. The names of the clones contained within each of these deposits are provided in Table 8 (inserted before the claims).

The above material has been deposited with the American Type Culture Collection, Rockville, Maryland, under the accession number indicated. These deposits will be maintained under the terms of the Budapest Treaty on the International Recognition of the Deposit of Microorganisms for the Purposes of Patent Procedure. The deposit will be maintained for a period of at least 30 years following issuance of this patent, or for the enforceable life of the patent, whichever is greater. Upon the granting of a patent, all restrictions on the availability to the public of the deposited material will be irrevocably removed.

The deposits described herein are provided merely as convenience to those of skill in the art, and is not an admission that a deposit is required under 35 U.S.C. §112. The sequence of the polynucleotides contained within the deposited material, as well as the amino acid sequence of the polypeptides encoded thereby, are incorporated herein by reference and are controlling in the event of any conflict with the written description of sequences herein. A license may be required to make, use, or sell the deposited material, and no such license is granted hereby.

Retrieval of Individual Clones from Deposit of Pooled Clones. Where the ATCC deposit is composed of a pool of cDNA clones or a library of cDNA clones, the deposit was prepared by first transfecting each of the clones into separate bacterial cells. The clones in the pool or library were then deposited as a pool of equal mixtures in the composite deposit. Particular clones can be obtained from the composite deposit using methods well known in the art. For example, a bacterial cell containing a particular clone can be identified by isolating single colonies, and identifying

colonies containing the specific clone through standard colony hybridization techniques, using an oligonucleotide probe or probes designed to specifically hybridize to a sequence of the clone insert (*e.g.*, a probe based upon unmasked sequence of the encoded polynucleotide having the indicated SEQ ID NO). The probe should be designed to have a T_m of approximately 80°C (assuming 2°C for each A or T and 4°C for each G or C). Positive colonies can then be picked, grown in culture, and the recombinant clone isolated. Alternatively, probes designed in this manner can be used to PCR to isolate a nucleic acid molecule from the pooled clones according to methods well known in the art, *e.g.*, by purifying the cDNA from the deposited culture pool, and using the probes in PCR reactions to produce an amplified product having the corresponding desired polynucleotide sequence.

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Table 1

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3	205329	RTA22200006F.d.09.2.P.Seq	F	M00056020:410	CH15CON
4	446680	RTA22200001F.f.07.1.P.Seq	F	M00042693:54	CH15CON
5	1261	RTA222000021F.j.18.3.P.Seq	F	M00054812:15	CH17COHLV
6	400258	RTA22200011F.k.23.1.P.Seq	F	M00056617:86	CH16COP
7	450559	RTA22200005F.e.21.1.P.Seq	F	M00055882:16	CH15CON
8	450959	RTA22200012F.e.11.1.P.Seq	F	M00056703:46	CH16COP
9	451794	RTA22200007F.l.16.1.P.Seq	F	M00056247:76	CH15CON
10	415058	RTA22200020F.d.11.1.P.Seq	F	M00054591:87	CH17COHLV
11	31506	RTA22200012F.b.08.1.P.Seq	F	M00056670:111	CH16COP
12	417155	RTA22200002F.f.10.1.P.Seq	F	M00055466:28	CH15CON
13	448925	RTA22200019F.e.21.1.P.Seq	F	M00043507:45	CH17COHLV
14	11329	RTA22200006F.d.10.2.P.Seq	F	M00056020:47	CH15CON
15	650422	RTA22200001F.n.14.1.P.Seq	F	M00042911:83	CH15CON
16	6863	RTA22200229F.f.13.1.P.Seq	F	M00006967:25	CH02COH
17	449690	RTA22200002F.g.18.1.P.Seq	F	M00055495:45	CH15CON
18	724616	RTA22200016F.j.23.1.P.Seq	F	M00057236:86	CH16COP
19	549722	RTA22200025F.m.01.2.P.Seq	F	M00055383:24	CH17COHLV
20	549722	RTA22200025F.l.24.1.P.Seq	F	M00055383:24	CH17COHLV
21	448110	RTA22200018F.m.04.1.P.Seq	F	M00043354:31	CH17COHLV
22	515631	RTA22200010F.j.14.1.P.Seq	F	M00056434:38	CH16COP
23	11881	RTA22200233F.k.04.1.P.Seq	F	M00008099:78	CH03MAH
24	650856	RTA22200012F.n.24.1.P.Seq	F	M00056772:14	CH16COP
25	449701	RTA22200012F.f.21.1.P.Seq	F	M00056710:89	CH16COP
26	651073	RTA22200007F.l.06.1.P.Seq	F	M00056243:710	CH15CON
27	10340	RTA22200234F.b.07.1.P.Seq	F	M00022189:23	CH03MAH
28	648310	RTA22200007F.m.04.1.P.Seq	F	M00056252:88	CH15CON
29	730336	RTA22200013F.l.02.1.P.Seq	F	M00056879:811	CH16COP
30	3060	RTA22200018F.b.10.1.P.Seq	F	M00042444:88	CH17COHLV
31	453016	RTA22200010F.l.06.1.P.Seq	F	M00056485:212	CH16COP
32	508931	RTA22200024F.i.13.1.P.Seq	F	M00055209:410	CH17COHLV
33	185461	RTA22200242F.b.06.1.P.Seq	F	M00026975:23	CH04MAL
34	452530	RTA22200015F.n.11.1.P.Seq	F	M00057131:21	CH16COP
35	448925	RTA22200026F.d.02.1.P.Seq	F	M00055419:71	CH17COHLV
36	1013	RTA22200005F.m.06.1.P.Seq	F	M00055945:811	CH15CON
37	6545	RTA22200241F.d.23.1.P.Seq	F	M00026879:410	CH04MAL
38	449891	RTA22200001F.b.23.1.P.Seq	F	M00042540:85	CH15CON
39	4045	RTA22200227F.n.06.1.P.Seq	F	M00006740:71	CH02COH
40	404475	RTA22200002F.b.23.1.P.Seq	F	M00055438:810	CH15CON
41	650297	RTA22200001F.n.10.1.P.Seq	F	M00042909:74	CH15CON
42	650493	RTA22200005F.n.03.1.P.Seq	F	M00055959:112	CH15CON
43	644884	RTA22200007F.k.04.1.P.Seq	F	M00056232:712	CH15CON
44	452212	RTA22200021F.k.21.3.P.Seq	F	M00054821:311	CH17COHLV
45	402727	RTA22200010F.n.09.1.P.Seq	F	M00056505:82	CH16COP
46	645194	RTA22200003F.m.24.1.P.Seq	F	M00055709:79	CH15CON
47	447501	RTA22200013F.f.14.1.P.Seq	F	M00056839:72	CH16COP
48	556326	RTA22200003F.o.06.1.P.Seq	F	M00055723:28	CH15CON
49	447035	RTA22200001F.e.15.1.P.Seq	F	M00042570:82	CH15CON
50	2551	RTA22200012F.o.07.1.P.Seq	F	M00056774:12	CH16COP
51	736154	RTA22200010F.i.17.1.P.Seq	F	M00056424:110	CH16COP
52	452028	RTA22200018F.k.24.1.P.Seq	F	M00043345:33	CH17COHLV
53	447441	RTA22200001F.m.13.1.P.Seq	F	M00042902:34	CH15CON
54	11028	RTA22200230F.g.12.1.P.Seq	F	M00007151:211	CH02COH

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56	555103	RTA22200022F.m.11.1.P.Seq	F	M00054973:110	CH17COHLV
57	446789	RTA22200001F.c.12.1.P.Seq	F	M00042547:62	CH15CON
58	644884	RTA22200007F.k.04.2.P.Seq	F	M00056232:712	CH15CON
59	9029	RTA22200222F.g.08.1.P.Seq	F	M00003792:111	CH01COH
60	419255	RTA22200007F.l.14.2.P.Seq	F	M00056246:77	CH15CON
61	4309	RTA22200225F.j.15.1.P.Seq	F	M00005491:23	CH02COH
62	554069	RTA22200022F.p.16.1.P.Seq	F	M00055008:28	CH17COHLV
63	4330	RTA22200227F.i.16.1.P.Seq	F	M00006686:27	CH02COH
64	644903	RTA22200015F.i.22.1.P.Seq	F	M00057103:511	CH16COP
65	549395	RTA22200024F.d.04.1.P.Seq	F	M00055163:32	CH17COHLV
66	4974	RTA22200225F.k.17.1.P.Seq	F	M00005500:53	CH02COH
67	447466	RTA22200006F.h.03.2.P.Seq	F	M00056053:19	CH15CON
68	645073	RTA22200004F.o.13.1.P.Seq	F	M00055829:79	CH15CON
69	447978	RTA22200025F.i.14.1.P.Seq	F	M00055361:81	CH17COHLV
70	607430	RTA22200004F.p.22.1.P.Seq	F	M00055841:45	CH15CON
71	556198	RTA22200014F.h.02.2.P.Seq	F	M00056972:65	CH16COP
72	450323	RTA22200018F.l.23.1.P.Seq	F	M00043352:59	CH17COHLV
73	21205	RTA22200249F.g.01.1.P.Seq	F	M00027660:53	CH04MAL
74	561109	RTA22200011F.m.10.1.P.Seq	F	M00056631:43	CH16COP
75	446673	RTA22200001F.a.14.1.P.Seq	F	M00042525:51	CH15CON
76	456026	RTA22200004F.m.04.1.P.Seq	F	M00055817:38	CH15CON
77	449142	RTA22200009F.c.13.2.P.Seq	F	M00042513:112	CH16COP
78	5830	RTA22200010F.c.23.1.P.Seq	F	M00056370:72	CH16COP
79	554109	RTA22200026F.g.07.1.P.Seq	F	M00055484:77	CH17COHLV
80	595506	RTA22200010F.l.16.1.P.Seq	F	M00056491:78	CH16COP
81	453981	RTA22200010F.p.11.1.P.Seq	F	M00056519:81	CH16COP
82	642461	RTA22200016F.j.11.1.P.Seq	F	M00057233:54	CH16COP
83	556198	RTA22200014F.h.02.1.P.Seq	F	M00056972:65	CH16COP
84	2082	RTA22200009F.g.21.1.P.Seq	F	M00042801:26	CH16COP
85	549435	RTA22200007F.j.06.1.P.Seq	F	M00056223:73	CH15CON
86	2286	RTA22200230F.j.03.1.P.Seq	F	M00007177:511	CH02COH
87	2737	RTA22200023F.d.17.1.P.Seq	F	M00055039:52	CH17COHLV
88	728115	RTA22200013F.f.13.1.P.Seq	F	M00056839:71	CH16COP
89	650856	RTA22200012F.o.01.1.P.Seq	F	M00056772:14	CH16COP
90	650476	RTA22200005F.g.21.1.P.Seq	F	M00055891:14	CH15CON
91	535208	RTA22200005F.b.02.1.P.Seq	F	M00055852:17	CH15CON
92	733849	RTA22200011F.m.24.1.P.Seq	F	M00056638:48	CH16COP
93	447978	RTA22200009F.g.19.1.P.Seq	F	M00042800:13	CH16COP
94	729483	RTA22200012F.i.12.1.P.Seq	F	M00056728:45	CH16COP
95	12018	RTA22200249F.e.19.1.P.Seq	F	M00027641:11	CH04MAL
96	4747	RTA22200227F.d.18.1.P.Seq	F	M00006630:311	CH02COH
97	4747	RTA22200225F.a.23.1.P.Seq	F	M00005415:612	CH02COH
98	185577	RTA22200240F.i.02.1.P.Seq	F	M00023409:78	CH04MAL
99	4126	RTA22200231F.m.17.1.P.Seq	F	M00007990:43	CH03MAH
100	11456	RTA22200226F.l.08.1.P.Seq	F	M00005765:67	CH02COH
101	729851	RTA22200010F.o.03.1.P.Seq	F	M00056508:210	CH16COP
102	449849	RTA22200019F.b.07.1.P.Seq	F	M00043394:26	CH17COHLV
103	2490	RTA22200237F.e.17.1.P.Seq	F	M00022720:111	CH03MAH
104	549041	RTA22200021F.h.21.3.P.Seq	F	M00054779:67	CH17COHLV
105	11881	RTA22200237F.i.01.1.P.Seq	F	M00022750:17	CH03MAH
106	724296	RTA22200014F.o.10.1.P.Seq	F	M00057025:18	CH16COP
107	726173	RTA22200014F.o.01.1.P.Seq	F	M00057023:89	CH16COP
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111	11881	RTA22200237F.h.24.1.P.Seq	F	M00022750:17	CH03MAH
112	7436	RTA22200237F.j.11.1.P.Seq	F	M00022791:611	CH03MAH
113	2110	RTA22200235F.a.19.1.P.Seq	F	M00022415:26	CH03MAH
114	10340	RTA22200235F.e.13.1.P.Seq	F	M00022457:75	CH03MAH
115	643594	RTA22200005F.a.24.1.P.Seq	F	M00055851:612	CH15CON
116	447035	RTA22200005F.d.11.1.P.Seq	F	M00055872:412	CH15CON
117	402707	RTA22200007F.c.21.1.P.Seq	F	M00056160:18	CH15CON
118	645799	RTA22200014F.d.22.1.P.Seq	F	M00056952:84	CH16COP
119	171511	RTA22200014F.c.05.1.P.Seq	F	M00056939:22	CH16COP
120	451607	RTA22200014F.h.15.2.P.Seq	F	M00056976:610	CH16COP
121	3138	RTA22200242F.k.08.1.P.Seq	F	M00027039:59	CH04MAL
122	2988	RTA22200229F.h.11.1.P.Seq	F	M00006987:711	CH02COH
123	447326	RTA22200014F.g.22.1.P.Seq	F	M00056969:21	CH16COP
124	561734	RTA22200014F.f.10.1.P.Seq	F	M00056961:712	CH16COP
125	454999	RTA22200009F.a.13.2.P.Seq	F	M00042432:810	CH16COP
126	185652	RTA22200242F.i.12.1.P.Seq	F	M00027028:37	CH04MAL
127	6725	RTA22200232F.d.17.1.P.Seq	F	M00021947:36	CH03MAH
128	726644	RTA22200013F.i.19.1.P.Seq	F	M00056864:89	CH16COP
129	11012	RTA22200227F.n.21.1.P.Seq	F	M00006745:12	CH02COH
130	726377	RTA22200013F.i.03.1.P.Seq	F	M00056860:612	CH16COP
131	735326	RTA22200013F.l.19.1.P.Seq	F	M00056886:311	CH16COP
132	650845	RTA22200013F.l.13.1.P.Seq	F	M00056884:36	CH16COP
133	9048	RTA22200222F.l.18.1.P.Seq	F	M00004101:81	CH01COH
134	732254	RTA22200012F.b.15.1.P.Seq	F	M00056674:84	CH16COP
135	452052	RTA22200013F.i.16.1.P.Seq	F	M00056863:53	CH16COP
136	554079	RTA22200012F.j.17.1.P.Seq	F	M00056735:28	CH16COP
137	9049	RTA22200222F.i.05.1.P.Seq	F	M00003948:212	CH01COH
138	1307	RTA22200244F.n.16.1.P.Seq	F	M00027222:39	CH04MAL
139	139730	RTA22200242F.g.11.1.P.Seq	F	M00027016:76	CH04MAL
140	7750	RTA22200241F.f.24.1.P.Seq	F	M00026899:711	CH04MAL
141	8050	RTA22200227F.p.20.1.P.Seq	F	M00006761:49	CH02COH
142	725222	RTA22200013F.k.24.1.P.Seq	F	M00056879:55	CH16COP
143	3275	RTA22200235F.j.22.2.P.Seq	F	M00022516:59	CH03MAH
144	7424	RTA22200235F.c.12.1.P.Seq	F	M00022430:44	CH03MAH
145	8953	RTA22200241F.c.05.1.P.Seq	F	M00026866:88	CH04MAL
146	8966	RTA22200243F.c.04.1.P.Seq	F	M00027088:86	CH04MAL
147	530883	RTA22200013F.i.22.1.P.Seq	F	M00056866:55	CH16COP
148	6725	RTA22200238F.l.09.1.P.Seq	F	M00022973:78	CH03MAH
149	4439	RTA22200222F.m.24.1.P.Seq	F	M00004167:411	CH01COH
150	648472	RTA22200012F.g.07.1.P.Seq	F	M00056712:17	CH16COP
151	735346	RTA22200011F.i.03.1.P.Seq	F	M00056618:22	CH16COP
152	732121	RTA22200011F.j.05.1.P.Seq	F	M00056600:87	CH16COP
153	650337	RTA22200005F.h.15.1.P.Seq	F	M00055900:25	CH15CON
154	533588	RTA22200005F.p.05.1.P.Seq	F	M00055981:17	CH15CON
155	649667	RTA22200007F.p.20.1.P.Seq	F	M00056290:82	CH15CON
156	394436	RTA22200015F.p.07.1.P.Seq	F	M00057145:45	CH16COP
157	649354	RTA22200007F.h.13.1.P.Seq	F	M00056210:53	CH15CON
158	2022	RTA22200240F.e.10.1.P.Seq	F	M00023347:312	CH04MAL
159	561359	RTA22200003F.m.08.1.P.Seq	F	M00055703:26	CH15CON
160	7607	RTA22200225F.m.20.1.P.Seq	F	M00005520:512	CH02COH
161	7750	RTA22200242F.f.06.1.P.Seq	F	M00027006:81	CH04MAL
162	410554	RTA22200012F.i.21.1.P.Seq	F	M00056729:812	CH16COP

Table 1

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165	4420	RTA22200229F.f.02.1.P.Seq	F	M00006964:111	CH02COH
166	559663	RTA22200012F.d.17.1.P.Seq	F	M00056697:53	CH16COP
167	7082	RTA22200235F.p.01.2.P.Seq	F	M00022565:15	CH03MAH
168	2315	RTA22200230F.f.01.1.P.Seq	F	M00007135:211	CH02COH
169	650472	RTA22200012F.j.21.1.P.Seq	F	M00056737:77	CH16COP
170	6482	RTA22200230F.a.10.1.P.Seq	F	M00007096:51	CH02COH
171	4584	RTA22200230F.a.09.1.P.Seq	F	M00007096:52	CH02COH
172	453846	RTA22200012F.b.14.1.P.Seq	F	M00056674:55	CH16COP
173	650820	RTA22200011F.p.05.1.P.Seq	F	M00056656:83	CH16COP
174	642906	RTA22200005F.g.06.1.P.Seq	F	M00055887:36	CH15CON
175	448805	RTA22200005F.i.23.1.P.Seq	F	M00055912:35	CH15CON
176	649667	RTA22200006F.k.18.2.P.Seq	F	M00056082:66	CH15CON
177	735786	RTA22200012F.m.12.1.P.Seq	F	M00056758:35	CH16COP
178	121457	RTA22200012F.p.18.1.P.Seq	F	M00056785:68	CH16COP
179	372960	RTA22200012F.m.06.1.P.Seq	F	M00056756:28	CH16COP
180	120049	RTA22200012F.j.10.1.P.Seq	F	M00056733:49	CH16COP
181	648996	RTA22200006F.p.20.2.P.Seq	F	M00056136:211	CH15CON
182	3765	RTA22200226F.a.16.1.P.Seq	F	M00005589:67	CH02COH
183	462642	RTA22200008F.e.08.1.P.Seq	F	M00056342:75	CH15CON
184	727181	RTA22200016F.f.18.1.P.Seq	F	M00057208:12	CH16COP
185	649259	RTA22200006F.k.06.2.P.Seq	F	M00056079:412	CH15CON
186	649717	RTA22200007F.e.08.1.P.Seq	F	M00056180:89	CH15CON
187	736860	RTA22200009F.p.24.1.P.Seq	F	M00056351:46	CH16COP
188	729175	RTA22200012F.o.05.1.P.Seq	F	M00056773:811	CH16COP
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190	4420	RTA22200232F.l.13.1.P.Seq	F	M00022123:45	CH03MAH
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192	648109	RTA22200015F.o.03.1.P.Seq	F	M00057135:84	CH16COP
193	2334	RTA22200011F.p.20.1.P.Seq	F	M00056661:19	CH16COP
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195	551907	RTA22200003F.n.12.1.P.Seq	F	M00055717:64	CH15CON
196	561382	RTA22200003F.m.20.1.P.Seq	F	M00055706:71	CH15CON
197	595506	RTA22200022F.a.01.1.P.Seq	F	M00054866:77	CH17COHLV
198	499424	RTA22200013F.f.16.1.P.Seq	F	M00056839:61	CH16COP
199	735477	RTA22200016F.f.08.1.P.Seq	F	M00057203:56	CH16COP
200	734370	RTA22200013F.g.21.1.P.Seq	F	M00056848:37	CH16COP
201	779	RTA22200230F.c.07.1.P.Seq	F	M00007112:112	CH02COH
202	649143	RTA22200007F.o.24.1.P.Seq	F	M00056283:52	CH15CON
203	489	RTA22200012F.m.16.1.P.Seq	F	M00056759:611	CH16COP
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205	2994	RTA22200229F.l.01.1.P.Seq	F	M00007028:34	CH02COH
206	11147	RTA22200227F.g.12.1.P.Seq	F	M00006664:29	CH02COH
207	549395	RTA22200021F.d.19.2.P.Seq	F	M00054745:13	CH17COHLV
208	559806	RTA22200022F.h.11.1.P.Seq	F	M00054937:63	CH17COHLV
209	452238	RTA22200009F.k.17.2.P.Seq	F	M00042838:511	CH16COP
210	225914	RTA22200023F.j.18.1.P.Seq	F	M00055075:85	CH17COHLV
211	463480	RTA22200022F.p.18.1.P.Seq	F	M00055008:29	CH17COHLV
212	184725	RTA22200007F.o.17.1.P.Seq	F	M00056281:54	CH15CON
213	557401	RTA22200023F.g.22.1.P.Seq	F	M00055056:26	CH17COHLV
214	455155	RTA22200003F.f.04.1.P.Seq	F	M00055633:711	CH15CON
215	551117	RTA22200023F.p.03.1.P.Seq	F	M00055131:210	CH17COHLV
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220	380412	RTA22200006F.c.23.2.P.Seq	F	M00056016:46	CH15CON
221	446614	RTA22200001F.e.01.1.P.Seq	F	M00042563:52	CH15CON
222	555911	RTA22200023F.f.21.1.P.Seq	F	M00055050:74	CH17COHLV
223	450828	RTA22200022F.g.23.1.P.Seq	F	M00054935:74	CH17COHLV
224	28	RTA22200006F.a.17.2.P.Seq	F	M00055999:710	CH15CON
225	446450	RTA22200001F.h.15.1.P.Seq	F	M00042717:44	CH15CON
226	452026	RTA22200010F.g.18.1.P.Seq	F	M00056411:54	CH16COP
227	643594	RTA22200006F.a.18.2.P.Seq	F	M00055999:76	CH15CON
228	1905	RTA22200012F.o.14.1.P.Seq	F	M00056775:38	CH16COP
229	651073	RTA22200007F.l.06.2.P.Seq	F	M00056243:710	CH15CON
230	553705	RTA22200006F.a.23.2.P.Seq	F	M00056001:27	CH15CON
231	521840	RTA22200004F.j.15.1.P.Seq	F	M00055802:84	CH15CON
232	648689	RTA22200006F.o.07.2.P.Seq	F	M00056111:82	CH15CON
233	447858	RTA22200022F.d.10.1.P.Seq	F	M00054895:49	CH17COHLV
234	556198	RTA22200010F.d.10.1.P.Seq	F	M00056374:82	CH16COP
235	394436	RTA22200003F.i.09.1.P.Seq	F	M00055662:14	CH15CON
236	639651	RTA22200003F.g.12.1.P.Seq	F	M00055647:24	CH15CON
237	499424	RTA22200010F.d.18.1.P.Seq	F	M00056382:82	CH16COP
238	468109	RTA22200001F.p.12.1.P.Seq	F	M00054915:57	CH15CON
239	185701	RTA22200248F.g.23.1.P.Seq	F	M00027561:34	CH04MAL
240	451811	RTA22200006F.h.04.2.P.Seq	F	M00056053:412	CH15CON
241	730670	RTA22200009F.m.14.1.P.Seq	F	M00042850:34	CH16COP
242	172013	RTA22200021F.l.15.3.P.Seq	F	M00054826:310	CH17COHLV
243	449142	RTA22200001F.f.10.1.P.Seq	F	M00042694:52	CH15CON
244	446964	RTA22200001F.h.23.1.P.Seq	F	M00042721:77	CH15CON
245	414739	RTA22200022F.i.16.1.P.Seq	F	M00054945:77	CH17COHLV
246	641124	RTA22200004F.k.12.1.P.Seq	F	M00055805:37	CH15CON
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249	643954	RTA22200002F.d.19.1.P.Seq	F	M00055451:711	CH15CON
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251	560526	RTA22200022F.f.10.1.P.Seq	F	M00054910:76	CH17COHLV
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253	7607	RTA22200004F.b.13.1.P.Seq	F	M00055744:69	CH15CON
254	559409	RTA22200019F.o.07.1.P.Seq	F	M00054551:73	CH17COHLV
255	650053	RTA22200002F.p.11.1.P.Seq	F	M00055560:62	CH15CON
256	448511	RTA22200009F.f.03.1.P.Seq	F	M00042777:46	CH16COP
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261	284586	RTA22200002F.d.17.1.P.Seq	F	M00055451:67	CH15CON
262	556198	RTA22200022F.l.06.1.P.Seq	F	M00054963:84	CH17COHLV
263	431601	RTA22200004F.j.04.1.P.Seq	F	M00055800:48	CH15CON
264	449891	RTA22200002F.n.21.1.P.Seq	F	M00055548:64	CH15CON
265	556561	RTA22200022F.p.01.1.P.Seq	F	M00054997:212	CH17COHLV
266	554188	RTA22200022F.o.20.1.P.Seq	F	M00054996:39	CH17COHLV
267	3247	RTA22200006F.a.22.2.P.Seq	F	M00056001:26	CH15CON
268	546705	RTA22200022F.k.20.1.P.Seq	F	M00054959:311	CH17COHLV
269	560984	RTA22200022F.p.02.1.P.Seq	F	M00054997:83	CH17COHLV
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Table 1

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274	454806	RTA22200004F.n.04.1.P.Seq	F	M00055822:84	CH15CON
275	724296	RTA22200014F.o.10.2.P.Seq	F	M00057025:18	CH16COP
276	559280	RTA22200015F.j.19.1.P.Seq	F	M00057106:26	CH16COP
277	171511	RTA22200014F.c.05.2.P.Seq	F	M00056939:22	CH16COP
278	644242	RTA22200002F.o.14.1.P.Seq	F	M00055553:84	CH15CON
279	734370	RTA22200016F.j.07.1.P.Seq	F	M00057232:46	CH16COP
280	639459	RTA22200002F.i.18.1.P.Seq	F	M00055512:76	CH15CON
281	641679	RTA22200003F.d.20.1.P.Seq	F	M00055613:52	CH15CON
282	644611	RTA22200002F.i.10.1.P.Seq	F	M00055509:89	CH15CON
283	550038	RTA22200021F.i.16.3.P.Seq	F	M00054802:72	CH17COHLV
284	452567	RTA22200002F.j.12.1.P.Seq	F	M00055519:36	CH15CON
285	411113	RTA22200024F.f.03.1.P.Seq	F	M00055185:21	CH17COHLV
286	650749	RTA22200002F.d.18.1.P.Seq	F	M00055451:611	CH15CON
287	558899	RTA22200026F.d.12.1.P.Seq	F	M00055421:44	CH17COHLV
288	452986	RTA22200002F.a.13.1.P.Seq	F	M00055426:22	CH15CON
289	393197	RTA22200015F.k.01.1.P.Seq	F	M00057108:59	CH16COP
290	499424	RTA22200024F.e.10.1.P.Seq	F	M00055179:42	CH17COHLV
291	21669	RTA22200025F.m.07.2.P.Seq	F	M00055384:13	CH17COHLV
292	640590	RTA22200004F.h.21.1.P.Seq	F	M00055794:711	CH15CON
293	549936	RTA22200024F.c.10.1.P.Seq	F	M00055157:311	CH17COHLV
294	448770	RTA22200016F.c.17.1.P.Seq	F	M00057174:712	CH16COP
295	559280	RTA22200015F.h.14.1.P.Seq	F	M00057093:69	CH16COP
296	648934	RTA22200003F.c.10.1.P.Seq	F	M00055591:81	CH15CON
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301	446673	RTA22200015F.c.01.1.P.Seq	F	M00057055:78	CH16COP
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304	463824	RTA22200004F.n.10.1.P.Seq	F	M00055823:43	CH15CON
305	393197	RTA22200015F.j.24.1.P.Seq	F	M00057108:59	CH16COP
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307	499424	RTA22200018F.h.13.1.P.Seq	F	M00043317:81	CH17COHLV
308	554500	RTA22200021F.o.20.2.P.Seq	F	M00054857:512	CH17COHLV
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310	595506	RTA22200015F.c.21.1.P.Seq	F	M00057061:44	CH16COP
311	2334	RTA22200016F.k.13.1.P.Seq	F	M00057242:85	CH16COP
312	647444	RTA22200002F.k.22.1.P.Seq	F	M00055527:711	CH15CON
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314	644849	RTA22200016F.a.22.1.P.Seq	F	M00057162:37	CH16COP
315	449457	RTA22200018F.g.23.1.P.Seq	F	M00043314:84	CH17COHLV
316	446673	RTA22200015F.b.24.1.P.Seq	F	M00057055:78	CH16COP
317	549069	RTA22200020F.e.05.1.P.Seq	F	M00054596:27	CH17COHLV
318	728884	RTA22200015F.d.02.1.P.Seq	F	M00057063:38	CH16COP
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323	449831	RTA22200018F.d.22.1.P.Seq	F	M00042518:16	CH17COHLV
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Table 1

Table 1

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327	5830	RTA22200011F.d.11.1.P.Seq	F	M00056552:110	CH16COP
328	8953	RTA22200248F.p.09.1.P.Seq	F	M00027608:87	CH04MAL
329	8012	RTA22200233F.i.02.1.P.Seq	F	M00008089:59	CH03MAH
330	185718	RTA22200250F.f.15.1.P.Seq	F	M00027829:42	CH04MAL
331	729851	RTA22200011F.b.18.1.P.Seq	F	M00056537:85	CH16COP
332	185597	RTA22200249F.a.20.1.P.Seq	F	M00027616:712	CH04MAL
333	9887	RTA22200234F.h.14.1.P.Seq	F	M00022253:53	CH03MAH
334	725825	RTA22200011F.c.16.1.P.Seq	F	M00056547:34	CH16COP
335	6545	RTA22200249F.e.12.1.P.Seq	F	M00027639:511	CH04MAL
336	21205	RTA22200249F.f.24.1.P.Seq	F	M00027660:53	CH04MAL
337	8867	RTA22200234F.j.23.1.P.Seq	F	M00022280:711	CH03MAH
338	729295	RTA22200010F.m.09.1.P.Seq	F	M00056499:65	CH16COP
339	730430	RTA22200010F.h.08.1.P.Seq	F	M00056416:212	CH16COP
340	7072	RTA22200233F.h.20.1.P.Seq	F	M00008085:39	CH03MAH
341	730533	RTA22200010F.n.17.1.P.Seq	F	M00056506:712	CH16COP
342	9121	RTA22200224F.g.11.1.P.Seq	F	M00005312:410	CH02COH
343	11131	RTA22200224F.c.08.1.P.Seq	F	M00004852:14	CH02COH
344	640116	RTA22200010F.n.01.1.P.Seq	F	M00056503:711	CH16COP
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346	550571	RTA22200019F.h.11.1.P.Seq	F	M00054502:52	CH17COHLV
347	1183	RTA22200248F.c.22.1.P.Seq	F	M00027527:74	CH04MAL
348	449437	RTA22200019F.g.09.1.P.Seq	F	M00054494:51	CH17COHLV
349	8966	RTA22200242F.d.21.1.P.Seq	F	M00026994:17	CH04MAL
350	6134	RTA22200006F.p.04.2.P.Seq	F	M00056125:49	CH15CON
351	95700	RTA22200241F.f.09.1.P.Seq	F	M00026896:510	CH04MAL
352	7066	RTA22200229F.a.23.1.P.Seq	F	M00006928:14	CH02COH
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355	736014	RTA22200012F.f.11.1.P.Seq	F	M00056708:411	CH16COP
356	646577	RTA22200012F.d.07.1.P.Seq	F	M00056693:38	CH16COP
357	732254	RTA22200014F.g.09.1.P.Seq	F	M00056967:57	CH16COP
358	7037	RTA22200229F.b.01.1.P.Seq	F	M00006928:41	CH02COH
359	7037	RTA22200229F.a.24.1.P.Seq	F	M00006928:41	CH02COH
360	6937	RTA22200232F.b.06.1.P.Seq	F	M00021864:57	CH03MAH
361	7572	RTA22200228F.k.06.2.P.Seq	F	M00006867:612	CH02COH
362	388085	RTA22200005F.c.21.1.P.Seq	F	M00055868:43	CH15CON
363	2676	RTA22200227F.p.19.1.P.Seq	F	M00006761:35	CH02COH
364	639240	RTA22200007F.k.18.1.P.Seq	F	M00056238:57	CH15CON
365	650472	RTA22200012F.e.19.1.P.Seq	F	M00056705:57	CH16COP
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367	2495	RTA22200238F.e.03.1.P.Seq	F	M00022895:211	CH03MAH
368	732254	RTA22200014F.g.09.2.P.Seq	F	M00056967:57	CH16COP
369	5268	RTA22200225F.m.13.1.P.Seq	F	M00005517:64	CH02COH
370	11881	RTA22200238F.e.09.1.P.Seq	F	M00022897:83	CH03MAH
371	448677	RTA22200009F.b.05.2.P.Seq	F	M00042440:55	CH16COP
372	1876	RTA22200235F.i.14.2.P.Seq	F	M00022496:64	CH03MAH
373	3441	RTA22200233F.e.23.1.P.Seq	F	M00008065:62	CH03MAH
374	726134	RTA22200011F.l.05.1.P.Seq	F	M00056618:611	CH16COP
375	9048	RTA22200222F.g.12.1.P.Seq	F	M00003804:19	CH01COH
376	26489	RTA22200242F.k.07.1.P.Seq	F	M00027039:66	CH04MAL
377	644205	RTA22200007F.c.24.1.P.Seq	F	M00056162:68	CH15CON
378	468689	RTA22200006F.f.04.2.P.Seq	F	M00056036:26	CH15CON

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381	6725	RTA22200232F.f.22.1.P.Seq	F	M00022013:85	CH03MAH
382	2488	RTA22200012F.l.21.1.P.Seq	F	M00056754:49	CH16COP
383	8366	RTA22200244F.c.08.1.P.Seq	F	M00027173:48	CH04MAL
384	502683	RTA22200007F.a.09.1.P.Seq	F	M00056139:71	CH15CON
385	450914	RTA22200012F.k.22.1.P.Seq	F	M00056747:45	CH16COP
386	21205	RTA22200243F.k.21.1.P.Seq	F	M00027140:311	CH04MAL
387	644205	RTA22200007F.d.01.1.P.Seq	F	M00056162:68	CH15CON
388	5268	RTA22200225F.m.05.1.P.Seq	F	M00005513:69	CH02COH
389	8012	RTA22200232F.n.17.1.P.Seq	F	M00022148:16	CH03MAH
390	11270	RTA22200227F.m.18.1.P.Seq	F	M00006734:18	CH02COH
391	10924	RTA22200237F.h.04.1.P.Seq	F	M00022738:46	CH03MAH
392	11619	RTA22200241F.g.14.1.P.Seq	F	M00026902:74	CH04MAL
393	3650	RTA22200236F.e.11.1.P.Seq	F	M00022617:32	CH03MAH
394	1655	RTA22200222F.e.14.1.P.Seq	F	M00001637:49	CH01COH
395	3275	RTA22200238F.b.21.1.P.Seq	F	M00022876:25	CH03MAH
396	3355	RTA22200238F.c.05.1.P.Seq	F	M00022880:79	CH03MAH
397	2078	RTA22200235F.g.18.1.P.Seq	F	M00022473:26	CH03MAH
398	4809	RTA22200222F.g.09.1.P.Seq	F	M00003794:47	CH01COH
399	6402	RTA22200236F.l.15.1.P.Seq	F	M00022660:24	CH03MAH
400	555244	RTA22200023F.e.03.1.P.Seq	F	M00055042:21	CH17COHLV
401	548965	RTA22200012F.g.16.1.P.Seq	F	M00056715:410	CH16COP
402	4747	RTA22200227F.m.12.1.P.Seq	F	M00006731:38	CH02COH
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404	14596	RTA22200241F.d.18.1.P.Seq	F	M00026879:22	CH04MAL
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406	7110	RTA22200232F.m.24.1.P.Seq	F	M00022143:41	CH03MAH
407	6592	RTA22200238F.p.20.1.P.Seq	F	M00023029:56	CH03MAH
408	6455	RTA22200232F.o.06.1.P.Seq	F	M00022151:75	CH03MAH
409	2738	RTA22200232F.g.16.1.P.Seq	F	M00022050:44	CH03MAH
410	696	RTA22200232F.m.02.1.P.Seq	F	M00022132:64	CH03MAH
411	379186	RTA22200012F.c.05.1.P.Seq	F	M00056682:610	CH16COP
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413	7007	RTA22200225F.e.05.1.P.Seq	F	M00005454:33	CH02COH
414	9025	RTA22200222F.k.23.1.P.Seq	F	M00004080:15	CH01COH
415	650749	RTA22200007F.i.16.2.P.Seq	F	M00056220:49	CH15CON
416	553158	RTA22200005F.e.13.1.P.Seq	F	M00055879:511	CH15CON
417	641703	RTA22200003F.e.18.1.P.Seq	F	M00055628:18	CH15CON
418	833	RTA22200006F.j.24.2.P.Seq	F	M00056077:512	CH15CON
419	649259	RTA22200006F.o.01.2.P.Seq	F	M00056108:212	CH15CON
420	451179	RTA22200011F.i.14.1.P.Seq	F	M00056596:88	CH16COP
421	9505	RTA22200231F.b.20.1.P.Seq	F	M00007935:15	CH03MAH
422	736728	RTA22200015F.n.19.1.P.Seq	F	M00057134:31	CH16COP
423	380412	RTA22200001F.p.23.1.P.Seq	F	M00054918:43	CH15CON
424	642425	RTA22200011F.k.12.1.P.Seq	F	M00056613:15	CH16COP
425	405073	RTA22200007F.o.05.1.P.Seq	F	M00056273:11	CH15CON
426	174250	RTA22200008F.h.09.1.P.Seq	F	M00056475:61	CH15CON
427	726281	RTA22200017F.d.08.1.P.Seq	F	M00057324:412	CH16COP
428	639029	RTA22200007F.k.05.2.P.Seq	F	M00056233:63	CH15CON
429	452245	RTA22200022F.l.05.1.P.Seq	F	M00054963:811	CH17COHLV
430	510254	RTA22200005F.p.22.1.P.Seq	F	M00055992:511	CH15CON
431	642425	RTA22200007F.g.19.1.P.Seq	F	M00056204:14	CH15CON
432	51939	RTA22200005F.i.22.1.P.Seq	F	M00055912:510	CH15CON

Table 1

Table 1

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435	734827	RTA22200011F.m.09.1.P.Seq	F	M00056631:38	CH16COP
436	2554	RTA22200231F.g.06.1.P.Seq	F	M00007961:65	CH03MAH
437	643285	RTA22200012F.a.16.1.P.Seq	F	M00056665:111	CH16COP
438	448770	RTA22200001F.o.07.1.P.Seq	F	M00054793:27	CH15CON
439	375380	RTA22200023F.e.20.1.P.Seq	F	M00055046:37	CH17COHLV
440	726134	RTA22200011F.l.10.1.P.Seq	F	M00056620:512	CH16COP
441	422687	RTA22200015F.p.03.1.P.Seq	F	M00057143:55	CH16COP
442	448436	RTA22200012F.n.02.1.P.Seq	F	M00056763:45	CH16COP
443	644893	RTA22200012F.l.24.1.P.Seq	F	M00056754:15	CH16COP
444	559104	RTA22200012F.n.21.1.P.Seq	F	M00056771:312	CH16COP
445	551172	RTA22200016F.g.09.1.P.Seq	F	M00057211:16	CH16COP
446	724296	RTA22200012F.f.22.1.P.Seq	F	M00056710:67	CH16COP
447	735936	RTA22200009F.p.13.1.P.Seq	F	M00056346:312	CH16COP
448	556326	RTA22200023F.k.20.1.P.Seq	F	M00055085:110	CH17COHLV
449	729699	RTA22200011F.o.04.1.P.Seq	F	M00056646:32	CH16COP
450	550694	RTA22200022F.a.05.1.P.Seq	F	M00054867:27	CH17COHLV
451	734738	RTA22200017F.e.11.1.P.Seq	F	M00057337:72	CH16COP
452	404502	RTA22200007F.p.08.1.P.Seq	F	M00056286:58	CH15CON
453	554151	RTA22200015F.o.18.1.P.Seq	F	M00057142:17	CH16COP
454	649852	RTA22200001F.n.24.1.P.Seq	F	M00042914:210	CH15CON
455	734063	RTA22200011F.m.16.1.P.Seq	F	M00056633:27	CH16COP
456	7279	RTA22200230F.b.22.1.P.Seq	F	M00007108:41	CH02COH
457	2676	RTA22200230F.l.05.1.P.Seq	F	M00007204:41	CH02COH
458	649148	RTA22200006F.k.08.2.P.Seq	F	M00056079:311	CH15CON
459	1953	RTA22200226F.p.21.1.P.Seq	F	M00006576:24	CH02COH
460	650108	RTA22200006F.d.04.2.P.Seq	F	M00056018:75	CH15CON
461	515350	RTA22200005F.g.04.1.P.Seq	F	M00055886:79	CH15CON
462	402494	RTA22200013F.a.15.1.P.Seq	F	M00056796:85	CH16COP
463	649148	RTA22200013F.d.09.1.P.Seq	F	M00056821:39	CH16COP
464	833	RTA22200006F.k.01.2.P.Seq	F	M00056077:512	CH15CON
465	139730	RTA22200242F.g.02.1.P.Seq	F	M00027014:74	CH04MAL
466	453079	RTA22200009F.k.11.2.P.Seq	F	M00042835:42	CH16COP
467	546705	RTA22200003F.p.11.1.P.Seq	F	M00055729:16	CH15CON
468	644903	RTA22200003F.f.09.1.P.Seq	F	M00055635:74	CH15CON
469	732254	RTA22200013F.g.01.1.P.Seq	F	M00056842:612	CH16COP
470	561180	RTA22200003F.e.19.1.P.Seq	F	M00055630:59	CH15CON
471	732254	RTA22200013F.f.24.1.P.Seq	F	M00056842:612	CH16COP
472	449204	RTA22200009F.k.07.2.P.Seq	F	M00042834:26	CH16COP
473	185651	RTA22200242F.f.20.1.P.Seq	F	M00027013:510	CH04MAL
474	639029	RTA22200013F.l.04.1.P.Seq	F	M00056880:24	CH16COP
475	452986	RTA22200007F.f.11.1.P.Seq	F	M00056192:54	CH15CON
476	729779	RTA22200011F.i.05.1.P.Seq	F	M00056594:36	CH16COP
477	646248	RTA22200005F.o.19.1.P.Seq	F	M00055979:29	CH15CON
478	650448	RTA22200012F.a.11.1.P.Seq	F	M00056664:27	CH16COP
479	642049	RTA22200003F.o.23.1.P.Seq	F	M00055726:28	CH15CON
480	728273	RTA22200012F.f.20.1.P.Seq	F	M00056710:65	CH16COP
481	446139	RTA22200007F.l.09.2.P.Seq	F	M00056244:37	CH15CON
482	2783	RTA22200008F.f.20.1.P.Seq	F	M00056456:62	CH15CON
483	642906	RTA22200012F.n.20.1.P.Seq	F	M00056771:612	CH16COP
484	8332	RTA22200236F.j.08.1.P.Seq	F	M00022651:24	CH03MAH
485	453470	RTA22200007F.j.08.2.P.Seq	F	M00056224:58	CH15CON
486	552277	RTA22200020F.p.05.1.P.Seq	F	M00054706:39	CH17COHLV

Table 1

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489	649722	RTA22200006F.m.10.2.P.Seq	F	M00056094:87	CH15CON
490	612572	RTA22200007F.l.08.2.P.Seq	F	M00056244:28	CH15CON
491	385980	RTA22200012F.p.15.1.P.Seq	F	M00056784:25	CH16COP
492	141185	RTA22200007F.i.02.2.P.Seq	F	M00056215:53	CH15CON
493	463824	RTA22200006F.p.16.2.P.Seq	F	M00056133:49	CH15CON
494	446139	RTA22200007F.g.14.1.P.Seq	F	M00056201:88	CH15CON
495	725994	RTA22200011F.h.16.1.P.Seq	F	M00056591:53	CH16COP
496	736679	RTA22200011F.o.02.1.P.Seq	F	M00056645:66	CH16COP
497	551718	RTA22200013F.a.18.1.P.Seq	F	M00056799:511	CH16COP
498	640525	RTA22200003F.m.23.1.P.Seq	F	M00055707:38	CH15CON
499	645210	RTA22200007F.m.03.1.P.Seq	F	M00056251:16	CH15CON
500	6567	RTA22200235F.p.09.2.P.Seq	F	M00022569:17	CH03MAH
501	646146	RTA22200005F.p.10.1.P.Seq	F	M00055985:41	CH15CON
502	4934	RTA22200227F.a.18.1.P.Seq	F	M00006587:18	CH02COH
503	450791	RTA22200011F.l.04.1.P.Seq	F	M00056618:66	CH16COP
504	227936	RTA22200009F.p.09.1.P.Seq	F	M00042879:69	CH16COP
505	9436	RTA22200020F.m.12.1.P.Seq	F	M00054679:412	CH17COHLV
506	2557	RTA22200226F.b.14.1.P.Seq	F	M00005610:211	CH02COH
507	11356	RTA22200228F.g.20.1.P.Seq	F	M00006831:85	CH02COH
508	7571	RTA22200226F.l.17.1.P.Seq	F	M00005769:13	CH02COH
509	558116	RTA22200007F.g.09.1.P.Seq	F	M00056199:19	CH15CON
510	216574	RTA22200012F.o.12.1.P.Seq	F	M00056775:17	CH16COP
511	455145	RTA22200005F.l.12.1.P.Seq	F	M00055936:57	CH15CON
512	649148	RTA22200007F.k.01.2.P.Seq	F	M00056231:79	CH15CON
513	648996	RTA22200007F.m.08.1.P.Seq	F	M00056253:612	CH15CON
514	304253	RTA22200013F.g.11.1.P.Seq	F	M00056844:110	CH16COP
515	649717	RTA22200008F.g.10.1.P.Seq	F	M00056466:13	CH15CON
516	5838	RTA22200226F.h.10.1.P.Seq	F	M00005685:412	CH02COH
517	454050	RTA22200005F.m.23.1.P.Seq	F	M00055956:52	CH15CON
518	557903	RTA22200011F.j.17.1.P.Seq	F	M00056608:54	CH16COP
519	1724	RTA22200240F.k.16.1.P.Seq	F	M00023518:14	CH04MAL
520	734803	RTA22200011F.n.23.1.P.Seq	F	M00056645:211	CH16COP
521	557948	RTA22200023F.b.07.1.P.Seq	F	M00055022:84	CH17COHLV
522	5838	RTA22200229F.i.24.1.P.Seq	F	M00006997:13	CH02COH
523	2334	RTA22200017F.c.04.1.P.Seq	F	M00057312:511	CH16COP
524	450953	RTA22200022F.h.12.1.P.Seq	F	M00054937:210	CH17COHLV
525	4840	RTA22200236F.i.16.1.P.Seq	F	M00022645:15	CH03MAH
526	728421	RTA22200011F.m.20.1.P.Seq	F	M00056635:111	CH16COP
527	4747	RTA22200228F.f.23.1.P.Seq	F	M00006822:19	CH02COH
528	648934	RTA22200005F.m.08.1.P.Seq	F	M00055945:510	CH15CON
529	1787	RTA22200226F.d.09.1.P.Seq	F	M00005627:210	CH02COH
530	558098	RTA22200006F.j.17.2.P.Seq	F	M00056074:710	CH15CON
531	1655	RTA22200222F.k.16.1.P.Seq	F	M00004066:42	CH01COH
532	158601	RTA22200242F.h.06.1.P.Seq	F	M00027021:811	CH04MAL
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534	7110	RTA22200232F.k.19.1.P.Seq	F	M00022106:44	CH03MAH
535	2543	RTA22200230F.k.02.1.P.Seq	F	M00007192:56	CH02COH
536	115762	RTA22200012F.f.06.1.P.Seq	F	M00056707:45	CH16COP
537	696	RTA22200243F.p.04.1.P.Seq	F	M00027163:411	CH04MAL
538	1948	RTA22200232F.l.23.1.P.Seq	F	M00022132:410	CH03MAH
539	696	RTA22200241F.o.01.1.P.Seq	F	M00026951:711	CH04MAL
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Table 1

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543	551982	RTA22200019F.m.15.1.P.Seq	F	M00054542:18	CH17COHLV
544	551982	RTA22200021F.k.10.3.P.Seq	F	M00054815:51	CH17COHLV
545	521840	RTA22200021F.c.20.2.P.Seq	F	M00054739:56	CH17COHLV
546	561180	RTA22200026F.d.16.1.P.Seq	F	M00055423:110	CH17COHLV
547	556245	RTA22200020F.i.02.1.P.Seq	F	M00054636:12	CH17COHLV
548	449792	RTA22200001F.a.07.1.P.Seq	F	M00042345:612	CH15CON
549	549722	RTA22200020F.d.22.1.P.Seq	F	M00054595:22	CH17COHLV
550	612572	RTA22200024F.i.24.1.P.Seq	F	M00055216:13	CH17COHLV
551	551235	RTA22200021F.i.12.3.P.Seq	F	M00054826:25	CH17COHLV
552	449701	RTA22200009F.h.04.1.P.Seq	F	M00042802:711	CH16COP
553	375380	RTA22200026F.e.18.1.P.Seq	F	M00055472:83	CH17COHLV
554	56940	RTA22200021F.i.14.3.P.Seq	F	M00054826:55	CH17COHLV
555	549160	RTA22200021F.c.19.2.P.Seq	F	M00054739:43	CH17COHLV
556	554151	RTA22200021F.i.13.3.P.Seq	F	M00054826:310	CH17COHLV
557	727331	RTA22200015F.b.19.1.P.Seq	F	M00057052:211	CH16COP
558	551502	RTA22200019F.o.20.1.P.Seq	F	M00054555:712	CH17COHLV
559	612572	RTA22200024F.j.01.1.P.Seq	F	M00055216:13	CH17COHLV
560	701221	RTA22200002F.o.23.1.P.Seq	F	M00055556:89	CH15CON
561	378041	RTA22200016F.b.17.1.P.Seq	F	M00057167:712	CH16COP
562	503491	RTA22200004F.i.16.1.P.Seq	F	M00055812:51	CH15CON
563	452833	RTA22200018F.e.01.1.P.Seq	F	M00042520:69	CH17COHLV
564	640974	RTA22200002F.i.20.1.P.Seq	F	M00055512:68	CH15CON
565	735326	RTA22200013F.n.08.1.P.Seq	F	M00056898:44	CH16COP
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567	447532	RTA22200001F.d.07.1.P.Seq	F	M00042556:44	CH15CON
568	455598	RTA22200002F.k.15.1.P.Seq	F	M00055526:69	CH15CON
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571	449862	RTA22200024F.i.07.1.P.Seq	F	M00055207:14	CH17COHLV
572	549591	RTA22200023F.o.03.1.P.Seq	F	M00055117:33	CH17COHLV
573	553877	RTA22200021F.c.23.2.P.Seq	F	M00054740:88	CH17COHLV
574	553501	RTA22200021F.a.01.2.P.Seq	F	M00054720:412	CH17COHLV
575	1905	RTA22200020F.p.14.1.P.Seq	F	M00054713:412	CH17COHLV
576	446599	RTA22200001F.h.20.1.P.Seq	F	M00042720:46	CH15CON
577	559409	RTA22200024F.d.17.1.P.Seq	F	M00055170:61	CH17COHLV
578	551982	RTA22200026F.g.14.1.P.Seq	F	M00055485:39	CH17COHLV
579	559057	RTA22200024F.d.23.1.P.Seq	F	M00055172:44	CH17COHLV
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583	506744	RTA22200021F.h.07.3.P.Seq	F	M00054772:36	CH17COHLV
584	401849	RTA22200002F.n.05.1.P.Seq	F	M00055544:22	CH15CON
585	453848	RTA22200009F.n.04.1.P.Seq	F	M00042853:14	CH16COP
586	456764	RTA22200004F.c.15.1.P.Seq	F	M00055755:42	CH15CON
587	446371	RTA22200003F.c.17.1.P.Seq	F	M00055594:11	CH15CON
588	406413	RTA22200021F.c.09.2.P.Seq	F	M00054734:810	CH17COHLV
589	555103	RTA22200024F.a.21.1.P.Seq	F	M00055148:411	CH17COHLV
590	735292	RTA22200015F.c.13.1.P.Seq	F	M00057059:89	CH16COP
591	558534	RTA22200023F.o.13.1.P.Seq	F	M00055125:61	CH17COHLV
592	727181	RTA22200016F.k.12.1.P.Seq	F	M00057242:29	CH16COP
593	551117	RTA22200021F.f.14.3.P.Seq	F	M00054760:112	CH17COHLV
594	464040	RTA22200024F.g.21.1.P.Seq	F	M00055198:77	CH17COHLV

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597	649259	RTA22200006F.n.24.2.P.Seq	F	M00056108:212	CH15CON
598	15414	RTA22200023F.n.18.1.P.Seq	F	M00055113:111	CH17COHLV
599	639240	RTA22200007F.k.18.2.P.Seq	F	M00056238:57	CH15CON
600	549722	RTA22200020F.a.09.1.P.Seq	F	M00054568:711	CH17COHLV
601	561499	RTA22200021F.b.16.2.P.Seq	F	M00054728:210	CH17COHLV
602	639029	RTA22200002F.k.07.1.P.Seq	F	M00055523:33	CH15CON
603	449512	RTA22200009F.p.02.1.P.Seq	F	M00042875:54	CH16COP
604	446987	RTA22200001F.b.20.1.P.Seq	F	M00042540:86	CH15CON
605	466302	RTA22200004F.m.18.1.P.Seq	F	M00055820:55	CH15CON
606	553802	RTA22200022F.f.04.1.P.Seq	F	M00054908:67	CH17COHLV
607	639662	RTA22200004F.h.15.1.P.Seq	F	M00055792:79	CH15CON
608	551527	RTA22200014F.k.03.2.P.Seq	F	M00056998:58	CH16COP
609	730389	RTA22200016F.b.02.1.P.Seq	F	M00057162:410	CH16COP
610	640974	RTA22200002F.n.03.1.P.Seq	F	M00055543:78	CH15CON
611	417155	RTA22200002F.o.01.1.P.Seq	F	M00055548:512	CH15CON
612	417155	RTA22200002F.n.24.1.P.Seq	F	M00055548:512	CH15CON
613	451784	RTA22200008F.d.18.1.P.Seq	F	M00056330:43	CH15CON
614	649152	RTA22200002F.f.04.1.P.Seq	F	M00055464:65	CH15CON
615	450867	RTA22200003F.d.19.1.P.Seq	F	M00055613:410	CH15CON
616	143436	RTA22200003F.d.04.1.P.Seq	F	M00055602:57	CH15CON
617	549395	RTA22200004F.o.05.1.P.Seq	F	M00055827:55	CH15CON
618	639273	RTA22200002F.h.02.1.P.Seq	F	M00055496:57	CH15CON
619	506744	RTA22200021F.m.24.2.P.Seq	F	M00054841:27	CH17COHLV
620	736595	RTA22200014F.i.22.2.P.Seq	F	M00056990:29	CH16COP
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622	451784	RTA22200019F.p.21.1.P.Seq	F	M00054563:39	CH17COHLV
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625	451092	RTA22200026F.h.02.1.P.Seq	F	M00055487:66	CH17COHLV
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627	553736	RTA22200022F.j.18.1.P.Seq	F	M00054952:61	CH17COHLV
628	394413	RTA22200002F.e.15.1.P.Seq	F	M00055456:612	CH15CON
629	556326	RTA22200021F.j.24.3.P.Seq	F	M00054812:37	CH17COHLV
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631	394413	RTA22200002F.k.19.1.P.Seq	F	M00055527:52	CH15CON
632	645633	RTA22200002F.j.09.1.P.Seq	F	M00055516:58	CH15CON
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634	556326	RTA22200021F.k.01.3.P.Seq	F	M00054812:37	CH17COHLV
635	540787	RTA22200004F.n.21.1.P.Seq	F	M00055827:42	CH15CON
636	648872	RTA22200004F.o.20.1.P.Seq	F	M00055833:111	CH15CON
637	643804	RTA22200004F.f.05.1.P.Seq	F	M00055775:36	CH15CON
638	446139	RTA22200001F.e.06.1.P.Seq	F	M00042565:18	CH15CON
639	640356	RTA22200002F.p.15.1.P.Seq	F	M00055563:12	CH15CON
640	379186	RTA22200015F.i.09.1.P.Seq	F	M00057099:38	CH16COP
641	454927	RTA22200021F.b.13.2.P.Seq	F	M00054728:58	CH17COHLV
642	401849	RTA22200004F.h.06.1.P.Seq	F	M00055790:82	CH15CON
643	452414	RTA22200004F.i.20.1.P.Seq	F	M00055798:36	CH15CON
644	446789	RTA22200004F.k.24.1.P.Seq	F	M00055807:710	CH15CON
645	189561	RTA22200022F.n.17.1.P.Seq	F	M00054985:67	CH17COHLV
646	640323	RTA22200003F.g.22.1.P.Seq	F	M00055653:84	CH15CON
647	558116	RTA22200024F.h.08.1.P.Seq	F	M00055201:27	CH17COHLV
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652	551907	RTA22200020F.l.04.1.P.Seq	F	M00054665:88	CH17COHLV
653	447532	RTA22200004F.a.12.1.P.Seq	F	M00055736:73	CH15CON
654	447532	RTA22200003F.b.14.1.P.Seq	F	M00055584:311	CH15CON
655	558454	RTA22200026F.c.17.1.P.Seq	F	M00055417:78	CH17COHLV
656	502683	RTA22200020F.j.12.1.P.Seq	F	M00054647:82	CH17COHLV
657	446909	RTA22200023F.n.17.1.P.Seq	F	M00055112:33	CH17COHLV
658	452506	RTA22200020F.c.23.1.P.Seq	F	M00054587:69	CH17COHLV
659	449792	RTA22200023F.c.02.1.P.Seq	F	M00055027:68	CH17COHLV
660	549395	RTA22200020F.i.08.1.P.Seq	F	M00054638:49	CH17COHLV
661	234653	RTA22200020F.g.14.1.P.Seq	F	M00054621:36	CH17COHLV
662	453911	RTA22200015F.f.01.1.P.Seq	F	M00057074:39	CH16COP
663	452071	RTA22200001F.a.18.1.P.Seq	F	M00042529:77	CH15CON
664	451032	RTA22200018F.g.04.1.P.Seq	F	M00043310:23	CH17COHLV
665	446680	RTA22200018F.g.17.1.P.Seq	F	M00043313:36	CH17COHLV
666	641884	RTA22200008F.b.08.1.P.Seq	F	M00056303:24	CH15CON
667	452800	RTA22200018F.e.16.1.P.Seq	F	M00043301:66	CH17COHLV
668	461835	RTA22200004F.f.08.1.P.Seq	F	M00055778:69	CH15CON
669	548965	RTA22200020F.g.08.1.P.Seq	F	M00054617:19	CH17COHLV
670	734793	RTA22200016F.c.20.1.P.Seq	F	M00057174:812	CH16COP
671	539955	RTA22200008F.a.12.1.P.Seq	F	M00056295:46	CH15CON
672	561892	RTA22200020F.f.11.1.P.Seq	F	M00054609:61	CH17COHLV
673	562292	RTA22200020F.e.06.1.P.Seq	F	M00054596:711	CH17COHLV
674	420686	RTA22200001F.j.02.1.P.Seq	F	M00042735:72	CH15CON
675	9436	RTA22200004F.f.20.1.P.Seq	F	M00055781:35	CH15CON
676	1013	RTA22200004F.e.21.1.P.Seq	F	M00055774:51	CH15CON
677	412364	RTA22200008F.b.07.1.P.Seq	F	M00056303:33	CH15CON
678	44424	RTA22200018F.j.01.1.P.Seq	F	M00043327:82	CH17COHLV
679	394413	RTA22200001F.j.18.1.P.Seq	F	M00042742:45	CH15CON
680	449617	RTA22200008F.c.08.1.P.Seq	F	M00056312:14	CH15CON
681	455032	RTA22200018F.l.07.1.P.Seq	F	M00043347:712	CH17COHLV
682	185400	RTA22200025F.b.17.1.P.Seq	F	M00055279:512	CH17COHLV
683	453911	RTA22200015F.e.24.1.P.Seq	F	M00057074:39	CH16COP
684	650297	RTA22200004F.e.23.1.P.Seq	F	M00055774:73	CH15CON
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690	375380	RTA22200025F.e.16.1.P.Seq	F	M00055319:11	CH17COHLV
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694	550195	RTA22200025F.j.07.1.P.Seq	F	M00055368:310	CH17COHLV
695	562221	RTA22200025F.k.09.1.P.Seq	F	M00055374:18	CH17COHLV
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698	6751	RTA22200248F.n.24.1.P.Seq	F	M00027604:710	CH04MAL
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700	2883	RTA22200249F.l.14.1.P.Seq	F	M00027717:75	CH04MAL
701	9784	RTA22200249F.c.12.1.P.Seq	F	M00027628:11	CH04MAL
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705	1649	RTA22200234F.g.21.1.P.Seq	F	M00022246:88	CH03MAH
706	4325	RTA22200234F.i.13.1.P.Seq	F	M00022259:27	CH03MAH
707	10882	RTA22200249F.f.21.1.P.Seq	F	M00027658:73	CH04MAL
708	10342	RTA22200233F.l.20.1.P.Seq	F	M00021628:47	CH03MAH
709	6474	RTA22200224F.e.16.1.P.Seq	F	M00004972:51	CH02COH
710	10340	RTA22200233F.o.24.1.P.Seq	F	M00021681:32	CH03MAH
711	734723	RTA22200010F.k.06.1.P.Seq	F	M00056480:312	CH16COP
712	452142	RTA22200010F.i.16.1.P.Seq	F	M00056424:86	CH16COP
713	185432	RTA22200249F.o.24.1.P.Seq	F	M00027742:21	CH04MAL
714	11456	RTA22200224F.m.02.1.P.Seq	F	M00005385:110	CH02COH
715	508892	RTA22200010F.p.07.1.P.Seq	F	M00056517:73	CH16COP
716	67	RTA22200224F.f.14.1.P.Seq	F	M00005019:42	CH02COH
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718	735028	RTA22200011F.e.08.1.P.Seq	F	M00056556:71	CH16COP
719	1924	RTA22200224F.n.16.1.P.Seq	F	M00005395:49	CH02COH
720	640116	RTA22200010F.m.24.1.P.Seq	F	M00056503:711	CH16COP
721	6546	RTA22200225F.b.13.1.P.Seq	F	M00005420:31	CH02COH
722	730866	RTA22200010F.p.03.1.P.Seq	F	M00056515:35	CH16COP
723	4829	RTA22200224F.c.02.1.P.Seq	F	M00004850:75	CH02COH
724	546632	RTA22200010F.o.12.1.P.Seq	F	M00056512:36	CH16COP
725	549934	RTA22200019F.i.19.1.P.Seq	F	M00054510:89	CH17COHLV
726	649655	RTA22200010F.o.22.1.P.Seq	F	M00056514:58	CH16COP
727	62016	RTA22200019F.k.05.1.P.Seq	F	M00054520:25	CH17COHLV
728	2783	RTA22200019F.k.18.1.P.Seq	F	M00054524:22	CH17COHLV
729	3876	RTA22200019F.e.03.1.P.Seq	F	M00043504:76	CH17COHLV
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731	644032	RTA22200013F.e.06.1.P.Seq	F	M00056824:51	CH16COP
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733	3428	RTA22200237F.e.01.1.P.Seq	F	M00022716:36	CH03MAH
734	643954	RTA22200012F.p.22.1.P.Seq	F	M00056789:510	CH16COP
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739	456528	RTA22200014F.n.13.1.P.Seq	F	M00057019:82	CH16COP
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742	1024	RTA22200244F.p.09.1.P.Seq	F	M00027229:56	CH04MAL
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Table 1

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761	649148	RTA22200007F.j.24.1.P.Seq	F	M00056231:79	CH15CON
762	234605	RTA22200009F.c.17.2.P.Seq	F	M00042515:110	CH16COP
763	2224	RTA22200232F.g.14.1.P.Seq	F	M00022049:27	CH03MAH
764	185642	RTA22200243F.a.07.1.P.Seq	F	M00027076:67	CH04MAL
765	649655	RTA22200007F.d.16.1.P.Seq	F	M00056171:811	CH15CON
766	2854	RTA22200231F.o.23.1.P.Seq	F	M00007998:67	CH03MAH
767	453470	RTA22200007F.j.08.1.P.Seq	F	M00056224:58	CH15CON
768	11012	RTA22200227F.k.14.1.P.Seq	F	M00006704:76	CH02COH
769	535208	RTA22200005F.c.23.1.P.Seq	F	M00055869:16	CH15CON
770	448606	RTA22200014F.j.14.1.P.Seq	F	M00056994:33	CH16COP
771	12304	RTA22200244F.b.17.1.P.Seq	F	M00027172:33	CH04MAL
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773	367	RTA22200005F.d.04.1.P.Seq	F	M00055871:65	CH15CON
774	11351	RTA22200229F.c.09.1.P.Seq	F	M00006937:63	CH02COH
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786	3416	RTA22200227F.k.16.1.P.Seq	F	M00006705:79	CH02COH
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788	2889	RTA22200228F.n.19.2.P.Seq	F	M00006894:13	CH02COH
789	7393	RTA22200241F.l.09.1.P.Seq	F	M00026934:59	CH04MAL
790	14390	RTA22200244F.i.10.1.P.Seq	F	M00027193:35	CH04MAL
791	661	RTA22200241F.a.15.1.P.Seq	F	M00026856:311	CH04MAL
792	452992	RTA22200013F.e.07.1.P.Seq	F	M00056826:212	CH16COP
793	1943	RTA22200235F.k.21.2.P.Seq	F	M00022528:812	CH03MAH
794	2027	RTA22200244F.l.20.1.P.Seq	F	M00027207:59	CH04MAL
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799	4316	RTA22200248F.e.15.1.P.Seq	F	M00027543:77	CH04MAL
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801	560367	RTA22200013F.e.03.1.P.Seq	F	M00056824:310	CH16COP
802	9997	RTA22200238F.o.18.1.P.Seq	F	M00023015:42	CH03MAH
803	649106	RTA22200012F.f.03.1.P.Seq	F	M00056707:52	CH16COP
804	461835	RTA22200007F.b.18.1.P.Seq	F	M00056150:312	CH15CON
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806	648340	RTA22200007F.a.08.1.P.Seq	F	M00056139:54	CH15CON
807	554812	RTA22200014F.g.21.2.P.Seq	F	M00056969:38	CH16COP
808	447035	RTA22200007F.m.06.1.P.Seq	F	M00056252:511	CH15CON
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Table 1
Page 16 of 45

Table 1

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868	640525	RTA22200007F.f.12.1.P.Seq	F	M00056192:82	CH15CON
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871	468109	RTA22200005F.e.18.1.P.Seq	F	M00055880:612	CH15CON
872	21669	RTA22200023F.h.20.1.P.Seq	F	M00055064:512	CH17COHLV
873	651088	RTA22200007F.j.07.2.P.Seq	F	M00056224:210	CH15CON
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875	556421	RTA22200005F.e.14.1.P.Seq	F	M00055879:44	CH15CON
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877	447539	RTA22200005F.e.22.1.P.Seq	F	M00055882:19	CH15CON
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879	236368	RTA22200006F.j.23.2.P.Seq	F	M00056077:56	CH15CON
880	644523	RTA22200012F.b.12.1.P.Seq	F	M00056673:56	CH16COP
881	729173	RTA22200012F.k.02.1.P.Seq	F	M00056739:411	CH16COP
882	8315	RTA22200231F.a.06.1.P.Seq	F	M00007927:31	CH03MAH
883	450463	RTA22200007F.i.11.2.P.Seq	F	M00056218:73	CH15CON
884	650856	RTA22200012F.o.13.1.P.Seq	F	M00056775:31	CH16COP
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886	726644	RTA22200013F.d.19.1.P.Seq	F	M00056822:711	CH16COP
887	727224	RTA22200013F.h.19.1.P.Seq	F	M00056859:412	CH16COP
888	557906	RTA22200023F.h.18.1.P.Seq	F	M00055063:71	CH17COHLV
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944	727224	RTA22200011F.h.19.1.P.Seq	F	M00056592:64	CH16COP
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962	729295	RTA22200014F.a.21.2.P.Seq	F	M00056925:37	CH16COP
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978	550107	RTA22200023F.p.02.1.P.Seq	F	M00055130:71	CH17COHLV
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982	549722	RTA22200002F.p.13.1.P.Seq	F	M00055560:66	CH15CON
983	640525	RTA22200004F.i.10.1.P.Seq	F	M00055796:510	CH15CON
984	455542	RTA22200009F.f.23.1.P.Seq	F	M00042787:59	CH16COP
985	9436	RTA22200016F.n.12.1.P.Seq	F	M00057270:54	CH16COP
986	380284	RTA22200004F.c.17.1.P.Seq	F	M00055755:83	CH15CON
987	556260	RTA22200020F.p.08.1.P.Seq	F	M00054707:55	CH17COHLV
988	650476	RTA22200013F.p.21.1.P.Seq	F	M00056916:64	CH16COP
989	554500	RTA22200006F.n.14.2.P.Seq	F	M00056103:812	CH15CON
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991	456528	RTA22200019F.l.23.1.P.Seq	F	M00054535:89	CH17COHLV
992	644190	RTA22200009F.m.23.1.P.Seq	F	M00042853:73	CH16COP
993	554080	RTA22200014F.o.19.3.P.Seq	F	M00057028:49	CH16COP
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997	645799	RTA22200014F.d.22.2.P.Seq	F	M00056952:84	CH16COP
998	456506	RTA22200001F.l.10.1.P.Seq	F	M00042889:19	CH15CON
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1030	449617	RTA22200026F.c.15.1.P.Seq	F	M00055415:811	CH17COHLV
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1032	607430	RTA22200024F.n.10.1.P.Seq	F	M00055247:111	CH17COHLV
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1035	646780	RTA22200004F.m.23.1.P.Seq	F	M00055820:710	CH15CON
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1063	403632	RTA22200020F.b.08.1.P.Seq	F	M00054575:31	CH17COHLV
1064	390124	RTA22200021F.n.17.2.P.Seq	F	M00054849:811	CH17COHLV
1065	390124	RTA22200016F.i.16.1.P.Seq	F	M00057230:412	CH16COP
1066	422687	RTA22200015F.e.14.1.P.Seq	F	M00057072:52	CH16COP
1067	394413	RTA22200001F.k.11.1.P.Seq	F	M00042750:29	CH15CON
1068	549178	RTA22200020F.a.18.1.P.Seq	F	M00054571:31	CH17COHLV
1069	453079	RTA22200004F.e.11.1.P.Seq	F	M00055771:111	CH15CON
1070	463824	RTA22200001F.j.03.1.P.Seq	F	M00042735:17	CH15CON
1071	736595	RTA22200016F.d.16.1.P.Seq	F	M00057182:211	CH16COP
1072	102655	RTA22200004F.m.02.1.P.Seq	F	M00055816:61	CH15CON
1073	448606	RTA22200014F.j.14.2.P.Seq	F	M00056994:33	CH16COP
1074	504513	RTA22200004F.n.12.1.P.Seq	F	M00055823:411	CH15CON
1075	20036	RTA22200004F.f.12.1.P.Seq	F	M00055779:12	CH15CON
1076	530883	RTA22200016F.d.08.1.P.Seq	F	M00057180:811	CH16COP
1077	447126	RTA22200004F.o.18.1.P.Seq	F	M00055832:512	CH15CON
1078	556561	RTA22200025F.d.13.1.P.Seq	F	M00055302:62	CH17COHLV
1079	455096	RTA22200020F.e.15.1.P.Seq	F	M00054600:77	CH17COHLV
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Table 1

Table 1

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1083	16556	RTA22200025F.c.02.1.P.Seq	F	M00055281:58	CH17COHLV
1084	402707	RTA22200018F.d.23.1.P.Seq	F	M00042520:64	CH17COHLV
1085	557903	RTA22200025F.b.15.1.P.Seq	F	M00055279:78	CH17COHLV
1086	451243	RTA22200018F.i.18.1.P.Seq	F	M00043324:44	CH17COHLV
1087	452506	RTA22200025F.b.06.1.P.Seq	F	M00055274:62	CH17COHLV
1088	554703	RTA22200025F.g.23.1.P.Seq	F	M00055345:811	CH17COHLV
1089	449580	RTA22200018F.c.03.1.P.Seq	F	M00042450:810	CH17COHLV
1090	3316	RTA22200025F.i.02.1.P.Seq	F	M00055356:36	CH17COHLV
1091	97507	RTA22200025F.i.22.1.P.Seq	F	M00055364:51	CH17COHLV
1092	556216	RTA22200025F.k.07.1.P.Seq	F	M00055373:410	CH17COHLV
1093	185401	RTA22200250F.d.22.1.P.Seq	F	M00027808:710	CH04MAL
1094	3758	RTA22200248F.o.08.1.P.Seq	F	M00027605:55	CH04MAL
1095	95700	RTA22200248F.l.15.1.P.Seq	F	M00027588:16	CH04MAL
1096	2478	RTA22200250F.d.12.1.P.Seq	F	M00027803:810	CH04MAL
1097	550267	RTA22200011F.d.14.1.P.Seq	F	M00056552:210	CH16COP
1098	185652	RTA22200250F.c.19.1.P.Seq	F	M00027786:21	CH04MAL
1099	55798	RTA22200250F.a.04.1.P.Seq	F	M00027757:26	CH04MAL
1100	5078	RTA22200011F.a.19.1.P.Seq	F	M00056529:89	CH16COP
1101	9784	RTA22200249F.h.22.1.P.Seq	F	M00027681:42	CH04MAL
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1103	11606	RTA22200234F.e.19.1.P.Seq	F	M00022221:46	CH03MAH
1104	2245	RTA22200234F.e.21.1.P.Seq	F	M00022221:46	CH03MAH
1105	551172	RTA22200011F.b.19.1.P.Seq	F	M00056537:19	CH16COP
1106	729175	RTA22200010F.i.01.1.P.Seq	F	M00056420:47	CH16COP
1107	6317	RTA22200224F.e.13.1.P.Seq	F	M00004971:74	CH02COH
1108	2478	RTA22200234F.f.21.1.P.Seq	F	M00022235:311	CH03MAH
1109	4727	RTA22200234F.f.10.1.P.Seq	F	M00022231:512	CH03MAH
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1111	736349	RTA22200010F.j.16.1.P.Seq	F	M00056434:57	CH16COP
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1115	560984	RTA22200019F.k.07.1.P.Seq	F	M00054521:64	CH17COHLV
1116	549945	RTA22200019F.j.03.1.P.Seq	F	M00054513:112	CH17COHLV
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1119	551235	RTA22200019F.e.14.1.P.Seq	F	M00043506:89	CH17COHLV
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1122	15625	RTA22200005F.n.15.1.P.Seq	F	M00055966:46	CH15CON
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1124	550267	RTA22200005F.b.15.1.P.Seq	F	M00055856:67	CH15CON
1125	7436	RTA22200237F.b.08.1.P.Seq	F	M00022697:412	CH03MAH
1126	451794	RTA22200005F.c.13.1.P.Seq	F	M00055866:12	CH15CON
1127	5744	RTA22200227F.l.15.1.P.Seq	F	M00006719:512	CH02COH
1128	3516	RTA22200228F.n.13.2.P.Seq	F	M00006892:69	CH02COH
1129	730555	RTA22200014F.j.23.1.P.Seq	F	M00056997:89	CH16COP
1130	3085	RTA22200237F.n.05.1.P.Seq	F	M00022829:86	CH03MAH
1131	638854	RTA22200005F.b.09.1.P.Seq	F	M00055854:54	CH15CON
1132	7379	RTA22200225F.l.06.1.P.Seq	F	M00005501:79	CH02COH
1133	185562	RTA22200248F.i.11.1.P.Seq	F	M00027571:311	CH04MAL
1134	452491	RTA22200005F.a.16.1.P.Seq	F	M00055849:48	CH15CON

Table 1

Table 1

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1138	6923	RTA22200237F.h.10.1.P.Seq	F	M00022741:211	CH03MAH
1139	6923	RTA22200237F.h.16.1.P.Seq	F	M00022745:37	CH03MAH
1140	901	RTA22200237F.o.03.1.P.Seq	F	M00022831:34	CH03MAH
1141	901	RTA22200237F.n.23.1.P.Seq	F	M00022831:19	CH03MAH
1142	367	RTA22200236F.h.18.1.P.Seq	F	M00022641:310	CH03MAH
1143	4043	RTA22200228F.l.13.2.P.Seq	F	M00006873:21	CH02COH
1144	3299	RTA22200236F.h.19.1.P.Seq	F	M00022641:56	CH03MAH
1145	11881	RTA22200238F.e.15.1.P.Seq	F	M00022899:39	CH03MAH
1146	9113	RTA22200230F.l.04.1.P.Seq	F	M00007204:712	CH02COH
1147	185460	RTA22200243F.p.24.1.P.Seq	F	M00027165:611	CH04MAL
1148	185716	RTA22200241F.d.03.1.P.Seq	F	M00026873:511	CH04MAL
1149	5753	RTA22200227F.o.22.1.P.Seq	F	M00006756:68	CH02COH
1150	24939	RTA22200012F.e.06.1.P.Seq	F	M00056701:58	CH16COP
1151	649684	RTA22200007F.a.14.1.P.Seq	F	M00056140:87	CH15CON
1152	642109	RTA22200012F.h.03.1.P.Seq	F	M00056717:34	CH16COP
1153	15035	RTA22200007F.l.11.1.P.Seq	F	M00056246:23	CH15CON
1154	649354	RTA22200007F.a.15.1.P.Seq	F	M00056140:57	CH15CON
1155	4465	RTA22200228F.e.19.1.P.Seq	F	M00006811:412	CH02COH
1156	647952	RTA22200007F.b.02.1.P.Seq	F	M00056144:39	CH15CON
1157	455601	RTA22200005F.p.18.1.P.Seq	F	M00055990:25	CH15CON
1158	641901	RTA22200005F.p.07.1.P.Seq	F	M00055984:32	CH15CON
1159	446878	RTA22200009F.b.21.2.P.Seq	F	M00042466:86	CH16COP
1160	7436	RTA22200232F.h.08.1.P.Seq	F	M00022058:11	CH03MAH
1161	2245	RTA22200230F.i.03.1.P.Seq	F	M00007166:56	CH02COH
1162	3531	RTA22200227F.o.01.1.P.Seq	F	M00006746:26	CH02COH
1163	9625	RTA22200240F.k.21.1.P.Seq	F	M00023520:77	CH04MAL
1164	727489	RTA22200012F.l.19.1.P.Seq	F	M00056754:14	CH16COP
1165	159925	RTA22200240F.j.14.1.P.Seq	F	M00023428:43	CH04MAL
1166	645210	RTA22200012F.g.17.1.P.Seq	F	M00056715:54	CH16COP
1167	157629	RTA22200235F.d.24.1.P.Seq	F	M00022453:84	CH03MAH
1168	8375	RTA22200231F.l.07.1.P.Seq	F	M00007982:611	CH03MAH
1169	4319	RTA22200230F.e.02.1.P.Seq	F	M00007129:68	CH02COH
1170	4045	RTA22200231F.n.07.1.P.Seq	F	M00007992:78	CH03MAH
1171	185642	RTA22200240F.p.21.1.P.Seq	F	M00026848:711	CH04MAL
1172	7436	RTA22200238F.l.11.1.P.Seq	F	M00022974:410	CH03MAH
1173	3531	RTA22200227F.n.24.1.P.Seq	F	M00006746:26	CH02COH
1174	644776	RTA22200012F.g.21.1.P.Seq	F	M00056715:58	CH16COP
1175	8354	RTA22200238F.d.13.1.P.Seq	F	M00022892:77	CH03MAH
1176	2099	RTA22200243F.f.05.1.P.Seq	F	M00027111:84	CH04MAL
1177	449956	RTA22200011F.l.18.1.P.Seq	F	M00056624:85	CH16COP
1178	649106	RTA22200003F.o.09.1.P.Seq	F	M00055723:55	CH15CON
1179	452414	RTA22200005F.i.09.1.P.Seq	F	M00055908:512	CH15CON
1180	732712	RTA22200011F.k.21.1.P.Seq	F	M00056616:110	CH16COP
1181	185562	RTA22200241F.m.01.1.P.Seq	F	M00026938:64	CH04MAL
1182	3516	RTA22200225F.i.17.1.P.Seq	F	M00005485:19	CH02COH
1183	185562	RTA22200241F.l.24.1.P.Seq	F	M00026938:64	CH04MAL
1184	185460	RTA22200241F.a.08.1.P.Seq	F	M00026854:57	CH04MAL
1185	10947	RTA22200237F.l.16.1.P.Seq	F	M00022813:18	CH03MAH
1186	452856	RTA22200007F.d.13.1.P.Seq	F	M00056169:66	CH15CON
1187	558767	RTA22200015F.m.17.1.P.Seq	F	M00057127:77	CH16COP
1188	15035	RTA22200008F.e.22.1.P.Seq	F	M00056438:16	CH15CON

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1192	3242	RTA22200230F.a.01.1.P.Seq	F	M00007092:63	CH02COH
1193	6660	RTA22200222F.i.24.1.P.Seq	F	M00003986:712	CH01COH
1194	547	RTA22200244F.j.02.1.P.Seq	F	M00027197:77	CH04MAL
1195	121213	RTA22200011F.i.23.1.P.Seq	F	M00056599:411	CH16COP
1196	4378	RTA22200226F.p.15.1.P.Seq	F	M00005830:410	CH02COH
1197	185554	RTA22200244F.m.17.1.P.Seq	F	M00027217:73	CH04MAL
1198	185482	RTA22200241F.d.04.1.P.Seq	F	M00026873:28	CH04MAL
1199	185715	RTA22200240F.l.14.1.P.Seq	F	M00026805:24	CH04MAL
1200	66017	RTA22200243F.d.10.1.P.Seq	F	M00027097:711	CH04MAL
1201	403111	RTA22200007F.j.14.1.P.Seq	F	M00056226:612	CH15CON
1202	3224	RTA22200222F.o.18.1.P.Seq	F	M00004296:711	CH01COH
1203	966	RTA22200238F.k.11.1.P.Seq	F	M00022961:211	CH03MAH
1204	3639	RTA22200235F.j.05.2.P.Seq	F	M00022509:26	CH03MAH
1205	5388	RTA22200243F.k.17.1.P.Seq	F	M00027139:36	CH04MAL
1206	3299	RTA22200238F.b.05.1.P.Seq	F	M00022872:25	CH03MAH
1207	23760	RTA22200241F.n.13.1.P.Seq	F	M00026949:810	CH04MAL
1208	729384	RTA22200012F.n.06.1.P.Seq	F	M00056765:512	CH16COP
1209	46559	RTA22200016F.g.16.1.P.Seq	F	M00057215:22	CH16COP
1210	449750	RTA22200022F.n.05.1.P.Seq	F	M00054980:32	CH17COHLV
1211	735936	RTA22200011F.i.02.1.P.Seq	F	M00056593:55	CH16COP
1212	607430	RTA22200005F.o.04.1.P.Seq	F	M00055971:57	CH15CON
1213	452856	RTA22200007F.g.23.1.P.Seq	F	M00056205:41	CH15CON
1214	557903	RTA22200016F.g.07.1.P.Seq	F	M00057211:67	CH16COP
1215	453112	RTA22200001F.g.01.1.P.Seq	F	M00042700:43	CH15CON
1216	645900	RTA22200006F.i.24.2.P.Seq	F	M00056067:48	CH15CON
1217	415114	RTA22200002F.m.20.1.P.Seq	F	M00055542:31	CH15CON
1218	418763	RTA22200004F.l.11.1.P.Seq	F	M00055811:18	CH15CON
1219	2245	RTA22200230F.a.12.1.P.Seq	F	M00007097:24	CH02COH
1220	403668	RTA22200012F.o.18.1.P.Seq	F	M00056777:33	CH16COP
1221	15427	RTA22200020F.m.08.1.P.Seq	F	M00054677:42	CH17COHLV
1222	555714	RTA22200020F.n.23.1.P.Seq	F	M00054691:55	CH17COHLV
1223	555830	RTA22200022F.d.19.1.P.Seq	F	M00054899:67	CH17COHLV
1224	4620	RTA22200231F.e.13.1.P.Seq	F	M00007951:15	CH03MAH
1225	171511	RTA22200012F.p.21.1.P.Seq	F	M00056789:34	CH16COP
1226	451401	RTA22200008F.h.08.1.P.Seq	F	M00056475:312	CH15CON
1227	447501	RTA22200002F.e.01.1.P.Seq	F	M00055453:51	CH15CON
1228	460445	RTA22200022F.p.12.1.P.Seq	F	M00055005:28	CH17COHLV
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1230	449356	RTA22200026F.d.19.1.P.Seq	F	M00055423:78	CH17COHLV
1231	468736	RTA22200022F.i.10.1.P.Seq	F	M00054943:33	CH17COHLV
1232	548858	RTA22200023F.a.04.1.P.Seq	F	M00055011:54	CH17COHLV
1233	3693	RTA22200240F.g.16.1.P.Seq	F	M00023393:32	CH04MAL
1234	642973	RTA22200005F.k.19.1.P.Seq	F	M00055931:13	CH15CON
1235	561180	RTA22200012F.n.04.1.P.Seq	F	M00056765:110	CH16COP
1236	453708	RTA22200020F.p.07.1.P.Seq	F	M00054707:28	CH17COHLV
1237	645305	RTA22200001F.p.17.1.P.Seq	F	M00054917:69	CH15CON
1238	463487	RTA22200007F.e.12.1.P.Seq	F	M00056184:48	CH15CON
1239	11131	RTA22200230F.b.14.1.P.Seq	F	M00007105:312	CH02COH
1240	561807	RTA22200020F.k.18.1.P.Seq	F	M00054660:65	CH17COHLV
1241	452800	RTA22200023F.n.03.1.P.Seq	F	M00055104:212	CH17COHLV
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SEQ ID	CLUSTER	SEQ NAME	ORIENTATION	CLONE ID	LIBRARY
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1245	9113	RTA22200226F.i.12.1.P.Seq	F	M00005704:410	CH02COH
1246	630259	RTA22200004F.k.14.1.P.Seq	F	M00055805:410	CH15CON
1247	3516	RTA22200226F.o.20.1.P.Seq	F	M00005819:211	CH02COH
1248	447494	RTA22200004F.j.14.1.P.Seq	F	M00055802:72	CH15CON
1249	554500	RTA22200019F.n.10.1.P.Seq	F	M00054547:59	CH17COHLV
1250	639662	RTA22200001F.p.19.1.P.Seq	F	M00054917:412	CH15CON
1251	421	RTA22200009F.o.23.1.P.Seq	F	M00042869:56	CH16COP
1252	736014	RTA22200016F.o.19.1.P.Seq	F	M00057277:39	CH16COP
1253	643061	RTA22200006F.m.24.2.P.Seq	F	M00056099:811	CH15CON
1254	9113	RTA22200229F.m.02.1.P.Seq	F	M00007035:56	CH02COH
1255	650856	RTA22200007F.i.19.2.P.Seq	F	M00056221:55	CH15CON
1256	476223	RTA22200009F.g.09.1.P.Seq	F	M00042792:64	CH16COP
1257	737088	RTA22200011F.f.01.1.P.Seq	F	M00056564:59	CH16COP
1258	449512	RTA22200022F.p.03.1.P.Seq	F	M00055000:64	CH17COHLV
1259	449457	RTA22200023F.m.21.1.P.Seq	F	M00055100:48	CH17COHLV
1260	521901	RTA22200022F.l.07.1.P.Seq	F	M00054964:811	CH17COHLV
1261	175799	RTA22200001F.f.12.1.P.Seq	F	M00042695:85	CH15CON
1262	550108	RTA22200012F.p.01.1.P.Seq	F	M00056779:810	CH16COP
1263	203605	RTA22200003F.e.03.1.P.Seq	F	M00055618:16	CH15CON
1264	450429	RTA22200013F.b.10.1.P.Seq	F	M00056805:29	CH16COP
1265	2478	RTA22200238F.j.18.1.P.Seq	F	M00022956:29	CH03MAH
1266	644099	RTA22200004F.b.06.1.P.Seq	F	M00055743:312	CH15CON
1267	552614	RTA22200008F.e.13.1.P.Seq	F	M00056344:73	CH15CON
1268	452523	RTA22200007F.g.15.1.P.Seq	F	M00056203:810	CH15CON
1269	446789	RTA22200004F.l.01.1.P.Seq	F	M00055807:710	CH15CON
1270	515631	RTA22200010F.c.15.1.P.Seq	F	M00056369:412	CH16COP
1271	452523	RTA22200009F.h.13.1.P.Seq	F	M00042805:88	CH16COP
1272	640116	RTA22200007F.l.23.2.P.Seq	F	M00056250:61	CH15CON
1273	9113	RTA22200230F.a.14.1.P.Seq	F	M00007097:47	CH02COH
1274	562221	RTA22200006F.b.03.2.P.Seq	F	M00056001:59	CH15CON
1275	455972	RTA22200012F.i.18.1.P.Seq	F	M00056729:44	CH16COP
1276	449137	RTA22200009F.e.12.1.P.Seq	F	M00042771:13	CH16COP
1277	5078	RTA22200013F.p.15.1.P.Seq	F	M00056914:29	CH16COP
1278	5078	RTA22200013F.g.09.1.P.Seq	F	M00056844:57	CH16COP
1279	4016	RTA22200228F.d.20.1.P.Seq	F	M00006807:712	CH02COH
1280	403111	RTA22200005F.m.11.1.P.Seq	F	M00055946:77	CH15CON
1281	562292	RTA22200023F.g.07.1.P.Seq	F	M00055053:23	CH17COHLV
1282	403111	RTA22200007F.j.14.2.P.Seq	F	M00056226:612	CH15CON
1283	403111	RTA22200007F.m.22.1.P.Seq	F	M00056262:28	CH15CON
1284	500959	RTA22200006F.i.23.2.P.Seq	F	M00056066:87	CH15CON
1285	763	RTA22200231F.g.24.1.P.Seq	F	M00007965:33	CH03MAH
1286	763	RTA22200231F.h.01.1.P.Seq	F	M00007965:33	CH03MAH
1287	500959	RTA22200008F.f.19.1.P.Seq	F	M00056456:19	CH15CON
1288	452071	RTA22200001F.g.03.1.P.Seq	F	M00042700:85	CH15CON
1289	468672	RTA22200026F.e.16.1.P.Seq	F	M00055472:62	CH17COHLV
1290	455492	RTA22200001F.j.08.1.P.Seq	F	M00042738:410	CH15CON
1291	639667	RTA22200015F.f.11.1.P.Seq	F	M00057079:59	CH16COP
1292	549829	RTA22200024F.e.11.1.P.Seq	F	M00055181:51	CH17COHLV
1293	553158	RTA22200021F.f.02.3.P.Seq	F	M00054752:17	CH17COHLV
1294	561485	RTA22200026F.d.14.1.P.Seq	F	M00055421:311	CH17COHLV
1295	639352	RTA22200002F.l.04.1.P.Seq	F	M00055528:66	CH15CON
1296	451401	RTA22200018F.h.16.1.P.Seq	F	M00043317:64	CH17COHLV

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1299	218416	RTA22200004F.b.09.1.P.Seq	F	M00055744:38	CH15CON
1300	447501	RTA22200002F.d.24.1.P.Seq	F	M00055453:51	CH15CON
1301	558371	RTA22200024F.m.15.1.P.Seq	F	M00055242:44	CH17COHLV
1302	561794	RTA22200015F.f.14.1.P.Seq	F	M00057080:32	CH16COP
1303	645065	RTA22200004F.b.15.1.P.Seq	F	M00055744:78	CH15CON
1304	451269	RTA22200001F.b.05.1.P.Seq	F	M00042534:27	CH15CON
1305	401553	RTA22200004F.e.16.1.P.Seq	F	M00055771:67	CH15CON
1306	555276	RTA22200022F.n.12.1.P.Seq	F	M00054984:212	CH17COHLV
1307	551617	RTA22200021F.f.21.3.P.Seq	F	M00054762:67	CH17COHLV
1308	463480	RTA22200001F.i.08.1.P.Seq	F	M00042727:812	CH15CON
1309	549178	RTA22200022F.n.07.1.P.Seq	F	M00054981:511	CH17COHLV
1310	374450	RTA22200003F.d.02.1.P.Seq	F	M00055601:49	CH15CON
1311	562835	RTA22200009F.o.07.1.P.Seq	F	M00042864:55	CH16COP
1312	730555	RTA22200014F.j.23.2.P.Seq	F	M00056997:89	CH16COP
1313	732978	RTA22200015F.f.09.1.P.Seq	F	M00057078:312	CH16COP
1314	1609	RTA22200001F.k.16.1.P.Seq	F	M00042883:612	CH15CON
1315	18591	RTA22200015F.c.09.1.P.Seq	F	M00057058:69	CH16COP
1316	553158	RTA22200021F.f.12.3.P.Seq	F	M00054759:28	CH17COHLV
1317	470602	RTA22200024F.i.03.1.P.Seq	F	M00055206:84	CH17COHLV
1318	639662	RTA22200003F.d.14.1.P.Seq	F	M00055609:612	CH15CON
1319	644721	RTA22200004F.p.13.1.P.Seq	F	M00055839:69	CH15CON
1320	453202	RTA22200025F.n.08.2.P.Seq	F	M00055390:48	CH17COHLV
1321	554655	RTA22200015F.e.19.1.P.Seq	F	M00057073:15	CH16COP
1322	641988	RTA22200002F.c.20.1.P.Seq	F	M00055446:26	CH15CON
1323	453112	RTA22200001F.f.24.1.P.Seq	F	M00042700:43	CH15CON
1324	550694	RTA22200020F.c.09.1.P.Seq	F	M00054583:65	CH17COHLV
1325	649106	RTA22200004F.h.02.1.P.Seq	F	M00055788:13	CH15CON
1326	638973	RTA22200002F.g.14.1.P.Seq	F	M00055494:39	CH15CON
1327	549911	RTA22200024F.h.16.1.P.Seq	F	M00055203:82	CH17COHLV
1328	648774	RTA22200013F.o.21.1.P.Seq	F	M00056909:511	CH16COP
1329	549911	RTA22200024F.g.03.1.P.Seq	F	M00055194:35	CH17COHLV
1330	639662	RTA22200003F.a.10.1.P.Seq	F	M00055572:212	CH15CON
1331	560455	RTA22200024F.l.03.1.P.Seq	F	M00055231:410	CH17COHLV
1332	735805	RTA22200016F.d.23.1.P.Seq	F	M00057191:13	CH16COP
1333	732712	RTA22200014F.p.03.2.P.Seq	F	M00057029:16	CH16COP
1334	446663	RTA22200026F.f.10.1.P.Seq	F	M00055479:72	CH17COHLV
1335	226324	RTA22200024F.e.17.1.P.Seq	F	M00055182:37	CH17COHLV
1336	453016	RTA22200013F.m.14.1.P.Seq	F	M00056893:86	CH16COP
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1338	452414	RTA22200008F.d.21.1.P.Seq	F	M00056331:41	CH15CON
1339	129535	RTA22200003F.a.13.1.P.Seq	F	M00055572:63	CH15CON
1340	447089	RTA22200001F.c.04.1.P.Seq	F	M00042543:82	CH15CON
1341	447850	RTA22200021F.c.07.2.P.Seq	F	M00054732:53	CH17COHLV
1342	556216	RTA22200021F.l.05.3.P.Seq	F	M00054823:87	CH17COHLV
1343	452523	RTA22200003F.d.13.1.P.Seq	F	M00055609:73	CH15CON
1344	44424	RTA22200015F.i.23.1.P.Seq	F	M00057103:89	CH16COP
1345	648872	RTA22200004F.m.05.1.P.Seq	F	M00055817:48	CH15CON
1346	451636	RTA22200018F.e.12.1.P.Seq	F	M00043300:811	CH17COHLV
1347	5078	RTA22200024F.a.14.1.P.Seq	F	M00055145:67	CH17COHLV
1348	403111	RTA22200002F.g.21.1.P.Seq	F	M00055495:52	CH15CON
1349	648959	RTA22200002F.d.02.1.P.Seq	F	M00055448:48	CH15CON
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Table 1

Table 1

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1354	450959	RTA22200018F.f.14.1.P.Seq	F	M00043306:27	CH17COHLV
1355	452833	RTA22200018F.d.24.1.P.Seq	F	M00042520:69	CH17COHLV
1356	550195	RTA22200020F.e.19.1.P.Seq	F	M00054602:34	CH17COHLV
1357	448927	RTA22200018F.i.10.1.P.Seq	F	M00043349:38	CH17COHLV
1358	551514	RTA22200020F.h.08.1.P.Seq	F	M00054629:59	CH17COHLV
1359	549829	RTA22200020F.f.14.1.P.Seq	F	M00054609:86	CH17COHLV
1360	551514	RTA22200025F.f.12.1.P.Seq	F	M00055327:88	CH17COHLV
1361	561485	RTA22200025F.i.07.1.P.Seq	F	M00055358:31	CH17COHLV
1362	453846	RTA22200025F.k.20.1.P.Seq	F	M00055376:21	CH17COHLV
1363	69863	RTA22200249F.j.23.1.P.Seq	F	M00027699:42	CH04MAL
1364	727181	RTA22200011F.d.23.1.P.Seq	F	M00056555:69	CH16COP
1365	454050	RTA22200011F.c.06.1.P.Seq	F	M00056541:18	CH16COP
1366	725994	RTA22200011F.b.07.1.P.Seq	F	M00056534:411	CH16COP
1367	1495	RTA22200234F.j.11.1.P.Seq	F	M00022273:19	CH03MAH
1368	5665	RTA22200233F.n.01.1.P.Seq	F	M00021654:14	CH03MAH
1369	5665	RTA22200233F.m.24.1.P.Seq	F	M00021654:14	CH03MAH
1370	646146	RTA22200010F.i.03.1.P.Seq	F	M00056421:612	CH16COP
1371	8371	RTA22200224F.e.18.1.P.Seq	F	M00005000:88	CH02COH
1372	73812	RTA22200250F.e.14.1.P.Seq	F	M00027817:211	CH04MAL
1373	4242	RTA22200233F.k.20.1.P.Seq	F	M00021620:610	CH03MAH
1374	5482	RTA22200225F.a.01.1.P.Seq	F	M00005411:37	CH02COH
1375	5474	RTA22200224F.p.13.1.P.Seq	F	M00005407:512	CH02COH
1376	5448	RTA22200225F.a.13.1.P.Seq	F	M00005413:63	CH02COH
1377	7607	RTA22200225F.c.10.1.P.Seq	F	M00005438:16	CH02COH
1378	555928	RTA22200010F.o.23.1.P.Seq	F	M00056514:71	CH16COP
1379	4046	RTA22200224F.j.04.1.P.Seq	F	M00005359:16	CH02COH
1380	554080	RTA22200019F.f.02.1.P.Seq	F	M00043508:18	CH17COHLV
1381	451092	RTA22200018F.p.13.1.P.Seq	F	M00043377:33	CH17COHLV
1382	551380	RTA22200018F.p.22.1.P.Seq	F	M00043381:510	CH17COHLV
1383	546642	RTA22200014F.o.20.1.P.Seq	F	M00057029:312	CH16COP
1384	1764	RTA22200228F.c.06.1.P.Seq	F	M00006789:111	CH02COH
1385	650773	RTA22200005F.c.05.1.P.Seq	F	M00055864:511	CH15CON
1386	644205	RTA22200005F.d.20.1.P.Seq	F	M00055874:26	CH15CON
1387	185718	RTA22200242F.m.05.1.P.Seq	F	M00027051:17	CH04MAL
1388	5538	RTA22200227F.k.23.1.P.Seq	F	M00006712:62	CH02COH
1389	7546	RTA22200222F.e.06.1.P.Seq	F	M00001625:28	CH01COH
1390	727789	RTA22200014F.b.21.1.P.Seq	F	M00056939:68	CH16COP
1391	3837	RTA22200232F.m.13.1.P.Seq	F	M00022137:74	CH03MAH
1392	380477	RTA22200007F.d.03.1.P.Seq	F	M00056162:46	CH15CON
1393	3299	RTA22200238F.a.22.1.P.Seq	F	M00022861:210	CH03MAH
1394	448853	RTA22200009F.b.12.2.P.Seq	F	M00042463:69	CH16COP
1395	736701	RTA22200012F.h.21.1.P.Seq	F	M00056723:410	CH16COP
1396	735296	RTA22200013F.k.05.1.P.Seq	F	M00056873:56	CH16COP
1397	13666	RTA22200241F.f.02.1.P.Seq	F	M00026893:11	CH04MAL
1398	732712	RTA22200013F.i.11.1.P.Seq	F	M00056883:17	CH16COP
1399	3765	RTA22200227F.o.19.1.P.Seq	F	M00006755:14	CH02COH
1400	185596	RTA22200243F.j.05.1.P.Seq	F	M00027134:72	CH04MAL
1401	1943	RTA22200233F.e.19.1.P.Seq	F	M00008065:25	CH03MAH
1402	448193	RTA22200009F.d.18.2.P.Seq	F	M00042764:24	CH16COP
1403	1793	RTA22200235F.d.08.1.P.Seq	F	M00022444:311	CH03MAH
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1407	641884	RTA22200003F.m.17.1.P.Seq	F	M00055705:77	CH15CON
1408	463487	RTA22200014F.f.09.2.P.Seq	F	M00056961:28	CH16COP
1409	5156	RTA22200225F.m.12.1.P.Seq	F	M00005516:86	CH02COH
1410	728408	RTA22200012F.h.05.1.P.Seq	F	M00056718:72	CH16COP
1411	73812	RTA22200242F.m.20.1.P.Seq	F	M00027054:23	CH04MAL
1412	1662	RTA22200231F.n.18.1.P.Seq	F	M00007994:15	CH03MAH
1413	736556	RTA22200012F.c.09.1.P.Seq	F	M00056683:29	CH16COP
1414	5240	RTA22200230F.i.16.1.P.Seq	F	M00007172:33	CH02COH
1415	6184	RTA22200230F.a.11.1.P.Seq	F	M00007096:82	CH02COH
1416	446404	RTA22200007F.m.11.1.P.Seq	F	M00056253:86	CH15CON
1417	646825	RTA22200005F.m.17.1.P.Seq	F	M00055951:32	CH15CON
1418	734929	RTA22200011F.i.01.1.P.Seq	F	M00056592:47	CH16COP
1419	648851	RTA22200007F.e.21.1.P.Seq	F	M00056185:13	CH15CON
1420	640135	RTA22200014F.o.14.2.P.Seq	F	M00057027:76	CH16COP
1421	7443	RTA22200234F.p.21.1.P.Seq	F	M00022411:712	CH03MAH
1422	454050	RTA22200007F.h.03.1.P.Seq	F	M00056206:56	CH15CON
1423	3765	RTA22200226F.l.11.1.P.Seq	F	M00005766:610	CH02COH
1424	648320	RTA22200003F.p.03.1.P.Seq	F	M00055726:710	CH15CON
1425	451269	RTA22200005F.g.17.1.P.Seq	F	M00055889:812	CH15CON
1426	535208	RTA22200005F.h.10.1.P.Seq	F	M00055896:611	CH15CON
1427	728115	RTA22200012F.i.04.1.P.Seq	F	M00056724:511	CH16COP
1428	5240	RTA22200228F.b.08.1.P.Seq	F	M00006783:67	CH02COH
1429	909	RTA22200233F.d.12.1.P.Seq	F	M00008043:211	CH03MAH
1430	447697	RTA22200001F.m.18.1.P.Seq	F	M00042905:611	CH15CON
1431	447737	RTA22200005F.k.16.1.P.Seq	F	M00055930:28	CH15CON
1432	651100	RTA22200010F.d.03.1.P.Seq	F	M00056371:612	CH16COP
1433	735477	RTA22200010F.d.20.1.P.Seq	F	M00056383:310	CH16COP
1434	3774	RTA22200230F.c.04.1.P.Seq	F	M00007110:63	CH02COH
1435	646146	RTA22200006F.a.09.2.P.Seq	F	M00055997:711	CH15CON
1436	643931	RTA22200005F.j.20.1.P.Seq	F	M00055921:211	CH15CON
1437	463487	RTA22200013F.h.14.1.P.Seq	F	M00056857:39	CH16COP
1438	650097	RTA22200016F.h.08.1.P.Seq	F	M00057218:31	CH16COP
1439	554469	RTA22200012F.o.20.1.P.Seq	F	M00056777:22	CH16COP
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1441	8738	RTA22200231F.c.10.1.P.Seq	F	M00007939:13	CH03MAH
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1446	734582	RTA22200013F.c.12.1.P.Seq	F	M00056816:110	CH16COP
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1448	558719	RTA22200004F.d.17.1.P.Seq	F	M00055766:83	CH15CON
1449	21669	RTA22200023F.j.14.1.P.Seq	F	M00055073:812	CH17COHLV
1450	470462	RTA22200006F.b.13.2.P.Seq	F	M00056005:55	CH15CON
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1452	553728	RTA22200021F.e.07.3.P.Seq	F	M00054747:61	CH17COHLV
1453	736014	RTA22200016F.p.01.1.P.Seq	F	M00057279:72	CH16COP
1454	237288	RTA22200002F.m.12.1.P.Seq	F	M00055538:811	CH15CON
1455	11141	RTA22200226F.m.20.1.P.Seq	F	M00005782:210	CH02COH
1456	556421	RTA22200022F.k.11.1.P.Seq	F	M00054957:22	CH17COHLV
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Table 1

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1463	549864	RTA22200022F.k.06.1.P.Seq	F	M00054954:33	CH17COHLV
1464	449836	RTA22200017F.a.23.1.P.Seq	F	M00057301:812	CH16COP
1465	554812	RTA22200023F.m.06.1.P.Seq	F	M00055094:89	CH17COHLV
1466	3316	RTA22200021F.l.17.3.P.Seq	F	M00054827:81	CH17COHLV
1467	649852	RTA22200003F.l.09.1.P.Seq	F	M00055689:712	CH15CON
1468	453592	RTA22200001F.g.17.1.P.Seq	F	M00042705:42	CH15CON
1469	455096	RTA22200026F.g.02.1.P.Seq	F	M00055482:11	CH17COHLV
1470	446199	RTA22200009F.n.08.1.P.Seq	F	M00042855:29	CH16COP
1471	558427	RTA22200024F.m.11.1.P.Seq	F	M00055242:56	CH17COHLV
1472	450255	RTA22200021F.j.13.3.P.Seq	F	M00054810:82	CH17COHLV
1473	452026	RTA22200003F.l.10.1.P.Seq	F	M00055689:62	CH15CON
1474	374971	RTA22200024F.p.11.1.P.Seq	F	M00055260:612	CH17COHLV
1475	446404	RTA22200003F.l.04.1.P.Seq	F	M00055686:511	CH15CON
1476	549591	RTA22200025F.p.19.2.P.Seq	F	M00055404:37	CH17COHLV
1477	640135	RTA22200014F.o.14.3.P.Seq	F	M00057027:76	CH16COP
1478	646248	RTA22200016F.k.06.1.P.Seq	F	M00057239:78	CH16COP
1479	639705	RTA22200004F.e.05.1.P.Seq	F	M00055770:71	CH15CON
1480	483084	RTA22200004F.m.03.1.P.Seq	F	M00055817:61	CH15CON
1481	464029	RTA22200026F.b.04.1.P.Seq	F	M00055408:63	CH17COHLV
1482	428005	RTA22200021F.c.03.2.P.Seq	F	M00054731:312	CH17COHLV
1483	91178	RTA22200024F.o.02.1.P.Seq	F	M00055252:32	CH17COHLV
1484	550571	RTA22200024F.k.21.1.P.Seq	F	M00055227:57	CH17COHLV
1485	735028	RTA22200015F.e.10.1.P.Seq	F	M00057070:28	CH16COP
1486	559409	RTA22200021F.m.17.2.P.Seq	F	M00054839:66	CH17COHLV
1487	551172	RTA22200021F.m.09.2.P.Seq	F	M00054836:25	CH17COHLV
1488	648872	RTA22200002F.g.23.1.P.Seq	F	M00055496:69	CH15CON
1489	446404	RTA22200001F.l.03.1.P.Seq	F	M00042887:47	CH15CON
1490	734063	RTA22200016F.j.24.1.P.Seq	F	M00057237:211	CH16COP
1491	467991	RTA22200008F.c.22.1.P.Seq	F	M00056320:82	CH15CON
1492	454050	RTA22200008F.d.06.1.P.Seq	F	M00056323:312	CH15CON
1493	734646	RTA22200015F.j.06.1.P.Seq	F	M00057104:68	CH16COP
1494	450192	RTA22200018F.n.06.1.P.Seq	F	M00043361:45	CH17COHLV
1495	403978	RTA22200018F.f.01.1.P.Seq	F	M00043304:35	CH17COHLV
1496	734209	RTA22200016F.c.16.1.P.Seq	F	M00057174:36	CH16COP
1497	14805	RTA22200021F.o.12.2.P.Seq	F	M00054856:12	CH17COHLV
1498	230995	RTA22200020F.f.01.1.P.Seq	F	M00054604:49	CH17COHLV
1499	120049	RTA22200020F.e.18.1.P.Seq	F	M00054601:58	CH17COHLV
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1502	386543	RTA22200018F.g.02.1.P.Seq	F	M00043309:87	CH17COHLV
1503	379105	RTA22200018F.a.14.1.P.Seq	F	M00042355:72	CH17COHLV
1504	450255	RTA22200018F.c.16.1.P.Seq	F	M00042455:411	CH17COHLV
1505	730143	RTA22200011F.a.03.1.P.Seq	F	M00056526:511	CH16COP
1506	734209	RTA22200010F.m.02.1.P.Seq	F	M00056496:11	CH16COP
1507	401553	RTA22200010F.m.16.1.P.Seq	F	M00056501:87	CH16COP
1508	72979	RTA22200019F.a.15.1.P.Seq	F	M00043388:39	CH17COHLV
1509	726307	RTA22200010F.o.16.1.P.Seq	F	M00056512:312	CH16COP
1510	230995	RTA22200019F.b.14.1.P.Seq	F	M00043397:29	CH17COHLV
1511	3524	RTA22200227F.f.19.1.P.Seq	F	M00006650:13	CH02COH
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1515	2676	RTA22200227F.k.01.1.P.Seq	F	M00006695:88	CH02COH
1516	736701	RTA22200014F.e.11.1.P.Seq	F	M00056955:79	CH16COP
1517	736701	RTA22200014F.e.11.2.P.Seq	F	M00056955:79	CH16COP
1518	8371	RTA22200229F.a.07.1.P.Seq	F	M00006921:88	CH02COH
1519	8336	RTA22200235F.f.24.1.P.Seq	F	M00022470:71	CH03MAH
1520	185542	RTA22200248F.h.05.1.P.Seq	F	M00027564:43	CH04MAL
1521	448046	RTA22200014F.d.13.1.P.Seq	F	M00056951:69	CH16COP
1522	185422	RTA22200242F.j.15.1.P.Seq	F	M00027034:411	CH04MAL
1523	650448	RTA22200005F.c.17.1.P.Seq	F	M00055868:66	CH15CON
1524	5753	RTA22200227F.n.02.1.P.Seq	F	M00006737:111	CH02COH
1525	8001	RTA22200222F.a.01.1.P.Seq	F	M00001340:51	CH01COH
1526	1644	RTA22200240F.j.17.1.P.Seq	F	M00023430:410	CH04MAL
1527	4453	RTA22200237F.o.18.1.P.Seq	F	M00022836:73	CH03MAH
1528	454152	RTA22200020F.j.08.1.P.Seq	F	M00054646:21	CH17COHLV
1529	9913	RTA22200231F.m.19.1.P.Seq	F	M00007991:71	CH03MAH
1530	1350	RTA22200227F.m.14.1.P.Seq	F	M00006731:51	CH02COH
1531	188	RTA22200244F.i.18.1.P.Seq	F	M00027194:15	CH04MAL
1532	4471	RTA22200232F.g.09.1.P.Seq	F	M00022025:42	CH03MAH
1533	2622	RTA22200248F.i.16.1.P.Seq	F	M00027573:69	CH04MAL
1534	185465	RTA22200248F.j.08.1.P.Seq	F	M00027578:54	CH04MAL
1535	19205	RTA22200244F.b.14.1.P.Seq	F	M00027171:27	CH04MAL
1536	185635	RTA22200242F.l.11.1.P.Seq	F	M00027046:55	CH04MAL
1537	5289	RTA22200235F.o.06.2.P.Seq	F	M00022559:49	CH03MAH
1538	779	RTA22200238F.f.01.1.P.Seq	F	M00022901:511	CH03MAH
1539	779	RTA22200238F.e.24.1.P.Seq	F	M00022901:511	CH03MAH
1540	5289	RTA22200235F.m.20.2.P.Seq	F	M00022550:24	CH03MAH
1541	456808	RTA22200013F.d.22.1.P.Seq	F	M00056823:17	CH16COP
1542	646620	RTA22200007F.n.14.1.P.Seq	F	M00056267:22	CH15CON
1543	546642	RTA22200013F.d.21.1.P.Seq	F	M00056823:25	CH16COP
1544	649732	RTA22200003F.n.10.1.P.Seq	F	M00055716:24	CH15CON
1545	5240	RTA22200231F.f.05.1.P.Seq	F	M00007953:89	CH03MAH
1546	448046	RTA22200009F.c.06.2.P.Seq	F	M00042511:14	CH16COP
1547	650476	RTA22200008F.f.07.1.P.Seq	F	M00056447:14	CH15CON
1548	379341	RTA22200016F.n.21.1.P.Seq	F	M00057272:84	CH16COP
1549	401849	RTA22200003F.p.02.1.P.Seq	F	M00055726:412	CH15CON
1550	11452	RTA22200227F.f.18.1.P.Seq	F	M00006649:211	CH02COH
1551	185417	RTA22200242F.b.12.1.P.Seq	F	M00026977:59	CH04MAL
1552	4471	RTA22200232F.c.20.1.P.Seq	F	M00021925:810	CH03MAH
1553	2557	RTA22200228F.e.11.1.P.Seq	F	M00006810:411	CH02COH
1554	3656	RTA22200227F.f.01.1.P.Seq	F	M00006641:83	CH02COH
1555	2327	RTA22200241F.i.20.1.P.Seq	F	M00026917:83	CH04MAL
1556	449026	RTA22200009F.o.17.1.P.Seq	F	M00042867:81	CH16COP
1557	730227	RTA22200013F.n.03.1.P.Seq	F	M00056896:610	CH16COP
1558	650864	RTA22200006F.e.08.2.P.Seq	F	M00056028:63	CH15CON
1559	530774	RTA22200004F.j.19.1.P.Seq	F	M00055803:111	CH15CON
1560	395341	RTA22200011F.g.06.1.P.Seq	F	M00056580:610	CH16COP
1561	557906	RTA22200004F.a.07.1.P.Seq	F	M00055735:75	CH15CON
1562	452531	RTA22200009F.l.08.2.P.Seq	F	M00042842:58	CH16COP
1563	559057	RTA22200021F.e.09.3.P.Seq	F	M00054747:36	CH17COHLV
1564	448046	RTA22200014F.d.13.2.P.Seq	F	M00056951:69	CH16COP
1565	553547	RTA22200022F.g.22.1.P.Seq	F	M00054935:51	CH17COHLV
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SEQ ID	CLUSTER	SEQ NAME	ORIENTATION	CLONE ID	LIBRARY
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1569	552597	RTA22200013F.a.02.1.P.Seq	F	M00056791:612	CH16COP
1570	446531	RTA22200001F.c.11.1.P.Seq	F	M00042547:411	CH15CON
1571	639352	RTA22200008F.a.09.1.P.Seq	F	M00056293:79	CH15CON
1572	642604	RTA22200004F.e.12.1.P.Seq	F	M00055771:65	CH15CON
1573	558534	RTA22200008F.c.04.1.P.Seq	F	M00056310:76	CH15CON
1574	556421	RTA22200026F.b.02.1.P.Seq	F	M00055408:59	CH17COHLV
1575	735477	RTA22200016F.k.10.1.P.Seq	F	M00057242:67	CH16COP
1576	640703	RTA22200014F.o.06.2.P.Seq	F	M00057024:52	CH16COP
1577	643878	RTA22200015F.j.14.1.P.Seq	F	M00057106:13	CH16COP
1578	557797	RTA22200004F.e.07.1.P.Seq	F	M00055771:111	CH15CON
1579	557200	RTA22200021F.b.08.2.P.Seq	F	M00054727:510	CH17COHLV
1580	729531	RTA22200015F.h.06.1.P.Seq	F	M00057091:512	CH16COP
1581	734554	RTA22200014F.o.09.2.P.Seq	F	M00057024:88	CH16COP
1582	418008	RTA22200020F.e.16.1.P.Seq	F	M00054601:810	CH17COHLV
1583	558614	RTA22200024F.k.16.1.P.Seq	F	M00055227:89	CH17COHLV
1584	452245	RTA22200025F.l.16.1.P.Seq	F	M00055381:59	CH17COHLV
1585	449891	RTA22200019F.b.13.1.P.Seq	F	M00043397:22	CH17COHLV
1586	547916	RTA22200011F.a.18.1.P.Seq	F	M00056529:612	CH16COP
1587	6162	RTA22200233F.l.19.1.P.Seq	F	M00021628:211	CH03MAH
1588	6162	RTA22200234F.f.14.1.P.Seq	F	M00022234:45	CH03MAH
1589	4809	RTA22200224F.d.21.1.P.Seq	F	M00004868:412	CH02COH
1590	3926	RTA22200242F.d.18.1.P.Seq	F	M00026993:86	CH04MAL
1591	185693	RTA22200248F.d.20.1.P.Seq	F	M00027532:32	CH04MAL
1592	641683	RTA22200007F.m.16.1.P.Seq	F	M00056256:811	CH15CON
1593	11351	RTA22200226F.o.18.1.P.Seq	F	M00005818:29	CH02COH
1594	650864	RTA22200008F.g.16.1.P.Seq	F	M00056467:57	CH15CON
1595	460445	RTA22200001F.i.11.1.P.Seq	F	M00042728:57	CH15CON
1596	447669	RTA22200011F.e.16.1.P.Seq	F	M00056561:48	CH16COP
1597	227936	RTA22200016F.m.13.1.P.Seq	F	M00057259:810	CH16COP
1598	639459	RTA22200002F.l.20.1.P.Seq	F	M00055532:78	CH15CON
1599	650195	RTA22200004F.a.04.1.P.Seq	F	M00055734:85	CH15CON
1600	734793	RTA22200016F.n.06.1.P.Seq	F	M00057268:510	CH16COP
1601	540787	RTA22200002F.m.10.1.P.Seq	F	M00055536:56	CH15CON
1602	400654	RTA22200003F.n.13.1.P.Seq	F	M00055718:65	CH15CON
1603	731467	RTA22200016F.f.21.1.P.Seq	F	M00057208:36	CH16COP
1604	4045	RTA22200232F.g.23.1.P.Seq	F	M00022052:18	CH03MAH
1605	447669	RTA22200011F.l.23.1.P.Seq	F	M00056628:61	CH16COP
1606	11351	RTA22200230F.c.20.1.P.Seq	F	M00007121:78	CH02COH
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1608	726786	RTA22200016F.e.08.1.P.Seq	F	M00057192:72	CH16COP
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1610	415058	RTA22200022F.h.07.1.P.Seq	F	M00054937:23	CH17COHLV
1611	450633	RTA22200006F.l.11.2.P.Seq	F	M00056085:811	CH15CON
1612	736955	RTA22200014F.h.05.2.P.Seq	F	M00056973:28	CH16COP
1613	729851	RTA22200013F.h.15.1.P.Seq	F	M00056858:23	CH16COP
1614	2512	RTA22200235F.c.11.1.P.Seq	F	M00022430:410	CH03MAH
1615	452704	RTA22200008F.f.21.1.P.Seq	F	M00056456:61	CH15CON
1616	4589	RTA22200230F.c.15.1.P.Seq	F	M00007117:83	CH02COH
1617	4727	RTA22200233F.e.16.1.P.Seq	F	M00008059:28	CH03MAH
1618	454380	RTA22200014F.d.23.1.P.Seq	F	M00056953:16	CH16COP
1619	553912	RTA22200021F.j.04.3.P.Seq	F	M00054808:47	CH17COHLV
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1623	448511	RTA22200023F.b.05.1.P.Seq	F	M00055021:411	CH17COHLV
1624	335	RTA22200012F.l.18.1.P.Seq	F	M00056753:110	CH16COP
1625	561382	RTA22200026F.c.05.1.P.Seq	F	M00055413:27	CH17COHLV
1626	3447	RTA22200227F.k.15.1.P.Seq	F	M00006705:19	CH02COH
1627	639896	RTA22200012F.c.15.1.P.Seq	F	M00056684:611	CH16COP
1628	1353	RTA22200241F.e.20.1.P.Seq	F	M00026890:42	CH04MAL
1629	3031	RTA22200229F.i.23.1.P.Seq	F	M00006996:610	CH02COH
1630	557928	RTA22200021F.g.03.3.P.Seq	F	M00054765:35	CH17COHLV
1631	4727	RTA22200237F.n.09.1.P.Seq	F	M00022829:810	CH03MAH
1632	4046	RTA22200226F.g.16.1.P.Seq	F	M00005655:68	CH02COH
1633	10882	RTA22200241F.b.11.1.P.Seq	F	M00026861:19	CH04MAL
1634	646283	RTA22200007F.c.22.1.P.Seq	F	M00056161:74	CH15CON
1635	646283	RTA22200002F.d.05.1.P.Seq	F	M00055448:57	CH15CON
1636	139516	RTA22200242F.e.16.1.P.Seq	F	M00027000:65	CH04MAL
1637	6184	RTA22200230F.e.13.1.P.Seq	F	M00007131:11	CH02COH
1638	6184	RTA22200228F.c.12.1.P.Seq	F	M00006795:13	CH02COH
1639	454653	RTA22200013F.e.17.1.P.Seq	F	M00056830:72	CH16COP
1640	3309	RTA22200232F.c.11.1.P.Seq	F	M00021911:83	CH03MAH
1641	1037	RTA22200248F.e.02.1.P.Seq	F	M00027535:58	CH04MAL
1642	450665	RTA22200002F.g.06.1.P.Seq	F	M00055491:78	CH15CON
1643	726307	RTA22200016F.b.16.1.P.Seq	F	M00057167:512	CH16COP
1644	447669	RTA22200001F.b.14.1.P.Seq	F	M00042538:56	CH15CON
1645	639651	RTA22200003F.b.15.1.P.Seq	F	M00055584:76	CH15CON
1646	736860	RTA22200015F.b.11.1.P.Seq	F	M00057049:76	CH16COP
1647	553705	RTA22200025F.j.22.1.P.Seq	F	M00055371:61	CH17COHLV
1648	451375	RTA22200018F.j.20.1.P.Seq	F	M00043336:58	CH17COHLV
1649	204862	RTA22200006F.h.24.2.P.Seq	F	M00056058:84	CH15CON
1650	530883	RTA22200011F.o.17.1.P.Seq	F	M00056652:64	CH16COP
1651	447539	RTA22200001F.e.22.1.P.Seq	F	M00042575:41	CH15CON
1652	455096	RTA22200020F.m.23.1.P.Seq	F	M00054680:211	CH17COHLV
1653	8336	RTA22200235F.g.01.1.P.Seq	F	M00022470:71	CH03MAH
1654	449142	RTA22200006F.f.09.2.P.Seq	F	M00056041:34	CH15CON
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1664	447494	RTA22200002F.e.05.1.P.Seq	F	M00055454:811	CH15CON
1665	551433	RTA22200021F.k.12.3.P.Seq	F	M00054816:411	CH17COHLV
1666	414739	RTA22200019F.f.07.1.P.Seq	F	M00043508:31	CH17COHLV
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1668	640525	RTA22200002F.m.24.1.P.Seq	F	M00055543:35	CH15CON
1669	233108	RTA22200002F.p.10.1.P.Seq	F	M00055560:212	CH15CON
1670	643594	RTA22200003F.l.06.1.P.Seq	F	M00055687:61	CH15CON
1671	1642	RTA22200231F.a.18.1.P.Seq	F	M00007931:110	CH03MAH
1672	643804	RTA22200003F.h.09.1.P.Seq	F	M00055656:59	CH15CON
1673	449701	RTA22200012F.h.22.1.P.Seq	F	M00056723:311	CH16COP
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Table 1

SEQ ID	CLUSTER	SEQ NAME	ORIENTATION	CLONE ID	LIBRARY
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1677	1609	RTA22200226F.g.09.1.P.Seq	F	M00005650:16	CH02COH
1678	643938	RTA22200005F.o.22.1.P.Seq	F	M00055980:110	CH15CON
1679	3656	RTA22200227F.e.24.1.P.Seq	F	M00006641:83	CH02COH
1680	16576	RTA22200248F.e.07.1.P.Seq	F	M00027536:712	CH04MAL
1681	9784	RTA22200243F.c.16.1.P.Seq	F	M00027093:28	CH04MAL
1682	2557	RTA22200228F.p.12.2.P.Seq	F	M00006917:48	CH02COH
1683	4620	RTA22200237F.o.15.1.P.Seq	F	M00022834:71	CH03MAH
1684	43642	RTA22200021F.p.23.2.P.Seq	F	M00054865:84	CH17COHLV
1685	555103	RTA22200016F.l.08.1.P.Seq	F	M00057249:36	CH16COP
1686	643341	RTA22200002F.g.16.1.P.Seq	F	M00055495:72	CH15CON
1687	185531	RTA22200248F.l.12.1.P.Seq	F	M00027588:31	CH04MAL
1688	4045	RTA22200224F.b.17.1.P.Seq	F	M00004842:27	CH02COH
1689	400258	RTA22200011F.e.10.1.P.Seq	F	M00056557:42	CH16COP
1690	96618	RTA22200248F.j.22.1.P.Seq	F	M00027581:51	CH04MAL
1691	646060	RTA22200007F.p.23.1.P.Seq	F	M00056291:71	CH15CON
1692	5665	RTA22200232F.a.17.1.P.Seq	F	M00021854:57	CH03MAH
1693	149265	RTA22200241F.o.03.1.P.Seq	F	M00026951:43	CH04MAL
1694	727314	RTA22200012F.g.14.1.P.Seq	F	M00056714:86	CH16COP
1695	736349	RTA22200014F.d.03.1.P.Seq	F	M00056947:69	CH16COP
1696	648931	RTA22200006F.k.13.2.P.Seq	F	M00056081:25	CH15CON
1697	553881	RTA22200003F.m.10.1.P.Seq	F	M00055703:79	CH15CON
1698	7444	RTA22200235F.d.02.1.P.Seq	F	M00022440:41	CH03MAH
1699	150	RTA22200235F.p.14.2.P.Seq	F	M00022571:411	CH03MAH
1700	2889	RTA22200228F.p.09.2.P.Seq	F	M00006917:15	CH02COH
1701	730670	RTA22200013F.a.09.1.P.Seq	F	M00056793:87	CH16COP
1702	560984	RTA22200021F.n.20.2.P.Seq	F	M00054851:53	CH17COHLV
1703	453708	RTA22200026F.e.10.1.P.Seq	F	M00055425:35	CH17COHLV
1704	48977	RTA22200024F.p.08.1.P.Seq	F	M00055259:64	CH17COHLV
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1707	97507	RTA22200023F.p.11.1.P.Seq	F	M00055134:82	CH17COHLV
1708	735966	RTA22200012F.n.08.1.P.Seq	F	M00056766:110	CH16COP
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1711	639705	RTA22200002F.i.11.1.P.Seq	F	M00055510:27	CH15CON
1712	185465	RTA22200013F.c.17.1.P.Seq	F	M00056817:33	CH16COP
1713	378525	RTA22200015F.h.03.1.P.Seq	F	M00057091:33	CH16COP
1714	2889	RTA22200228F.p.10.2.P.Seq	F	M00006917:14	CH02COH
1715	557686	RTA22200025F.f.19.1.P.Seq	F	M00055334:89	CH17COHLV
1716	735786	RTA22200010F.h.02.1.P.Seq	F	M00056414:15	CH16COP
1717	455145	RTA22200003F.f.10.1.P.Seq	F	M00055636:610	CH15CON
1718	639667	RTA22200002F.k.13.1.P.Seq	F	M00055525:27	CH15CON
1719	446913	RTA22200001F.m.21.1.P.Seq	F	M00042905:310	CH15CON
1720	402494	RTA22200014F.c.09.2.P.Seq	F	M00056941:52	CH16COP
1721	734256	RTA22200014F.l.11.1.P.Seq	F	M00057005:43	CH16COP
1722	734256	RTA22200012F.g.05.1.P.Seq	F	M00056711:15	CH16COP
1723	559362	RTA22200023F.n.21.1.P.Seq	F	M00055115:55	CH17COHLV
1724	639651	RTA22200003F.c.22.1.P.Seq	F	M00055597:58	CH15CON
1725	419774	RTA22200008F.g.11.1.P.Seq	F	M00056466:52	CH15CON
1726	555318	RTA22200025F.a.17.1.P.Seq	F	M00055271:35	CH17COHLV
1727	449956	RTA22200010F.b.08.1.P.Seq	F	M00056359:111	CH16COP
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1732	447035	RTA22200003F.f.08.1.P.Seq	F	M00055635:510	CH15CON
1733	446913	RTA22200001F.j.16.1.P.Seq	F	M00042742:16	CH15CON
1734	446900	RTA22200022F.g.20.1.P.Seq	F	M00054934:43	CH17COHLV
1735	504513	RTA22200003F.f.07.1.P.Seq	F	M00055635:810	CH15CON
1736	380477	RTA22200014F.j.09.1.P.Seq	F	M00056993:26	CH16COP
1737	1213	RTA22200244F.p.13.1.P.Seq	F	M00027231:13	CH04MAL
1738	8259	RTA22200222F.l.14.1.P.Seq	F	M00004093:310	CH01COH
1739	8259	RTA22200222F.h.23.1.P.Seq	F	M00003922:83	CH01COH
1740	552968	RTA22200019F.d.20.1.P.Seq	F	M00043503:38	CH17COHLV
1741	650845	RTA22200010F.o.09.1.P.Seq	F	M00056511:812	CH16COP
1742	648594	RTA22200014F.h.17.1.P.Seq	F	M00056977:73	CH16COP
1743	648594	RTA22200014F.h.17.2.P.Seq	F	M00056977:73	CH16COP
1744	2796	RTA22200240F.c.13.1.P.Seq	F	M00023331:111	CH04MAL
1745	5753	RTA22200227F.f.13.1.P.Seq	F	M00006648:15	CH02COH
1746	734256	RTA22200014F.l.11.2.P.Seq	F	M00057005:43	CH16COP
1747	449580	RTA22200007F.p.19.1.P.Seq	F	M00056290:58	CH15CON
1748	553705	RTA22200021F.a.23.2.P.Seq	F	M00054726:68	CH17COHLV
1749	730670	RTA22200011F.n.02.1.P.Seq	F	M00056638:21	CH16COP
1750	15035	RTA22200001F.c.07.1.P.Seq	F	M00042544:610	CH15CON
1751	394436	RTA22200002F.o.12.1.P.Seq	F	M00055552:39	CH15CON
1752	726810	RTA22200011F.h.22.1.P.Seq	F	M00056592:33	CH16COP
1753	352763	RTA22200022F.j.12.1.P.Seq	F	M00054949:17	CH17COHLV
1754	3506	RTA22200240F.i.14.1.P.Seq	F	M00023414:63	CH04MAL
1755	726377	RTA22200015F.i.14.1.P.Seq	F	M00057100:23	CH16COP
1756	562111	RTA22200018F.d.10.1.P.Seq	F	M00042460:17	CH17COHLV
1757	404475	RTA22200010F.m.04.1.P.Seq	F	M00056496:89	CH16COP
1758	13824	RTA22200234F.m.16.1.P.Seq	F	M00022370:72	CH03MAH
1759	558222	RTA22200019F.h.07.1.P.Seq	F	M00054502:41	CH17COHLV
1760	2834	RTA22200224F.p.09.1.P.Seq	F	M00005406:111	CH02COH
1761	453470	RTA22200001F.a.10.1.P.Seq	F	M00042523:35	CH15CON
1762	558682	RTA22200015F.o.16.1.P.Seq	F	M00057141:22	CH16COP
1763	641710	RTA22200016F.j.03.1.P.Seq	F	M00057231:79	CH16COP
1764	640221	RTA22200013F.k.12.1.P.Seq	F	M00056874:71	CH16COP
1765	559057	RTA22200016F.n.11.1.P.Seq	F	M00057270:89	CH16COP
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1767	5729	RTA22200228F.f.10.1.P.Seq	F	M00006819:25	CH02COH
1768	352763	RTA22200022F.g.09.1.P.Seq	F	M00054931:19	CH17COHLV
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1770	644032	RTA22200012F.m.04.1.P.Seq	F	M00056756:15	CH16COP
1771	185562	RTA22200240F.j.15.1.P.Seq	F	M00023428:611	CH04MAL
1772	736349	RTA22200014F.d.03.2.P.Seq	F	M00056947:69	CH16COP
1773	638870	RTA22200012F.h.13.1.P.Seq	F	M00056721:67	CH16COP
1774	649719	RTA22200012F.k.03.1.P.Seq	F	M00056739:48	CH16COP
1775	62016	RTA22200026F.d.09.1.P.Seq	F	M00055420:74	CH17COHLV
1776	2889	RTA22200229F.p.17.1.P.Seq	F	M00007084:74	CH02COH
1777	647135	RTA22200010F.k.08.1.P.Seq	F	M00056480:110	CH16COP
1778	8283	RTA22200224F.g.10.1.P.Seq	F	M00005309:55	CH02COH
1779	732121	RTA22200014F.d.06.1.P.Seq	F	M00056949:66	CH16COP
1780	532307	RTA22200022F.h.09.1.P.Seq	F	M00054937:112	CH17COHLV
1781	6589	RTA22200226F.n.24.1.P.Seq	F	M00005810:67	CH02COH
1782	554678	RTA22200010F.b.19.1.P.Seq	F	M00056363:26	CH16COP

Table 1

Table 1

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1786	451811	RTA22200003F.k.17.1.P.Seq	F	M00055681:72	CH15CON
1787	453059	RTA22200003F.b.22.1.P.Seq	F	M00055586:62	CH15CON
1788	453457	RTA22200021F.a.06.2.P.Seq	F	M00054721:611	CH17COHLV
1789	558454	RTA22200020F.a.20.1.P.Seq	F	M00054572:31	CH17COHLV
1790	417467	RTA22200025F.c.11.1.P.Seq	F	M00055289:42	CH17COHLV
1791	447850	RTA22200001F.a.23.1.P.Seq	F	M00042532:68	CH15CON
1792	557948	RTA22200024F.n.05.1.P.Seq	F	M00055245:19	CH17COHLV
1793	452685	RTA22200022F.b.14.1.P.Seq	F	M00054877:812	CH17COHLV
1794	446964	RTA22200019F.e.05.1.P.Seq	F	M00043504:78	CH17COHLV
1795	550318	RTA22200021F.d.04.2.P.Seq	F	M00054741:310	CH17COHLV
1796	407077	RTA22200023F.p.13.1.P.Seq	F	M00055134:23	CH17COHLV
1797	650864	RTA22200007F.o.19.1.P.Seq	F	M00056282:44	CH15CON
1798	644721	RTA22200003F.p.16.1.P.Seq	F	M00055731:812	CH15CON
1799	485431	RTA22200013F.l.17.1.P.Seq	F	M00056885:36	CH16COP
1800	651073	RTA22200007F.f.05.1.P.Seq	F	M00056186:62	CH15CON
1801	725811	RTA22200012F.o.17.1.P.Seq	F	M00056776:49	CH16COP
1802	645139	RTA22200005F.k.02.1.P.Seq	F	M00055924:811	CH15CON
1803	185478	RTA22200248F.j.05.1.P.Seq	F	M00027578:65	CH04MAL
1804	1441	RTA22200228F.j.04.2.P.Seq	F	M00006859:44	CH02COH
1805	640005	RTA22200002F.i.16.1.P.Seq	F	M00055511:59	CH15CON
1806	728273	RTA22200015F.h.04.1.P.Seq	F	M00057091:34	CH16COP
1807	185579	RTA22200242F.e.07.1.P.Seq	F	M00026996:16	CH04MAL
1808	724473	RTA22200012F.f.23.1.P.Seq	F	M00056711:31	CH16COP
1809	559674	RTA22200014F.h.06.1.P.Seq	F	M00056974:64	CH16COP
1810	456026	RTA22200005F.d.13.1.P.Seq	F	M00055873:53	CH15CON
1811	549320	RTA22200022F.a.02.1.P.Seq	F	M00054867:37	CH17COHLV
1812	447338	RTA22200001F.k.04.1.P.Seq	F	M00042746:29	CH15CON
1813	560700	RTA22200002F.b.09.1.P.Seq	F	M00055430:82	CH15CON
1814	3070	RTA22200021F.g.19.3.P.Seq	F	M00054769:67	CH17COHLV
1815	3070	RTA22200002F.f.03.1.P.Seq	F	M00055463:810	CH15CON
1816	380477	RTA22200014F.j.09.2.P.Seq	F	M00056993:26	CH16COP
1817	735040	RTA22200015F.b.05.1.P.Seq	F	M00057047:32	CH16COP
1818	378525	RTA22200009F.j.16.2.P.Seq	F	M00042826:33	CH16COP
1819	284586	RTA22200009F.c.23.2.P.Seq	F	M00042756:21	CH16COP
1820	640276	RTA22200014F.e.15.2.P.Seq	F	M00056956:61	CH16COP
1821	3344	RTA22200230F.j.07.1.P.Seq	F	M00007178:43	CH02COH
1822	555830	RTA22200005F.b.23.1.P.Seq	F	M00055861:43	CH15CON
1823	726307	RTA22200011F.i.10.1.P.Seq	F	M00056595:62	CH16COP
1824	416	RTA22200011F.m.06.1.P.Seq	F	M00056631:75	CH16COP
1825	2543	RTA22200225F.o.10.1.P.Seq	F	M00005545:18	CH02COH
1826	639352	RTA22200001F.n.09.1.P.Seq	F	M00042908:71	CH15CON
1827	453592	RTA22200009F.l.04.2.P.Seq	F	M00042842:31	CH16COP
1828	450633	RTA22200006F.n.19.2.P.Seq	F	M00056107:56	CH15CON
1829	448383	RTA22200009F.l.15.2.P.Seq	F	M00042844:312	CH16COP
1830	648719	RTA22200008F.a.08.1.P.Seq	F	M00056293:65	CH15CON
1831	730655	RTA22200012F.h.16.1.P.Seq	F	M00056722:71	CH16COP
1832	141185	RTA22200007F.j.21.2.P.Seq	F	M00056228:17	CH15CON
1833	640498	RTA22200003F.m.07.1.P.Seq	F	M00055703:28	CH15CON
1834	9029	RTA22200222F.l.08.1.P.Seq	F	M00004087:211	CH01COH
1835	559674	RTA22200014F.h.06.2.P.Seq	F	M00056974:64	CH16COP
1836	555734	RTA22200021F.n.09.2.P.Seq	F	M00054844:66	CH17COHLV

Table 1

Table 1

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1839	558098	RTA22200024F.p.10.1.P.Seq	F	M00055260:15	CH17COHLV
1840	468672	RTA22200004F.h.23.1.P.Seq	F	M00055794:26	CH15CON
1841	456596	RTA22200022F.f.19.1.P.Seq	F	M00054926:61	CH17COHLV
1842	649722	RTA22200012F.n.07.1.P.Seq	F	M00056765:410	CH16COP
1843	550708	RTA22200022F.o.19.1.P.Seq	F	M00054996:211	CH17COHLV
1844	643931	RTA22200005F.n.14.1.P.Seq	F	M00055966:13	CH15CON
1845	726927	RTA22200011F.j.08.1.P.Seq	F	M00056603:41	CH16COP
1846	459012	RTA22200007F.b.13.1.P.Seq	F	M00056149:21	CH15CON
1847	397773	RTA22200003F.c.13.1.P.Seq	F	M00055592:15	CH15CON
1848	450004	RTA22200011F.f.04.1.P.Seq	F	M00056566:81	CH16COP
1849	649732	RTA22200007F.o.23.1.P.Seq	F	M00056282:89	CH15CON
1850	553955	RTA22200021F.f.08.3.P.Seq	F	M00054755:86	CH17COHLV
1851	646309	RTA22200012F.h.04.1.P.Seq	F	M00056718:21	CH16COP
1852	402727	RTA22200024F.m.16.1.P.Seq	F	M00055243:64	CH17COHLV
1853	468736	RTA22200024F.m.17.1.P.Seq	F	M00055243:71	CH17COHLV
1854	650422	RTA22200007F.a.16.1.P.Seq	F	M00056141:45	CH15CON
1855	730533	RTA22200013F.b.15.1.P.Seq	F	M00056808:212	CH16COP
1856	726307	RTA22200015F.a.17.1.P.Seq	F	M00057044:66	CH16COP
1857	450311	RTA22200005F.j.22.1.P.Seq	F	M00055922:32	CH15CON
1858	450940	RTA22200001F.j.15.1.P.Seq	F	M00042742:83	CH15CON
1859	726786	RTA22200015F.f.06.1.P.Seq	F	M00057077:42	CH16COP
1860	7634	RTA22200235F.b.19.1.P.Seq	F	M00022420:83	CH03MAH
1861	230995	RTA22200016F.e.14.1.P.Seq	F	M00057196:64	CH16COP
1862	374770	RTA22200003F.n.21.1.P.Seq	F	M00055720:16	CH15CON
1863	9275	RTA22200249F.g.11.1.P.Seq	F	M00027665:41	CH04MAL
1864	553860	RTA22200023F.k.02.1.P.Seq	F	M00055077:611	CH17COHLV
1865	452010	RTA22200001F.m.07.1.P.Seq	F	M00042900:37	CH15CON
1866	649560	RTA22200015F.j.16.1.P.Seq	F	M00057106:52	CH16COP
1867	452704	RTA22200008F.b.18.1.P.Seq	F	M00056307:812	CH15CON
1868	447594	RTA22200007F.j.10.1.P.Seq	F	M00056225:79	CH15CON
1869	555444	RTA22200015F.n.10.1.P.Seq	F	M00057130:811	CH16COP
1870	736556	RTA22200017F.c.20.1.P.Seq	F	M00057318:13	CH16COP
1871	5289	RTA22200235F.l.12.2.P.Seq	F	M00022533:56	CH03MAH
1872	732121	RTA22200015F.c.11.1.P.Seq	F	M00057059:66	CH16COP
1873	452567	RTA22200009F.f.12.1.P.Seq	F	M00042783:13	CH16COP
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1875	644099	RTA22200005F.g.07.1.P.Seq	F	M00055887:67	CH15CON
1876	726788	RTA22200012F.h.08.1.P.Seq	F	M00056719:19	CH16COP
1877	638802	RTA22200012F.a.02.1.P.Seq	F	M00056662:63	CH16COP
1878	646283	RTA22200002F.o.18.1.P.Seq	F	M00055553:82	CH15CON
1879	8403	RTA22200238F.n.03.1.P.Seq	F	M00022998:38	CH03MAH
1880	2224	RTA22200233F.g.23.1.P.Seq	F	M00008079:33	CH03MAH
1881	650053	RTA22200008F.g.02.1.P.Seq	F	M00056459:47	CH15CON
1882	380477	RTA22200008F.e.20.1.P.Seq	F	M00056437:87	CH15CON
1883	450867	RTA22200019F.a.09.1.P.Seq	F	M00043386:16	CH17COHLV
1884	456764	RTA22200003F.n.22.1.P.Seq	F	M00055720:11	CH15CON
1885	641373	RTA22200003F.b.11.1.P.Seq	F	M00055583:24	CH15CON
1886	555882	RTA22200004F.m.12.1.P.Seq	F	M00055818:510	CH15CON
1887	644046	RTA22200008F.b.04.1.P.Seq	F	M00056302:612	CH15CON
1888	447250	RTA22200009F.d.15.2.P.Seq	F	M00042760:37	CH16COP
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Table 1

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1894	649062	RTA22200002F.j.14.1.P.Seq	F	M00055519:87	CH15CON
1895	12808	RTA22200233F.m.15.1.P.Seq	F	M00021649:512	CH03MAH
1896	468672	RTA22200001F.g.11.1.P.Seq	F	M00042704:64	CH15CON
1897	650773	RTA22200008F.d.12.1.P.Seq	F	M00056324:42	CH15CON
1898	732237	RTA22200014F.j.12.2.P.Seq	F	M00056994:67	CH16COP
1899	650773	RTA22200001F.o.15.1.P.Seq	F	M00054798:61	CH15CON
1900	550216	RTA22200021F.b.09.2.P.Seq	F	M00054727:86	CH17COHLV
1901	639189	RTA22200002F.n.20.1.P.Seq	F	M00055547:55	CH15CON
1902	3447	RTA22200227F.l.17.1.P.Seq	F	M00006719:87	CH02COH
1903	2012	RTA22200248F.c.03.1.P.Seq	F	M00027524:211	CH04MAL
1904	642876	RTA22200005F.b.13.1.P.Seq	F	M00055856:64	CH15CON
1905	449690	RTA22200009F.j.10.2.P.Seq	F	M00042823:74	CH16COP
1906	451208	RTA22200004F.k.07.1.P.Seq	F	M00055804:63	CH15CON
1907	725811	RTA22200011F.k.18.1.P.Seq	F	M00056616:38	CH16COP
1908	1256	RTA22200232F.b.11.1.P.Seq	F	M00021869:41	CH03MAH
1909	446599	RTA22200004F.f.18.1.P.Seq	F	M00055780:78	CH15CON
1910	446537	RTA22200001F.c.05.1.P.Seq	F	M00042544:42	CH15CON
1911	726281	RTA22200010F.l.02.1.P.Seq	F	M00056484:72	CH16COP
1912	11286	RTA22200226F.n.17.1.P.Seq	F	M00005802:810	CH02COH
1913	556082	RTA22200022F.p.11.1.P.Seq	F	M00055005:811	CH17COHLV
1914	97507	RTA22200005F.a.21.1.P.Seq	F	M00055851:711	CH15CON
1915	535955	RTA22200022F.b.11.1.P.Seq	F	M00054876:73	CH17COHLV
1916	728251	RTA22200011F.i.08.1.P.Seq	F	M00056595:37	CH16COP
1917	733849	RTA22200015F.g.08.1.P.Seq	F	M00057085:13	CH16COP
1918	447574	RTA22200014F.k.20.2.P.Seq	F	M00057002:25	CH16COP
1919	7607	RTA22200229F.g.17.1.P.Seq	F	M00006976:45	CH02COH
1920	644032	RTA22200010F.i.21.1.P.Seq	F	M00056425:23	CH16COP
1921	454087	RTA22200012F.f.13.1.P.Seq	F	M00056709:15	CH16COP
1922	412364	RTA22200007F.p.02.1.P.Seq	F	M00056283:33	CH15CON
1923	535208	RTA22200002F.m.04.1.P.Seq	F	M00055534:81	CH15CON
1924	644609	RTA22200002F.m.21.1.P.Seq	F	M00055542:66	CH15CON
1925	645073	RTA22200004F.o.14.1.P.Seq	F	M00055830:710	CH15CON
1926	417467	RTA22200012F.g.08.1.P.Seq	F	M00056712:26	CH16COP
1927	554188	RTA22200004F.n.02.1.P.Seq	F	M00055821:712	CH15CON
1928	647185	RTA22200005F.n.02.1.P.Seq	F	M00055958:62	CH15CON
1929	736679	RTA22200012F.a.20.1.P.Seq	F	M00056666:38	CH16COP
1930	553547	RTA22200022F.j.02.1.P.Seq	F	M00054947:712	CH17COHLV
1931	641524	RTA22200016F.c.06.1.P.Seq	F	M00057170:83	CH16COP
1932	649717	RTA22200003F.f.02.1.P.Seq	F	M00055633:12	CH15CON
1933	451041	RTA22200018F.a.16.1.P.Seq	F	M00042355:31	CH17COHLV
1934	3483	RTA22200225F.e.24.1.P.Seq	F	M00005459:21	CH02COH
1935	500959	RTA22200008F.c.24.1.P.Seq	F	M00056323:810	CH15CON
1936	500959	RTA22200008F.d.01.1.P.Seq	F	M00056323:810	CH15CON
1937	697	RTA22200233F.b.10.1.P.Seq	F	M00008020:33	CH03MAH
1938	736955	RTA22200013F.f.22.1.P.Seq	F	M00056840:89	CH16COP
1939	554742	RTA22200004F.l.14.1.P.Seq	F	M00055811:312	CH15CON
1940	642973	RTA22200015F.n.14.1.P.Seq	F	M00057132:68	CH16COP
1941	449437	RTA22200008F.b.13.1.P.Seq	F	M00056304:711	CH15CON
1942	467991	RTA22200002F.j.11.1.P.Seq	F	M00055517:43	CH15CON
1943	650204	RTA22200004F.n.13.1.P.Seq	F	M00055825:53	CH15CON
1944	640618	RTA22200004F.p.17.1.P.Seq	F	M00055840:46	CH15CON

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SEQ ID	CLUSTER	SEQ NAME	ORIENTATION	CLONE ID	LIBRARY
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1947	554101	RTA22200012F.f.24.1.P.Seq	F	M00056711:65	CH16COP
1948	185432	RTA22200249F.p.01.1.P.Seq	F	M00027742:21	CH04MAL
1949	455598	RTA22200022F.m.06.1.P.Seq	F	M00054970:73	CH17COHLV
1950	649354	RTA22200001F.o.05.1.P.Seq	F	M00054792:59	CH15CON
1951	4408	RTA22200242F.j.13.1.P.Seq	F	M00027034:49	CH04MAL
1952	452366	RTA22200006F.o.03.2.P.Seq	F	M00056110:49	CH15CON
1953	452366	RTA22200001F.e.02.1.P.Seq	F	M00042563:79	CH15CON
1954	727331	RTA22200016F.a.19.1.P.Seq	F	M00057161:59	CH16COP
1955	644853	RTA22200008F.a.05.1.P.Seq	F	M00056293:58	CH15CON
1956	554079	RTA22200014F.k.21.2.P.Seq	F	M00057002:26	CH16COP
1957	556245	RTA22200023F.l.05.1.P.Seq	F	M00055088:112	CH17COHLV
1958	557388	RTA22200012F.p.13.1.P.Seq	F	M00056783:711	CH16COP
1959	449468	RTA22200012F.l.11.1.P.Seq	F	M00056752:51	CH16COP
1960	556245	RTA22200023F.o.12.1.P.Seq	F	M00055125:56	CH17COHLV
1961	455327	RTA22200013F.b.03.1.P.Seq	F	M00056804:56	CH16COP
1962	546632	RTA22200015F.a.10.1.P.Seq	F	M00057041:211	CH16COP
1963	558762	RTA22200022F.a.03.1.P.Seq	F	M00054867:22	CH17COHLV
1964	550818	RTA22200020F.d.10.1.P.Seq	F	M00054590:72	CH17COHLV
1965	554079	RTA22200021F.p.09.2.P.Seq	F	M00054862:27	CH17COHLV
1966	452430	RTA22200016F.e.07.1.P.Seq	F	M00057192:52	CH16COP
1967	452430	RTA22200008F.e.11.1.P.Seq	F	M00056342:611	CH15CON
1968	556082	RTA22200019F.i.02.1.P.Seq	F	M00054507:311	CH17COHLV
1969	514418	RTA22200023F.e.23.1.P.Seq	F	M00055046:511	CH17COHLV
1970	426895	RTA22200021F.p.14.2.P.Seq	F	M00054863:73	CH17COHLV
1971	560803	RTA22200025F.c.05.1.P.Seq	F	M00055283:65	CH17COHLV
1972	447737	RTA22200018F.c.11.1.P.Seq	F	M00042453:51	CH17COHLV
1973	373432	RTA22200018F.l.18.1.P.Seq	F	M00043350:89	CH17COHLV
1974	779	RTA22200250F.f.02.1.P.Seq	F	M00027820:32	CH04MAL
1975	455327	RTA22200015F.m.05.1.P.Seq	F	M00057124:410	CH16COP
1976	554742	RTA22200004F.k.16.1.P.Seq	F	M00055806:812	CH15CON
1977	455327	RTA22200022F.g.14.1.P.Seq	F	M00054933:47	CH17COHLV
1978	11043	RTA22200228F.j.10.2.P.Seq	F	M00006861:18	CH02COH
1979	727447	RTA22200012F.c.14.1.P.Seq	F	M00056684:15	CH16COP
1980	552905	RTA22200011F.i.16.1.P.Seq	F	M00056597:67	CH16COP
1981	446900	RTA22200001F.g.23.1.P.Seq	F	M00042711:711	CH15CON
1982	644190	RTA22200005F.j.02.1.P.Seq	F	M00055913:45	CH15CON
1983	455327	RTA22200021F.c.18.2.P.Seq	F	M00054739:73	CH17COHLV
1984	422375	RTA22200020F.g.01.1.P.Seq	F	M00054613:49	CH17COHLV
1985	422375	RTA22200020F.f.24.1.P.Seq	F	M00054613:49	CH17COHLV
1986	530774	RTA22200025F.p.22.2.P.Seq	F	M00055405:49	CH17COHLV
1987	554101	RTA22200012F.g.01.1.P.Seq	F	M00056711:65	CH16COP
1988	5268	RTA22200226F.g.10.1.P.Seq	F	M00005650:44	CH02COH
1989	642461	RTA22200012F.g.18.1.P.Seq	F	M00056715:71	CH16COP
1990	770	RTA22200003F.a.18.1.P.Seq	F	M00055575:48	CH15CON
1991	3837	RTA22200231F.b.24.1.P.Seq	F	M00007936:29	CH03MAH
1992	561382	RTA22200022F.d.20.1.P.Seq	F	M00054899:71	CH17COHLV
1993	4408	RTA22200248F.e.13.1.P.Seq	F	M00027543:29	CH04MAL
1994	5686	RTA22200234F.j.21.1.P.Seq	F	M00022279:84	CH03MAH
1995	374609	RTA22200013F.e.23.1.P.Seq	F	M00056833:31	CH16COP
1996	734793	RTA22200012F.h.06.1.P.Seq	F	M00056719:46	CH16COP
1997	452430	RTA22200014F.f.18.2.P.Seq	F	M00056964:12	CH16COP
1998	450940	RTA22200020F.n.11.1.P.Seq	F	M00054684:812	CH17COHLV

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Table 1

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2001	555276	RTA22200018F.g.13.1.P.Seq	F	M00043313:77	CH17COHLV
2002	426895	RTA22200015F.l.18.1.P.Seq	F	M00057120:512	CH16COP
2003	1833	RTA22200224F.f.16.1.P.Seq	F	M00005293:46	CH02COH
2004	446450	RTA22200009F.h.08.1.P.Seq	F	M00042805:56	CH16COP
2005	650517	RTA22200007F.l.18.2.P.Seq	F	M00056248:19	CH15CON
2006	554785	RTA22200026F.f.14.1.P.Seq	F	M00055479:312	CH17COHLV
2007	607430	RTA22200002F.i.06.1.P.Seq	F	M00055508:53	CH15CON
2008	446673	RTA22200012F.a.18.1.P.Seq	F	M00056665:55	CH16COP
2009	734685	RTA22200014F.i.17.2.P.Seq	F	M00056986:71	CH16COP
2010	11630	RTA22200248F.h.02.1.P.Seq	F	M00027562:32	CH04MAL
2011	2930	RTA22200228F.c.13.1.P.Seq	F	M00006795:47	CH02COH
2012	44424	RTA22200006F.f.07.2.P.Seq	F	M00056038:64	CH15CON
2013	452052	RTA22200001F.e.19.1.P.Seq	F	M00042574:88	CH15CON
2014	449356	RTA22200009F.j.14.2.P.Seq	F	M00042826:35	CH16COP
2015	726225	RTA22200010F.d.04.1.P.Seq	F	M00056372:310	CH16COP
2016	453708	RTA22200022F.j.14.1.P.Seq	F	M00054950:76	CH17COHLV
2017	447858	RTA22200003F.n.20.1.P.Seq	F	M00055720:79	CH15CON
2018	451613	RTA22200018F.e.18.1.P.Seq	F	M00043301:89	CH17COHLV
2019	650337	RTA22200008F.c.18.1.P.Seq	F	M00056319:71	CH15CON
2020	62016	RTA22200019F.k.10.1.P.Seq	F	M00054522:811	CH17COHLV
2021	447250	RTA22200014F.f.02.2.P.Seq	F	M00056960:35	CH16COP
2022	3837	RTA22200231F.c.01.1.P.Seq	F	M00007936:29	CH03MAH
2023	640614	RTA22200017F.e.22.1.P.Seq	F	M00057340:312	CH16COP
2024	729531	RTA22200013F.g.24.1.P.Seq	F	M00056850:511	CH16COP
2025	729531	RTA22200013F.h.01.1.P.Seq	F	M00056850:511	CH16COP
2026	647952	RTA22200004F.j.07.1.P.Seq	F	M00055800:38	CH15CON
2027	446913	RTA22200004F.k.19.1.P.Seq	F	M00055806:67	CH15CON
2028	2675	RTA22200233F.a.20.1.P.Seq	F	M00008015:68	CH03MAH
2029	643481	RTA22200003F.i.13.1.P.Seq	F	M00055664:18	CH15CON
2030	1345	RTA22200012F.l.22.1.P.Seq	F	M00056754:84	CH16COP
2031	26	RTA22200231F.a.03.1.P.Seq	F	M00007926:15	CH03MAH
2032	945	RTA22200230F.h.02.1.P.Seq	F	M00007156:56	CH02COH
2033	449169	RTA22200009F.b.09.2.P.Seq	F	M00042461:110	CH16COP
2034	394193	RTA22200007F.h.10.1.P.Seq	F	M00056209:612	CH15CON
2035	452212	RTA22200006F.h.13.2.P.Seq	F	M00056055:21	CH15CON
2036	394193	RTA22200007F.i.15.2.P.Seq	F	M00056220:42	CH15CON
2037	1310	RTA22200235F.o.10.2.P.Seq	F	M00022561:16	CH03MAH
2038	734094	RTA22200016F.k.07.1.P.Seq	F	M00057241:24	CH16COP
2039	646579	RTA22200002F.h.08.1.P.Seq	F	M00055498:89	CH15CON
2040	4471	RTA22200233F.j.22.1.P.Seq	F	M00008098:81	CH03MAH
2041	729173	RTA22200016F.e.13.1.P.Seq	F	M00057196:53	CH16COP
2042	450323	RTA22200009F.i.11.2.P.Seq	F	M00042814:211	CH16COP
2043	4652	RTA22200241F.n.17.1.P.Seq	F	M00026950:612	CH04MAL
2044	553316	RTA22200021F.a.10.2.P.Seq	F	M00054722:38	CH17COHLV
2045	642604	RTA22200016F.j.10.1.P.Seq	F	M00057233:67	CH16COP
2046	553316	RTA22200002F.i.02.1.P.Seq	F	M00055504:48	CH15CON
2047	4097	RTA22200249F.f.14.1.P.Seq	F	M00027652:73	CH04MAL
2048	6818	RTA22200006F.f.12.2.P.Seq	F	M00056042:11	CH15CON
2049	395341	RTA22200024F.c.22.1.P.Seq	F	M00055161:111	CH17COHLV
2050	649143	RTA22200007F.o.20.1.P.Seq	F	M00056282:31	CH15CON
2051	649143	RTA22200007F.o.18.1.P.Seq	F	M00056282:611	CH15CON
2052	648310	RTA22200007F.e.16.1.P.Seq	F	M00056184:61	CH15CON

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Table 1

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2055	6878	RTA22200231F.a.01.1.P.Seq	F	M00007926:17	CH03MAH
2056	452238	RTA22200009F.d.09.2.P.Seq	F	M00042758:812	CH16COP
2057	1870	RTA22200238F.g.09.1.P.Seq	F	M00022911:71	CH03MAH
2058	559259	RTA22200002F.n.12.1.P.Seq	F	M00055545:812	CH15CON
2059	453457	RTA22200004F.a.06.1.P.Seq	F	M00055735:37	CH15CON
2060	8868	RTA22200233F.l.13.1.P.Seq	F	M00021626:64	CH03MAH
2061	453059	RTA22200001F.b.21.1.P.Seq	F	M00042540:63	CH15CON
2062	236368	RTA22200008F.d.09.1.P.Seq	F	M00056323:17	CH15CON
2063	453059	RTA22200001F.b.18.1.P.Seq	F	M00042539:55	CH15CON
2064	549979	RTA22200007F.c.06.1.P.Seq	F	M00056153:41	CH15CON
2065	515631	RTA22200014F.j.22.2.P.Seq	F	M00056996:112	CH16COP
2066	2235	RTA22200234F.f.22.1.P.Seq	F	M00022236:12	CH03MAH
2067	448193	RTA22200016F.n.15.1.P.Seq	F	M00057271:51	CH16COP
2068	530774	RTA22200010F.c.12.1.P.Seq	F	M00056368:64	CH16COP
2069	650204	RTA22200002F.d.14.1.P.Seq	F	M00055450:28	CH15CON
2070	644240	RTA22200005F.j.19.1.P.Seq	F	M00055921:53	CH15CON
2071	552614	RTA22200022F.l.11.1.P.Seq	F	M00054965:82	CH17COHLV
2072	727331	RTA22200011F.b.04.1.P.Seq	F	M00056532:76	CH16COP
2073	185457	RTA22200244F.n.05.1.P.Seq	F	M00027220:212	CH04MAL
2074	454531	RTA22200022F.a.11.1.P.Seq	F	M00054869:41	CH17COHLV
2075	643485	RTA22200006F.g.19.2.P.Seq	F	M00056050:13	CH15CON
2076	733669	RTA22200013F.m.22.1.P.Seq	F	M00056895:17	CH16COP
2077	452344	RTA22200016F.b.19.1.P.Seq	F	M00057167:27	CH16COP
2078	63602	RTA22200002F.b.11.1.P.Seq	F	M00055431:59	CH15CON
2079	454155	RTA22200004F.j.13.1.P.Seq	F	M00055802:48	CH15CON
2080	549903	RTA22200013F.b.22.1.P.Seq	F	M00056811:34	CH16COP
2081	515631	RTA22200014F.j.22.1.P.Seq	F	M00056996:112	CH16COP
2082	6878	RTA22200248F.j.20.1.P.Seq	F	M00027580:510	CH04MAL
2083	2977	RTA22200231F.l.18.1.P.Seq	F	M00007983:86	CH03MAH
2084	553823	RTA22200006F.i.02.2.P.Seq	F	M00056060:210	CH15CON
2085	3070	RTA22200026F.a.07.1.P.Seq	F	M00055405:77	CH17COHLV
2086	728884	RTA22200012F.k.06.1.P.Seq	F	M00056740:25	CH16COP
2087	8166	RTA22200009F.c.03.2.P.Seq	F	M00042469:84	CH16COP
2088	644190	RTA22200010F.b.18.1.P.Seq	F	M00056362:75	CH16COP
2089	733669	RTA22200015F.l.05.1.P.Seq	F	M00057117:711	CH16COP
2090	728273	RTA22200011F.i.07.1.P.Seq	F	M00056595:12	CH16COP
2091	406499	RTA22200004F.a.13.1.P.Seq	F	M00055736:77	CH15CON
2092	557720	RTA22200022F.k.07.1.P.Seq	F	M00054954:61	CH17COHLV
2093	732050	RTA22200015F.d.10.1.P.Seq	F	M00057065:44	CH16COP
2094	450867	RTA22200020F.j.18.1.P.Seq	F	M00054648:810	CH17COHLV
2095	650297	RTA22200016F.a.01.1.P.Seq	F	M00057151:24	CH16COP
2096	448064	RTA22200009F.f.08.1.P.Seq	F	M00042781:16	CH16COP
2097	452530	RTA22200018F.p.03.1.P.Seq	F	M00043374:26	CH17COHLV
2098	7592	RTA22200225F.m.10.1.P.Seq	F	M00005515:84	CH02COH
2099	733669	RTA22200016F.b.13.1.P.Seq	F	M00057165:512	CH16COP
2100	11028	RTA22200228F.d.13.1.P.Seq	F	M00006806:39	CH02COH
2101	1013	RTA22200001F.h.22.1.P.Seq	F	M00042720:710	CH15CON
2102	549265	RTA22200002F.h.03.1.P.Seq	F	M00055496:39	CH15CON
2103	376600	RTA22200013F.p.08.1.P.Seq	F	M00056911:62	CH16COP
2104	643804	RTA22200004F.p.14.1.P.Seq	F	M00055839:110	CH15CON
2105	454927	RTA22200026F.d.08.1.P.Seq	F	M00055420:610	CH17COHLV
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Table 1

SEQ ID	CLUSTER	SEQ NAME	ORIENTATION	CLONE ID	LIBRARY
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2109	84895	RTA22200014F.m.13.2.P.Seq	F	M00057013:41	CH16COP
2110	157629	RTA22200242F.c.11.1.P.Seq	F	M00026984:410	CH04MAL
2111	2930	RTA22200229F.h.22.1.P.Seq	F	M00006990:52	CH02COH
2112	7037	RTA22200230F.k.08.1.P.Seq	F	M00007194:24	CH02COH
2113	559806	RTA22200002F.i.04.1.P.Seq	F	M00055505:110	CH15CON
2114	452076	RTA22200004F.g.03.1.P.Seq	F	M00055783:311	CH15CON
2115	454869	RTA22200004F.e.14.1.P.Seq	F	M00055771:44	CH15CON
2116	559674	RTA22200023F.j.05.1.P.Seq	F	M00055071:12	CH17COHLV
2117	2235	RTA22200232F.n.21.1.P.Seq	F	M00022149:31	CH03MAH
2118	7545	RTA22200222F.k.06.1.P.Seq	F	M00004054:75	CH01COH
2119	729173	RTA22200016F.n.22.1.P.Seq	F	M00057272:11	CH16COP
2120	650448	RTA22200004F.m.09.1.P.Seq	F	M00055818:612	CH15CON
2121	172013	RTA22200002F.j.16.1.P.Seq	F	M00055520:16	CH15CON
2122	651088	RTA22200014F.c.15.1.P.Seq	F	M00056945:211	CH16COP
2123	651088	RTA22200014F.c.15.2.P.Seq	F	M00056945:211	CH16COP
2124	726810	RTA22200015F.o.06.1.P.Seq	F	M00057136:61	CH16COP
2125	406499	RTA22200004F.n.23.1.P.Seq	F	M00055827:12	CH15CON
2126	556325	RTA22200023F.i.03.1.P.Seq	F	M00055087:110	CH17COHLV
2127	644836	RTA22200004F.i.13.1.P.Seq	F	M00055797:48	CH15CON
2128	649062	RTA22200007F.d.04.1.P.Seq	F	M00056162:59	CH15CON
2129	454776	RTA22200011F.d.07.1.P.Seq	F	M00056551:62	CH16COP
2130	377579	RTA22200025F.f.17.1.P.Seq	F	M00055332:711	CH17COHLV
2131	728131	RTA22200014F.o.08.1.P.Seq	F	M00057024:75	CH16COP
2132	475203	RTA22200016F.a.05.1.P.Seq	F	M00057154:24	CH16COP
2133	727314	RTA22200011F.p.15.1.P.Seq	F	M00056659:78	CH16COP
2134	552025	RTA22200019F.k.13.1.P.Seq	F	M00054523:110	CH17COHLV
2135	561382	RTA22200004F.d.11.1.P.Seq	F	M00055765:25	CH15CON
2136	732579	RTA22200017F.a.22.1.P.Seq	F	M00057300:62	CH16COP
2137	167	RTA22200012F.o.22.1.P.Seq	F	M00056779:512	CH16COP
2138	185585	RTA22200241F.l.21.1.P.Seq	F	M00026937:28	CH04MAL
2139	728131	RTA22200014F.o.08.2.P.Seq	F	M00057024:75	CH16COP
2140	475203	RTA22200014F.m.07.2.P.Seq	F	M00057011:43	CH16COP
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2143	645222	RTA22200008F.a.16.1.P.Seq	F	M00056300:15	CH15CON
2144	400362	RTA22200024F.j.22.1.P.Seq	F	M00055222:85	CH17COHLV
2145	646583	RTA22200009F.m.15.1.P.Seq	F	M00042850:310	CH16COP
2146	475203	RTA22200014F.m.07.1.P.Seq	F	M00057011:43	CH16COP
2147	550001	RTA22200002F.e.03.1.P.Seq	F	M00055454:17	CH15CON
2148	640703	RTA22200002F.i.19.1.P.Seq	F	M00055512:47	CH15CON
2149	646583	RTA22200007F.k.10.2.P.Seq	F	M00056236:71	CH15CON
2150	449468	RTA22200014F.l.23.1.P.Seq	F	M00057008:59	CH16COP
2151	449468	RTA22200016F.h.22.1.P.Seq	F	M00057223:36	CH16COP
2152	551628	RTA22200001F.l.16.1.P.Seq	F	M00042891:34	CH15CON
2153	449468	RTA22200014F.l.23.2.P.Seq	F	M00057008:59	CH16COP
2154	417259	RTA22200021F.i.19.3.P.Seq	F	M00054804:812	CH17COHLV
2155	448029	RTA22200009F.n.10.1.P.Seq	F	M00042856:67	CH16COP
2156	524363	RTA22200024F.h.07.1.P.Seq	F	M00055201:13	CH17COHLV
2157	446531	RTA22200023F.n.24.1.P.Seq	F	M00055116:22	CH17COHLV
2158	561359	RTA22200008F.a.11.1.P.Seq	F	M00056295:67	CH15CON
2159	711297	RTA22200007F.f.10.1.P.Seq	F	M00056190:72	CH15CON
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2163	560515	RTA22200023F.g.10.1.P.Seq	F	M00055054:32	CH17COHLV
2164	3441	RTA22200235F.l.18.2.P.Seq	F	M00022537:311	CH03MAH
2165	729273	RTA22200016F.i.03.1.P.Seq	F	M00057224:310	CH16COP
2166	557039	RTA22200004F.g.15.1.P.Seq	F	M00055786:45	CH15CON
2167	711297	RTA22200015F.k.22.1.P.Seq	F	M00057114:210	CH16COP
2168	711297	RTA22200014F.g.08.2.P.Seq	F	M00056967:42	CH16COP
2169	2860	RTA22200012F.i.07.1.P.Seq	F	M00056726:75	CH16COP
2170	558534	RTA22200020F.l.05.1.P.Seq	F	M00054665:511	CH17COHLV
2171	711297	RTA22200014F.g.08.1.P.Seq	F	M00056967:42	CH16COP
2172	378457	RTA22200025F.g.08.1.P.Seq	F	M00055338:87	CH17COHLV
2173	646583	RTA22200007F.n.04.1.P.Seq	F	M00056263:31	CH15CON
2174	646583	RTA22200006F.p.06.2.P.Seq	F	M00056128:210	CH15CON
2175	1996	RTA22200012F.m.23.1.P.Seq	F	M00056762:55	CH16COP
2176	7962	RTA22200235F.d.18.1.P.Seq	F	M00022452:27	CH03MAH
2177	645139	RTA22200013F.n.18.1.P.Seq	F	M00056902:812	CH16COP
2178	449468	RTA22200018F.g.12.1.P.Seq	F	M00043313:13	CH17COHLV
2179	9898	RTA22200238F.f.06.1.P.Seq	F	M00022902:810	CH03MAH
2180	406499	RTA22200004F.i.15.1.P.Seq	F	M00055797:57	CH15CON
2181	1257	RTA22200230F.h.06.1.P.Seq	F	M00007156:68	CH02COH
2182	549903	RTA22200004F.g.12.1.P.Seq	F	M00055785:58	CH15CON
2183	557906	RTA22200004F.j.22.1.P.Seq	F	M00055803:48	CH15CON
2184	3538	RTA22200222F.c.09.1.P.Seq	F	M00001491:38	CH01COH
2185	3114	RTA22200231F.n.12.1.P.Seq	F	M00007994:311	CH03MAH
2186	426895	RTA22200018F.l.24.1.P.Seq	F	M00043352:25	CH17COHLV
2187	923	RTA22200015F.c.15.1.P.Seq	F	M00057060:112	CH16COP
2188	645194	RTA22200007F.h.17.1.P.Seq	F	M00056212:71	CH15CON
2189	550161	RTA22200014F.a.06.1.P.Seq	F	M00056921:37	CH16COP
2190	650119	RTA22200005F.d.21.1.P.Seq	F	M00055874:43	CH15CON
2191	642142	RTA22200016F.g.21.1.P.Seq	F	M00057217:27	CH16COP
2192	419255	RTA22200004F.l.20.1.P.Seq	F	M00055814:411	CH15CON
2193	552905	RTA22200019F.j.20.1.P.Seq	F	M00054518:43	CH17COHLV
2194	511997	RTA22200005F.b.22.1.P.Seq	F	M00055860:18	CH15CON
2195	551434	RTA22200003F.m.02.1.P.Seq	F	M00055701:410	CH15CON
2196	727447	RTA22200012F.m.18.1.P.Seq	F	M00056759:73	CH16COP
2197	378786	RTA22200025F.o.11.2.P.Seq	F	M00055396:77	CH17COHLV
2198	649152	RTA22200006F.p.11.2.P.Seq	F	M00056131:312	CH15CON
2199	18853	RTA22200023F.p.10.1.P.Seq	F	M00055134:53	CH17COHLV
2200	643481	RTA22200005F.f.05.1.P.Seq	F	M00055884:510	CH15CON
2201	644417	RTA22200004F.p.08.1.P.Seq	F	M00055838:712	CH15CON
2202	726788	RTA22200011F.i.17.1.P.Seq	F	M00056597:32	CH16COP
2203	206	RTA22200248F.m.13.1.P.Seq	F	M00027594:33	CH04MAL
2204	395930	RTA22200011F.c.20.1.P.Seq	F	M00056548:311	CH16COP
2205	185589	RTA22200244F.a.15.1.P.Seq	F	M00027168:810	CH04MAL
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2207	14522	RTA22200241F.h.19.1.P.Seq	F	M00026909:73	CH04MAL
2208	203605	RTA22200013F.n.02.1.P.Seq	F	M00056896:65	CH16COP
2209	551527	RTA22200019F.g.15.1.P.Seq	F	M00054496:29	CH17COHLV
2210	4509	RTA22200225F.m.07.1.P.Seq	F	M00005514:16	CH02COH
2211	447737	RTA22200001F.g.12.1.P.Seq	F	M00042704:69	CH15CON
2212	447388	RTA22200004F.k.08.1.P.Seq	F	M00055804:61	CH15CON
2213	451932	RTA22200002F.c.24.1.P.Seq	F	M00055447:84	CH15CON
2214	559043	RTA22200025F.c.20.1.P.Seq	F	M00055294:44	CH17COHLV

Table 1

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2217	451932	RTA22200002F.d.01.1.P.Seq	F	M00055447:84	CH15CON
2218	447939	RTA22200002F.d.12.1.P.Seq	F	M00055450:79	CH15CON
2219	1181	RTA22200250F.c.03.1.P.Seq	F	M00027781:54	CH04MAL
2220	376600	RTA22200017F.a.06.1.P.Seq	F	M00057288:58	CH16COP
2221	234761	RTA22200001F.j.10.1.P.Seq	F	M00042739:41	CH15CON
2222	644417	RTA22200014F.d.20.1.P.Seq	F	M00056952:16	CH16COP
2223	639048	RTA22200004F.c.05.1.P.Seq	F	M00055749:811	CH15CON
2224	11452	RTA22200226F.d.16.1.P.Seq	F	M00005628:310	CH02COH
2225	452076	RTA22200001F.c.17.1.P.Seq	F	M00042551:49	CH15CON
2226	644523	RTA22200005F.c.07.1.P.Seq	F	M00055864:82	CH15CON
2227	554678	RTA22200021F.h.11.3.P.Seq	F	M00054776:61	CH17COHLV
2228	3550	RTA22200236F.k.16.1.P.Seq	F	M00022656:511	CH03MAH
2229	450311	RTA22200007F.d.12.1.P.Seq	F	M00056167:28	CH15CON
2230	647280	RTA22200005F.o.13.1.P.Seq	F	M00055976:61	CH15CON
2231	548858	RTA22200026F.f.18.1.P.Seq	F	M00055480:810	CH17COHLV
2232	4204	RTA22200225F.p.22.1.P.Seq	F	M00005568:29	CH02COH
2233	540690	RTA22200011F.f.19.1.P.Seq	F	M00056574:17	CH16COP
2234	404774	RTA22200009F.k.06.2.P.Seq	F	M00042833:71	CH16COP
2235	557823	RTA22200023F.h.01.1.P.Seq	F	M00055057:63	CH17COHLV
2236	1458	RTA22200242F.g.04.1.P.Seq	F	M00027014:74	CH04MAL
2237	485431	RTA22200020F.e.01.1.P.Seq	F	M00054595:89	CH17COHLV
2238	2245	RTA22200229F.l.11.1.P.Seq	F	M00007032:69	CH02COH
2239	3242	RTA22200226F.p.09.1.P.Seq	F	M00005826:710	CH02COH
2240	648747	RTA22200007F.m.12.1.P.Seq	F	M00056254:82	CH15CON
2241	3805	RTA22200222F.c.01.1.P.Seq	F	M00001470:71	CH01COH
2242	475203	RTA22200012F.c.17.1.P.Seq	F	M00056688:65	CH16COP
2243	12018	RTA22200240F.h.11.1.P.Seq	F	M00023399:38	CH04MAL
2244	475203	RTA22200009F.i.18.2.P.Seq	F	M00042818:512	CH16COP
2245	3805	RTA22200222F.b.24.1.P.Seq	F	M00001470:71	CH01COH
2246	496132	RTA22200018F.e.23.1.P.Seq	F	M00043304:41	CH17COHLV
2247	650600	RTA22200005F.m.01.1.P.Seq	F	M00055941:212	CH15CON
2248	650749	RTA22200004F.g.10.1.P.Seq	F	M00055785:63	CH15CON
2249	223148	RTA22200023F.n.05.1.P.Seq	F	M00055106:47	CH17COHLV
2250	449	RTA22200018F.m.12.1.P.Seq	F	M00043355:811	CH17COHLV
2251	735620	RTA22200013F.g.07.1.P.Seq	F	M00056843:89	CH16COP
2252	650600	RTA22200005F.l.24.1.P.Seq	F	M00055941:212	CH15CON
2253	218	RTA22200021F.m.03.2.P.Seq	F	M00054832:59	CH17COHLV
2254	4161	RTA22200222F.d.07.1.P.Seq	F	M00001561:71	CH01COH
2255	373202	RTA22200025F.f.01.1.P.Seq	F	M00055322:51	CH17COHLV
2256	724339	RTA22200010F.l.14.1.P.Seq	F	M00056490:52	CH16COP
2257	113291	RTA22200007F.p.17.1.P.Seq	F	M00056290:65	CH15CON
2258	736753	RTA22200016F.f.22.1.P.Seq	F	M00057208:48	CH16COP
2259	650600	RTA22200003F.m.18.1.P.Seq	F	M00055706:11	CH15CON
2260	451569	RTA22200013F.l.03.1.P.Seq	F	M00056879:12	CH16COP
2261	1297	RTA22200233F.n.06.1.P.Seq	F	M00021655:82	CH03MAH
2262	3680	RTA22200241F.h.12.1.P.Seq	F	M00026906:310	CH04MAL
2263	63602	RTA22200005F.g.11.1.P.Seq	F	M00055888:25	CH15CON
2264	2757	RTA22200238F.l.07.1.P.Seq	F	M00022973:77	CH03MAH
2265	373128	RTA22200020F.a.11.1.P.Seq	F	M00054569:87	CH17COHLV
2266	641479	RTA22200014F.l.16.2.P.Seq	F	M00057007:212	CH16COP
2267	450380	RTA22200015F.b.12.1.P.Seq	F	M00057049:85	CH16COP
2268	133512	RTA22200024F.i.12.1.P.Seq	F	M00055209:18	CH17COHLV

Table 1

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2271	645222	RTA22200013F.b.01.1.P.Seq	F	M00056802:81	CH16COP
2272	17372	RTA22200002F.i.22.1.P.Seq	F	M00055513:46	CH15CON
2273	451619	RTA22200025F.m.23.2.P.Seq	F	M00055388:88	CH17COHLV
2274	2510	RTA22200238F.m.21.1.P.Seq	F	M00022995:52	CH03MAH
2275	643974	RTA22200007F.n.15.1.P.Seq	F	M00056268:24	CH15CON
2276	500630	RTA22200013F.j.19.1.P.Seq	F	M00056872:16	CH16COP
2277	3101	RTA22200225F.n.05.1.P.Seq	F	M00005530:17	CH02COH
2278	446938	RTA22200004F.c.11.1.P.Seq	F	M00055751:41	CH15CON
2279	554469	RTA22200013F.f.23.1.P.Seq	F	M00056841:79	CH16COP
2280	554469	RTA22200003F.n.24.1.P.Seq	F	M00055721:66	CH15CON
2281	2894	RTA22200016F.b.05.1.P.Seq	F	M00057163:21	CH16COP
2282	650600	RTA22200008F.e.04.1.P.Seq	F	M00056338:210	CH15CON
2283	3101	RTA22200226F.j.12.1.P.Seq	F	M00005710:41	CH02COH
2284	554469	RTA22200003F.o.01.1.P.Seq	F	M00055721:66	CH15CON
2285	9910	RTA22200236F.n.06.1.P.Seq	F	M00022667:35	CH03MAH
2286	400608	RTA22200008F.g.03.1.P.Seq	F	M00056460:711	CH15CON
2287	555051	RTA22200021F.o.07.2.P.Seq	F	M00054854:58	CH17COHLV
2288	185400	RTA22200002F.j.21.1.P.Seq	F	M00055522:57	CH15CON
2289	3059	RTA22200233F.g.05.1.P.Seq	F	M00008075:112	CH03MAH
2290	647185	RTA22200004F.b.20.1.P.Seq	F	M00055747:49	CH15CON
2291	1669	RTA22200237F.p.19.1.P.Seq	F	M00022853:311	CH03MAH
2292	7158	RTA22200232F.l.21.1.P.Seq	F	M00022129:512	CH03MAH
2293	496132	RTA22200005F.d.06.1.P.Seq	F	M00055871:76	CH15CON
2294	378623	RTA22200024F.k.20.1.P.Seq	F	M00055227:52	CH17COHLV
2295	1257	RTA22200227F.i.05.1.P.Seq	F	M00006679:34	CH02COH
2296	648499	RTA22200012F.d.21.1.P.Seq	F	M00056698:512	CH16COP
2297	185627	RTA22200242F.k.21.1.P.Seq	F	M00027042:711	CH04MAL
2298	640005	RTA22200008F.c.15.1.P.Seq	F	M00056312:33	CH15CON
2299	553462	RTA22200021F.e.14.3.P.Seq	F	M00054750:412	CH17COHLV
2300	649852	RTA22200002F.g.01.1.P.Seq	F	M00055470:71	CH15CON
2301	422375	RTA22200018F.e.04.1.P.Seq	F	M00043296:210	CH17COHLV
2302	10910	RTA22200227F.n.22.1.P.Seq	F	M00006745:42	CH02COH
2303	2737	RTA22200023F.c.21.1.P.Seq	F	M00055034:71	CH17COHLV
2304	3438	RTA22200225F.o.18.1.P.Seq	F	M00005548:12	CH02COH
2305	3438	RTA22200228F.m.18.2.P.Seq	F	M00006885:711	CH02COH
2306	3763	RTA22200225F.o.12.1.P.Seq	F	M00005546:72	CH02COH
2307	648966	RTA22200007F.a.18.1.P.Seq	F	M00056141:29	CH15CON
2308	724339	RTA22200013F.m.10.1.P.Seq	F	M00056892:11	CH16COP
2309	451569	RTA22200018F.l.17.1.P.Seq	F	M00043350:86	CH17COHLV
2310	554109	RTA22200007F.d.17.1.P.Seq	F	M00056171:812	CH15CON
2311	380339	RTA22200006F.h.10.2.P.Seq	F	M00056055:17	CH15CON
2312	729903	RTA22200014F.g.06.1.P.Seq	F	M00056966:111	CH16COP
2313	45	RTA22200025F.l.10.1.P.Seq	F	M00055379:38	CH17COHLV
2314	454653	RTA22200019F.d.21.1.P.Seq	F	M00043503:55	CH17COHLV
2315	11536	RTA22200237F.n.02.1.P.Seq	F	M00022828:36	CH03MAH
2316	373134	RTA22200001F.h.02.1.P.Seq	F	M00042711:34	CH15CON
2317	185691	RTA22200241F.g.04.1.P.Seq	F	M00026900:32	CH04MAL
2318	234761	RTA22200011F.o.06.1.P.Seq	F	M00056646:75	CH16COP
2319	724339	RTA22200012F.f.19.1.P.Seq	F	M00056710:31	CH16COP
2320	732740	RTA22200016F.j.04.1.P.Seq	F	M00057231:19	CH16COP
2321	35895	RTA22200017F.d.10.1.P.Seq	F	M00057325:310	CH16COP
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Table 1

SEQ ID	CLUSTER	SEQ NAME	ORIENTATION	CLONE ID	LIBRARY
2323	2974	RTA22200227F.b.03.1.P.Seq	F	M00006590:310	CH02COH
2324	500	RTA22200231F.l.13.1.P.Seq	F	M00007983:43	CH03MAH
2325	376919	RTA22200020F.m.09.1.P.Seq	F	M00054678:57	CH17COHLV
2326	8403	RTA22200233F.g.08.1.P.Seq	F	M00008076:62	CH03MAH
2327	3643	RTA22200227F.e.11.1.P.Seq	F	M00006638:72	CH02COH
2328	447211	RTA22200001F.j.13.1.P.Seq	F	M00042741:410	CH15CON
2329	447211	RTA22200001F.b.15.1.P.Seq	F	M00042538:18	CH15CON
2330	14929	RTA22200025F.i.20.1.P.Seq	F	M00055363:712	CH17COHLV
2331	648934	RTA22200006F.k.14.2.P.Seq	F	M00056081:29	CH15CON
2332	731785	RTA22200014F.j.11.2.P.Seq	F	M00056993:43	CH16COP
2333	639908	RTA22200005F.g.08.1.P.Seq	F	M00055887:54	CH15CON
2334	344577	RTA22200014F.m.20.1.P.Seq	F	M00057015:312	CH16COP
2335	2906	RTA22200015F.m.13.1.P.Seq	F	M00057127:611	CH16COP
2336	446938	RTA22200002F.c.18.1.P.Seq	F	M00055445:76	CH15CON
2337	2493	RTA22200234F.h.08.1.P.Seq	F	M00022251:19	CH03MAH
2338	38	RTA22200006F.o.08.2.P.Seq	F	M00056112:82	CH15CON
2339	13818	RTA22200238F.e.13.1.P.Seq	F	M00022898:64	CH03MAH
2340	8371	RTA22200229F.o.12.1.P.Seq	F	M00007065:611	CH02COH
2341	402494	RTA22200012F.o.16.1.P.Seq	F	M00056776:16	CH16COP
2342	731785	RTA22200014F.j.11.1.P.Seq	F	M00056993:43	CH16COP
2343	4621	RTA22200235F.f.15.1.P.Seq	F	M00022468:510	CH03MAH
2344	9750	RTA22200229F.g.23.1.P.Seq	F	M00006979:210	CH02COH
2345	133512	RTA22200024F.p.23.1.P.Seq	F	M00055263:79	CH17COHLV
2346	162626	RTA22200250F.f.03.1.P.Seq	F	M00027823:77	CH04MAL
2347	730059	RTA22200011F.a.20.1.P.Seq	F	M00056530:41	CH16COP
2348	2069	RTA22200224F.k.12.1.P.Seq	F	M00005373:86	CH02COH
2349	5868	RTA22200242F.i.17.1.P.Seq	F	M00027030:38	CH04MAL
2350	2683	RTA22200226F.o.08.1.P.Seq	F	M00005813:510	CH02COH
2351	380409	RTA22200012F.h.07.1.P.Seq	F	M00056719:612	CH16COP
2352	639991	RTA22200002F.k.20.1.P.Seq	F	M00055527:54	CH15CON
2353	535	RTA22200233F.a.19.1.P.Seq	F	M00008015:210	CH03MAH
2354	14929	RTA22200025F.f.21.1.P.Seq	F	M00055335:83	CH17COHLV
2355	134702	RTA22200249F.n.23.1.P.Seq	F	M00027733:45	CH04MAL
2356	642477	RTA22200004F.j.16.1.P.Seq	F	M00055802:612	CH15CON
2357	14929	RTA22200014F.i.15.2.P.Seq	F	M00056986:611	CH16COP
2358	134702	RTA22200241F.n.23.1.P.Seq	F	M00026951:76	CH04MAL
2359	185649	RTA22200250F.g.08.1.P.Seq	F	M00027833:41	CH04MAL
2360	10702	RTA22200241F.b.05.1.P.Seq	F	M00026860:51	CH04MAL
2361	643955	RTA22200001F.k.21.1.P.Seq	F	M00042886:33	CH15CON
2362	643955	RTA22200004F.p.19.1.P.Seq	F	M00055841:29	CH15CON
2363	4455	RTA22200233F.o.08.1.P.Seq	F	M00021670:75	CH03MAH
2364	185567	RTA22200242F.c.16.1.P.Seq	F	M00026985:25	CH04MAL
2365	9115	RTA22200226F.e.04.1.P.Seq	F	M00005632:82	CH02COH
2366	14929	RTA22200015F.i.12.1.P.Seq	F	M00057100:59	CH16COP
2367	14929	RTA22200014F.i.15.1.P.Seq	F	M00056986:611	CH16COP
2368	4181	RTA22200244F.k.18.1.P.Seq	F	M00027203:88	CH04MAL
2369	5206	RTA22200238F.n.19.1.P.Seq	F	M00023002:710	CH03MAH
2370	825	RTA22200237F.c.05.1.P.Seq	F	M00022702:24	CH03MAH
2371	825	RTA22200238F.o.24.1.P.Seq	F	M00023020:79	CH03MAH
2372	825	RTA22200231F.d.09.1.P.Seq	F	M00007943:32	CH03MAH
2373	2748	RTA22200225F.d.18.1.P.Seq	F	M00005449:510	CH02COH
2374	2748	RTA22200238F.i.02.1.P.Seq	F	M00022934:23	CH03MAH
2375	2748	RTA22200225F.d.08.1.P.Seq	F	M00005445:12	CH02COH
2376	133512	RTA22200014F.a.15.2.P.Seq	F	M00056923:59	CH16COP

Table 1

[illegible]

Table 1
Page 45 of 45

Table 2B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)

SEQ ID	ACCESSION	DESCRIPTION1	P VALUE
63	3236249	(AC004684) hypothetical protein [Arabidopsis thaliana]	9.9
64	123111	H-2 CLASS II HISTOCOMPATIBILITY ANTIGEN, GAMMA CHAIN (HLA-DR ANTIGENS ASSOCIATED INVARIANT CHAIN) >gi 92086 pir S04362 class II histocompatibility antigen-associated gamma chain, long splice form - rat	9.7
65	94377	hypothetical protein 221 - turnip yellow mosaic virus	9.6
66	2736449	(AF039047) contains similarity to the BPTI/kunitz family of inhibitors [Caenorhabditis elegans]	9.5
67	543894	BETA-LACTAMASE PRECURSOR	8.2
68	3881525	(Z70038) cDNA EST EMBL:D32579 comes from this gene; cDNA EST EMBL:D35254 comes from this gene; cDNA EST yk224b3.5 comes from this gene; cDNA EST yk357f10.5 comes from this gene	7.6
69	3128358	(AF010496) ribose transport system permease protein RbsC	7.5
70	3875771	(Z68297) Weak similarity to Mouse DNA-binding protein BMI-1 (SW:BMI1_MOUSE); cDNA EST EMBL:C07407 comes from this gene; cDNA EST EMBL:C07408 comes from this gene	7.3
71	21293	(Y00759) 20 kDa protein (AA 1-212) [Spinacia oleracea]	7.3
72	2131007	(Z95890) pknE [Mycobacterium tuberculosis]	7.2
73	245923	(S83583) multiple-epitope polypeptide 1, MEP-1 construct]	7
74	115347	PROCOLLAGEN ALPHA 2(IV) CHAIN PRECURSOR >gi 84486 pir S16366 collagen alpha 2(IV) chain precursor - pig roundworm >gi 159649 (M67507) putative [Ascaris suum]	6.9
75	2072674	(Z95120) rhIE [Mycobacterium tuberculosis]	5.8
76	807646	(M17294) unknown protein [Human herpesvirus 4]	5.8
77	131706	URIDINE 5'-MONOPHOSPHATE SYNTHASE OROTIDINE 5'-PHOSPHATE DECARBOXYLASE	5.6
78	631593	glucose transport protein homolog - sheep	5
79	854064	(X83413) U87 [Human herpesvirus 6]	4.8
80	484695	vascular cell adhesion molecule 1 - human	4.2
81	1236146	(U49864) fus1 protein [Chlamydomonas reinhardtii]	3.8
82	1083846	acetyl-CoA carboxylase (EC 6.4.1.2) - Cyclotella cryptica >gi 409450 (L20784) acetyl-CoA carboxylase [Cyclotella cryptica]	3.5
83	2245054	(Z97342) protein kinase homolog	3.4
84	1717863	UBIQUITIN-CONJUGATING ENZYME E2-21.2 KD (UBIQUITIN-PROTEIN LIGASE) (UBIQUITIN CARRIER PROTEIN) >gi 1077331 pir S51438 probable membrane protein YLR306w -	3.4
85	1363331	transcription factor IIIC alpha chain - rat alpha-subunit [Rattus	3.4
86	2736327	(AF038615) No definition line found [Caenorhabditis elegans]	3.1
87	4587895	(AF072509) glutamate receptor interacting protein 2 [Rattus	3.1
88	1480746	(U62529) matrix metalloproteinase 3 [Equus caballus]	3
89	225858	thyroid/steroid receptor related gene [Homo sapiens]	3
90	3861293	(AJ235273) 3-OXOACYL-[ACYL-CARRIER-PROTEIN]	2.4
91	103812	hypothetical protein 1 - zebra fish	2
92	3256583	(AP000001) 361aa long hypothetical protein [Pyrococcus horikoshii]	1.7
93	1684985	(U20633) NADH dehydrogenase subunit [Neuwiedia veratrifolia]	1.5
94	452517	(D26361) KIAA0042 [Homo sapiens]	1.4
95	4218558	(AJ011500) gra-orf26 [Streptomyces violaceoruber]	1.1
96	4539280	(AL049498) putative transcription factor	0.28
97	4539280	(AL049498) putative transcription factor	0.26
98	3881842	(Z78201) Similarity to E.coli 2-oxoglutarate dehydrogenase (SW:ODO1_ECOLI); cDNA EST EMBL:D32590 comes from this gene; cDNA EST EMBL:D32841 comes from this gene; cDNA EST EMBL:D34051 comes from this gene; cDNA EST EMBL:D35268	4e-019
99	4102877	(AF017152) Shc binding protein [Mus musculus]	6e-050

Table 2B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)

SEQ ID	ACCESSION	DESCRIPTION1	P VALUE
100	3327062	(AB014524) KIAA0624 protein [Homo sapiens]	5e-050
102	3126979	(AF062483) SDP3 [Homo sapiens]	6.1
103	3930776	(AF099149) TRIAD1 type I [Homo sapiens]	9e-068
106	2708741	(AC003952) hypothetical protein [Arabidopsis thaliana]	3.6
107	733554	(U23450) similar to RNA-binding protein [Caenorhabditis elegans]	1e-014
108	3851703	(AF100421) p80 [Rattus norvegicus]	7e-055
112	2120729	GumG protein - Xanthomonas campestris	6
120	3334526	(AL021306) predicted using FGENEH [Homo sapiens]	7.7
121	2407956	(X87612) mono ATP-ribosyltransferase [Mus musculus]	5.9
122	3877701	(Z69662) predicted using Genefinder; similar to collagen; cDNA EST EMBL:D75049 comes from this gene; cDNA EST EMBL:D72067 comes from this gene; cDNA EST EMBL:D72223 comes from this gene; cDNA EST EMBL:D72768 comes from this	5.9
123	2117780	serine/threonine protein kinase - quail	3.5
124	1722738	MINOR CAPSID PROTEIN L2 >gi 1020224 type 36]	3.4
125	2494448	HYPOTHETICAL PROTEIN MJ0208 Methanococcus jannaschii >gi 1498983 (U67476) 4Fe-4S iron-sulfur protein [Methanococcus	3.4
126	2494294	NEUROGENIC LOCUS NOTCH 3 PROTEIN	3.4
127	4493971	(AL034559) predicted using hexExon; MAL3P7.11 (PFC0910w), Hypothetical protein, len: 430 aa	0.61
138	3025005	HYPOTHETICAL 28.8 KD PROTEIN IN MOAE-RHLE INTERGENIC REGION >gi 1787008 (AE000181) orf, hypothetical	9.8
139	3881856	(Z79759) Similarity to Yeast endosomal P24A protein (SW:EM70_YEAST); cDNA EST CEMSB40F comes from this gene; cDNA EST EMBL:C13538 comes from this gene; cDNA EST	9.6
140	1945493	(U56965) Similar to NAD(P) transhydrogenase, mitochondrial; coded for by C. elegans cDNA yk27c1.5; coded for by C. elegans cDNA yk35b9.5; coded for by C. elegans cDNA yk35b9.3; coded for by C. elegans cDNA yk161c9.3; coded for by C. elegans ...	5.6
141	3746071	(AC005311) putative GTP-binding protein [Arabidopsis thaliana]	5.6
142	2088843	(AF003386) F59E12.9 gene product [Caenorhabditis elegans]	3.2
143	1706551	GLUCAN ENDO-1,3-BETA-GLUCOSIDASE PRECURSOR ((1->3)-BETA-GLUCAN ENDOHYDROLASE) aestivum]	1.9
144	629778	chitinase (EC 3.2.1.14) - barley vulgare]	1.9
145	2791276	(Z95327) Cleavage Stimulation Factor sapiens]	0.85
146	736767	helper component protease [Turnip mosaic virus]	0.5
147	1731209	HYPOTHETICAL 35.4 KD PROTEIN CY20G9.19C >gi 1449291 emb CAB00954 (Z77162) hypothetical protein	0.22
148	3877063	(Z37092) F44F4.10 [Caenorhabditis elegans]	0.075
149	3878739	(Z73428) similar to Zinc finger, C3HC4 type (RING finger); cDNA EST EMBL:D67323 comes from this gene [Caenorhabditis elegans] >gi 3881096 emb CAB16481 finger); cDNA EST EMBL:D67323 comes from this gene	2e-029
159	4454483	(AC006234) putative kinase, 5' partial	9.1
160	3044086	(AF055904) unknown [Myxococcus xanthus]	5.4
161	1945493	(U56965) Similar to NAD(P) transhydrogenase, mitochondrial; coded for by C. elegans cDNA yk27c1.5; coded for by C. elegans cDNA yk35b9.5; coded for by C. elegans cDNA yk35b9.3; coded for by C. elegans cDNA yk161c9.3; coded for by C. elegans ...	5.4
162	730883	SYNAPTIC VESICLE PROTEIN 2 (SV2) norvegicus]	5.4
163	2351212	(D88386) gag-pol polyprotein (precursor protein) [Friend murine leukemia virus]	4.2
164	1722738	MINOR CAPSID PROTEIN L2 >gi 1020224 type 36]	3.2

Table 2B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)

SEQ ID	ACCESSION	DESCRIPTION1	P VALUE
165	4115922	(AF118222) contains similarity to ubiquitin carboxyl-terminal hydrolase family 2 (Pfam:PF00443, score=48.3, E=3.5e-13, N=2) and (Pfam:PF00442, Score=40.0 E=5.2e-08, N=1) [Arabidopsis]	2.4
166	1351639	VERY HYPOTHETICAL 52.7 KD PROTEIN C8A4.05C IN CHROMOSOME I >gi 2130446 pir S62521 hypothetical protein	2.4
167	4506857	small inducible cytokine subfamily D (Cys-X3-Cys), member 1 (fractalkine, neurotactin) >gi 1888523 (U84487) CX3C chemokine precursor [Homo sapiens] >gi 1899259 (U91835) CX3C chemokine	2.4
168	4505637	protocadherin 8; PCDH8 sapiens]	1.9
169	3249055	(AF071210) casein kinase II alpha subunit [Spodoptera frugiperda]	1.4
170	854065	(X83413) U88 [Human herpesvirus 6]	1e-005
171	854065	(X83413) U88 [Human herpesvirus 6]	1e-005
191	3150072	(AF046996) preS1 surface protein [woolly monkey hepatitis B Virus]	6.9
192	2622845	(AE000928) corrinoid/iron-sulfur protein, large subunit	6.9
193	1083554	tyrosine phosphoprotein SLP-76 - mouse	6.9
194	1708868	LOW-DENSITY LIPOPROTEIN RECEPTOR-RELATED PROTEIN PRECURSOR (LRP) Caenorhabditis elegans >gi 156360 (M96150) LDL receptor-related protein [Caenorhabditis elegans] Genefinder; Identity to C.elegans Low density lipid (LDL) receptor-	5.2
195	3169030	(AL023702) putative insertion element IS1647 transposase [Streptomyces coelicolor]	4
196	728835	!!!! ALU SUBFAMILY SC WARNING ENTRY	4
197	484695	vascular cell adhesion molecule 1 - human	3.9
198	2204102	(Y13898) glutathione-S-transferase	3.9
199	1118071	(U41554) coded for by C. elegans cDNA yk38a7.3; coded for by C. elegans cDNA yk8c6.3; coded for by C. elegans cDNA yk25d12.5; coded for by C. elegans cDNA yk25d12.3; coded for by C. elegans cDNA yk8c6.5; coded for by C. elegans cDNA yk7f8.5;...	2.3
200	799146	(U24495) 2a protein [Broad bean mottle virus]	1.4
201	73416	E2 protein - human papillomavirus type 18 papillomavirus type 18]	1.4
202	294529	(L14933) convertase PC5 [Rattus norvegicus]	0.45
203	124141	TRANS-ACTING TRANSCRIPTIONAL PROTEIN ICP4 (TRANSCRIPTIONAL ACTIVATOR IE175) (ALPHA-4 PROTEIN) human herpesvirus 1 >gi 59558 emb CAA32286 (X14112) RS1 RS1 [human herpesvirus 1] >gi 59849 emb CAA29763 1298) [human herpesvirus 1]	0.031
204	4503511	UNKNOWN >gi 3264861 (U97670) eukaryotic translation initiation factor eIF3, p35 subunit [Homo sapiens]	3e-010
205	4503511	UNKNOWN >gi 3264861 (U97670) eukaryotic translation initiation factor eIF3, p35 subunit [Homo sapiens]	3e-010
206	3298605	(AF057365) UDP N-acetylglucosamine transporter [Canis familiaris]	8e-033
221	3116148	(AL023290) putative ATP-dependent RNA helicase [Schizosaccharomyces pombe]	8.7
222	4544400	(AC007047) hypothetical protein [Arabidopsis thaliana]	8.7
223	1086982	E1 replication protein [bovine papillomavirus type 1 BPV-1, Peptide,	8.6
224	1762434	(U59924) nitric oxide synthase [Sus scrofa]	8.6
225	731689	HYPOTHETICAL 433.2 KD PROTEIN IN HXT5-NRK1 INTERGENIC REGION >gi 626646 pir S46715 hypothetical protein YHR099w - yeast (Saccharomyces cerevisiae) >gi 487929 (U00060)	8.5
226	2351132	(D85200) S glycoprotein [Brassica oleracea]	8.5
227	1762434	(U59924) nitric oxide synthase [Sus scrofa]	8.5
228	4493995	(AL034559) predicted using hexExon; MAL3P7.47 (PFC1080c), Hypothetical protein, len: 232 aa	6.7

Table 2B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)

SEQ ID	ACCESSION	DESCRIPTION1	P VALUE
229	462685	NUCLEOCAPSID PROTEIN coronavirus (strain K378) >gi 58850 emb CAA47246	5.2
230	4519268	(AB024314) CREA [<i>Aspergillus aculeatus</i>]	5
231	1364138	probable polymerase - soybean dwarf virus polymerase [Soybean]	5
232	1709938	ADENYLOSUCCINATE SYNTHETASE adenylosuccinate synthase (EC 6.3.4.4) - <i>Thiobacillus ferrooxidans</i> >gi 48168 emb CAA40593 (X57324) purA adenylosuccinate synthetase [<i>Thiobacillus</i> (AF000262) the second exon has similarity to collagen alpha in a glycine- and proline-rich region	3.8
233	1947132	(Z97342) protein kinase homolog	2.9
234	2245054	(Z97342) protein kinase homolog	2.9
235	2736517	(AF039052) contains similarity to helicases	1.7
236	1620170	(U42580) a499L [<i>Paramecium bursaria</i> Chlorella virus 1]	1.7
237	4336718	(AF104031) caudal-related homeobox protein	1.3
238	114969	BETA-GLUCOSIDASE A (GENTIOBIASE) 3.2.1.21) - <i>Caldocellum saccharolyticum</i> 1-455) [Caldicellulosiruptor	0.76
239	1170313	HOMEBOX PROTEIN CDX-1 (CAUDAL-TYPE HOMEBOX PROTEIN 1) >gi 1083361 pir A49303 homeotic protein Cdx-1 - (U44834) polyphosphate glucokinase [<i>Mycobacterium tuberculosis</i>] >gi 1588398 prf 2208389A phosphate glucokinase [<i>Mycobacterium</i>	0.44
258	1172222	(AJ002303) synaptogyrin 1c [<i>Homo sapiens</i>]	8.4
259	2959862	(AJ002303) synaptogyrin 1c [<i>Homo sapiens</i>]	8.1
260	2983552	(AE000721) cation efflux system (czcD-like) [<i>Aquifex aeolicus</i>]	8
261	104800	nicotinic acetylcholine receptor alpha-5 chain precursor - chicken (Z78013) predicted using Genefinder; cDNA EST EMBL:D72806 comes from this gene; cDNA EST EMBL:D75743 comes from this gene; cDNA EST yk417b6.3 comes from this gene; cDNA EST yk417b6.5 comes from this gene; cDNA EST yk276c6.3 com...	4.8
262	3875957	(U23511) No definition line found [<i>Caenorhabditis elegans</i>]	4.7
263	746475	(U90333) aquarius gene product [<i>Mus musculus</i>]	2.8
264	1899232	(U90333) aquarius gene product [<i>Mus musculus</i>]	2.8
265	3123186	AFLATOXIN BIOSYNTHESIS REGULATORY PROTEIN NUCLEOLYSIN TIAR (TIA-1 RELATED PROTEIN) >gi 1592563 (U55861) RNA binding protein TIAR	2.8
266	2500589	(U55861) RNA binding protein TIAR	2.8
267	90253	leukocyte common antigen precursor - mouse musculus]	1.7
268	2827553	(AL021635) predicted protein [<i>Arabidopsis thaliana</i>]	1.6
269	3695397	(AF096372) No definition line found [<i>Arabidopsis thaliana</i>]	0.42
270	2564330	(AB006629) KIAA0291 [<i>Homo sapiens</i>]	8e-006
271	3413860	(AB007918) KIAA0449 protein [<i>Homo sapiens</i>]	3e-009
272	4454698	(AF070661) HSPC005 [<i>Homo sapiens</i>]	1e-010
289	266328	PROBABLE PROCESSING AND TRANSPORT PROTEIN (INFECTED CELL PROTEIN 18.5) murine cytomegalovirus (strain	6
290	2204102	(Y13898) glutathione-S-transferase	3.5
291	2887280	(AJ002140) DNA	3.5
292	4567223	(AC007119) hypothetical protein	3.1
303	2077849	(AB003348) E1 protein [Rubella virus]	9.9
304	845311	(L40021) polyprotein [Feline calicivirus]	7.3
305	266328	PROBABLE PROCESSING AND TRANSPORT PROTEIN (INFECTED CELL PROTEIN 18.5) murine cytomegalovirus (strain	5.6
306	103469	homeotic protein bicoid - fruit fly pseudoobscura]	5.6
307	2204102	(Y13898) glutathione-S-transferase	3.3
308	125394	HOMOSERINE KINASE (HK) <i>Pseudomonas aeruginosa</i> >gi 45425 emb CAA46169 (X65034) homoserine kinase [<i>Pseudomonas aeruginosa</i>]	3.3
309	2353163	(AF015560) RO11 [<i>Neurospora crassa</i>]	0.66
310	484695	vascular cell adhesion molecule 1 - human	0.64

Table 2B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)

SEQ ID	ACCESSION	DESCRIPTION1	P VALUE
311	3874146	(Z72502) Similarity with proline-rich proteoglycan (PIR accession number B48013); cDNA EST EMBL:D66054 comes from this gene; cDNA EST EMBL:D69700 comes from this gene; cDNA EST yk446b10.3 comes from this gene; cDNA EST yk446b10...	0.52
312	117589	CIRCUMSPOROZOITE PROTEIN PRECURSOR precursor - Plasmodium knowlesi (strain Nuri) >gi 160198	9e-005
313	2781381	(AC004013) Similar to rabbit A-kinase-anchoring protein sapiens]	1e-019
317	730269	PAN1 PROTEIN >gi 626783 pir S48440 poly(A)-specific ribonuclease (EC 3.1.13.4) - yeast PAN1_YEAST P32521 PAB-DEPENDENT POLY(A)-SPECIFIC RIBONUCLEASE but	7.2
318	3201610	(AC004669) unknown protein [Arabidopsis thaliana]	5.4
319	3129975	(AL023516) Complement C4 [Gallus gallus]	2.4
322	1850592	(U88295) carnitine palmitoyltransferase II [Rattus norvegicus]	6.9
323	3881650	(Z70757) Weak similarity to the XFIN protein (Swiss Prot accession number P08045)	6.6
324	2653998	(AF032884) tnsC [Thiobacillus ferrooxidans]	8.2
326	145111	(M18083) periplasmic [NiFe]hydrogenase protein small subunit precursor [Desulfovibrio gigas]	0.37
327	2244839	(Z97337) hypothetical protein [Arabidopsis thaliana]	3.1
328	3935180	(AC004557) F17L21.23 [Arabidopsis thaliana]	4.6
332	3328899	(AE001320) hypothetical protein [Chlamydia trachomatis]	7.4
333	4096264	(U26528) Ig heavy chain [Oryctolagus cuniculus]	7.1
334	3023209	168 KD SURFACE-LAYER PROTEIN PRECURSOR [CONTAINS: 120 KD SURFACE-EXPOSED PROTEIN MEMBRANE PROTEIN OMPB]; 32 KD BETA PEPTIDE] precursor - Rickettsia typhi >gi 1871223 (L04661) crystalline surface	5.8
335	4589400	(AB009958) polypeptide [satsuma dwarf virus]	5.7
336	1709356	SODIUM-DEPENDENT NORADRENALINE TRANSPORTER (NOREPINEPHRINE TRANSPORTER) (NET) bovine >gi 1050439 emb CAA55645 (X79015) norepinephrine transporter	5.4
337	4512671	(AC006931) unknown protein [Arabidopsis thaliana]	1.9
343	3757516	(AC005167) putative TMV resistance protein [Arabidopsis thaliana]	3.8
344	586480	HYPOTHETICAL 62.6 KD PROTEIN IN CDS1-RPL2 INTERGENIC REGION >gi 626496 pir S45886 hypothetical protein YBR030w - yeast (Saccharomyces cerevisiae)	0.26
345	423981	88K E-26-specific domain protein Pok - Drosophila >gi 217342 dbj BAA01080 (D10228) Ets domain protein	0.054
347	1653153	(D90911) acriflavin resistance protein	5.5
348	2147342	E4 protein - human papillomavirus type 14D	0.67
349	3914412	GENOME POLYPROTEIN [CONTAINS: N-TERMINAL PROTEIN (P1); HELPER COMPONENT PROTEINASE INCLUSION PROTEIN (CI); 6 KD PROTEIN 2 (6K2); GENOME-LINKED PROTEIN (VPG); NUCLEA... mosaic virus]	0.95
350	2997741	(AF054838) tetraspan TM4SF; Tspan-1 [Homo sapiens]	1e-017
351	1086900	(U41278) contains similarity to G beta repeats	3e-027
372	129036	2-OXOGLUTARATE DEHYDROGENASE E1 COMPONENT (ALPHA-KETOGLUTARATE DEHYDROGENASE) dehydrogenase [Azotobacter vinelandii]	9.8
373	2120777	cellulose synthase - Agrobacterium tumefaciens >gi 710493 (L38609) cellulose synthase celA gene [Agrobacterium tumefaciens]	9.7
374	628527	hypothetical protein - Pseudomonas syringae syringae]	9.6
375	123395	HOMEBOX PROTEIN NK-1 (S59/2) fly (Drosophila melanogaster) >gi 8531 emb CAA39067 sp.]	7.8
376	3722000	(AF035323) survival motor neuron protein	7.8

Table 2B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)

SEQ ID	ACCESSION	DESCRIPTION1	P VALUE
377	3881030	(AL021493) Y51A2B.2 [Caenorhabditis elegans]	7.4
378	4505777	PHD finger protein 1 >gi 2660720 1) [Homo sapiens]	6
379	2190501	(X53706) immunoglobulin alpha-2 heavy chain [Pan troglodytes]	5.8
380	2688643	(AE001171) conserved hypothetical integral membrane protein [Borrelia burgdorferi]	5.7
381	1086832	(U41264) coded for by C. elegans cDNA cm13g1; Similar to bumetanide-sensitive Na-K-Cl cotransporter.	5.4
382	1931639	(U95973) lysophospholipase isolog [Arabidopsis thaliana]	4.6
383	3757516	(AC005167) putative TMV resistance protein [Arabidopsis thaliana]	4.5
384	4504567	interferon consensus sequence binding protein 1 >gi 2275153 (M91196) DNA-binding protein [Homo sapiens]	4.4
385	464822	SUR1 PROTEIN >gi 542362 pir S41798 SUR1 protein - yeast (Saccharomyces cerevisiae) cerevisiae >gi 976268 dbj BAA05628	4.4
386	3023738	EXOSTOSIN-L (MULTIPLE EXOSTOSIS-LIKE PROTEIN) >gi 1524413 (U67191) multiple exostosis-like protein [Homo]	4.3
387	3878603	(Z83116) M01B2.3 [Caenorhabditis elegans]	3.4
388	3745858	(L33180) BRO-a [Bombyx mori nuclear polyhedrosis virus]	3.3
389	4321758	(AF060669) polyprotein [Hepatitis E virus]	3.3
390	2661037	(AF035285) dihydroxyacetone phosphate acyltransferase	3.3
391	2950355	(AJ223300) homebox protein DRx [Drosophila melanogaster]	2.7
392	3821973	(AF061140) merozoite surface protein 1 [Plasmodium falciparum]	2.5
393	1552187	(D84375) ORF3 [Oryzias latipes]	2
394	2493417	S100 CALCIUM-BINDING PROTEIN A13 calcium-binding protein A13 [Mus musculus]	1.6
395	3550082	(AF071186) WW domain binding protein 11 [Mus musculus]	1.5
396	1082665	oligodendrocyte-specific proline-rich protein 2 - human >gi 1408050 dbj BAA05660 (D28114) MOBP [Homo sapiens]	1.5
397	3874925	(Z68296) Similarity to Mouse A-RAF proto-oncogene serine/threonine-protein kinase gene; cDNA EST EMBL:T01018 comes from this gene; cDNA EST EMBL:D33256 comes from this PROBABLE SIGNAL RECOGNITION 54 KD PROTEIN (SRP54) >gi 2129283 pir E64312 signal recognition particle protein -	1.2
398	2500886	Methanococcus jannaschii subunit SRP54 [Methanococcus (AF016428) contains similarity to Vaccinia virus 37 kd envelope protein [Caenorhabditis elegans]	1.2
399	2291241	(L06798) class D tetracycline/H+ antiporter [Plasmid pRA1] >gi 575937 dbj BAA03719 (D16172) PP-TETA protein	1.1
400	309958	(Z46267) F49E2.2 [Caenorhabditis elegans]	0.91
401	3877379	(AL049498) putative transcription factor	0.39
402	4539280	(U96413) putative opine synthase [Agrobacterium tumefaciens]	0.29
403	3293235	(AF078786) No definition line found [Caenorhabditis elegans]	0.097
404	3329636	(AL023828) cDNA EST yk491f8.5 comes from this gene [Caenorhabditis elegans]	0.003
405	3947614	(AL023828) cDNA EST yk491f8.5 comes from this gene [Caenorhabditis elegans]	8e-019
406	3947614	(AL023828) cDNA EST yk491f8.5 comes from this gene [Caenorhabditis elegans]	1e-019
407	3880930	(AL021481) similar to Phosphoglucosyltransferase and phosphomannomutase phosphoserine; cDNA EST EMBL:D36168 comes from this gene; cDNA EST EMBL:D70697 comes from this gene; cDNA EST yk373h9.5 comes from this gene; cDNA EST	1e-022
408	3184082	(AL023781) N-terminal acetyltransferase 1 PUTATIVE RIBONUCLEASE III (RNASE III)	1e-028
409	2500558	>gi 3876420 emb CAB03005 (Z81070) similar to ribonuclease	7e-030

Table 2B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)

SEQ ID	ACCESSION	DESCRIPTION1	P VALUE
410	3877493	(Z48583) similar to ATPases associated with various cellular activities (AAA); cDNA EST EMBL:Z14623 comes from this gene; cDNA EST EMBL:D75090 comes from this gene; cDNA EST EMBL:D72255 comes from this gene; cDNA EST yk200e4.5 ...	5e-044
411	3298605	(AF057365) UDP N-acetylglucosamine transporter [Canis familiaris]	1e-051
412	4103604	(AF026031) putative mitochondrial outer membrane protein import receptor [Homo sapiens]	1e-059
413	2662165	(AB007902) HH0712 cDNA clone for KIAA0442 has a 574-bp insertion at position 1474 of the sequence of KIAA0442. [Homo	4e-070
414	3882145	(AB018255) KIAA0712 protein [Homo sapiens]	9e-072
477	117552	CHAPERONE PROTEIN CS3-1 PRECURSOR Escherichia coli >gi 41156 emb CAA34815 (X16944) 27kD protein (AA 1 to 241) [Escherichia coli]	9.3
478	2983622	(AE000726) hypothetical protein [Aquifex aeolicus]	9.3
479	2088694	(AF003135) W03F11.1 gene product [Caenorhabditis elegans]	9.3
480	4240237	(AB020681) KIAA0874 protein [Homo sapiens]	9.2
481	1864073	(U63002) T-cell receptor beta chain [Callithrix jacchus]	9
482	2147334	DNA helicase II 70K chain homolog - Rhipicephalus appendiculatus >gi 1063592 (L41356) ku autoantigen p70 homologue [Rhipicephalus appendiculatus]	8.9
483	3323145	(AE001253) T. pallidum predicted coding region TP0827	8.7
484	2183251	(AF002227) putative polyprotein [border disease virus strain C413]	8.6
485	3875768	(Z92830) cDNA EST yk223c7.5 comes from this gene; cDNA EST yk307b2.5 comes from this gene; cDNA EST yk377h2.5 comes from this gene; cDNA EST yk223c7.3 comes from this gene; cDNA EST yk307b2.3 comes from this gene [Caenorhabditis...]	8.6
486	1351589	HYPOTHETICAL PROTEIN MG456 Mycoplasma genitalium (SGC3) >gi 1046175 (U39732) M. genitalium predicted coding region MG456 [Mycoplasma genitalium] >gi 3845050 (U39727) conserved hypothetical protein [Mycoplasma genitalium]	8.4
487	3023800	GLUCOSE-6-PHOSPHATASE (G6PASE) familiaris]	6.9
488	450722	(X71982) ORF j11R [African swine fever virus]	6.8
489	2633756	(Z99111) similar to heavy metal-transporting ATPase [Bacillus	6.6
490	4049887	(AF063866) ORF MSV024 ALI motif gene family protein	6.5
491	1363994	abdominal-A homeodomain protein - Junonia coenia >gi 797277 (L41931) abdominal-A homeodomain protein [Junonia coenia]	5.3
492	2370493	(Z98944) hypothetical protein	5.3
493	140631	HYPOTHETICAL 25.9 KD PROTEIN FP25.9 [Fowlpox virus]	5.3
494	400927	RIBONUCLEOPROTEIN RB97D ribonucleoprotein [Drosophila	5.1
495	2462935	(Y12321) open reading frame 1 [Brassica oleracea]	5
496	2160189	(AC000132) Similar to A. thaliana receptor-like protein kinase (gb RLK5_ARATH). ESTs gb ATTS0475,gb ATTS4362 come from this gene. [Arabidopsis thaliana]	5
497	1850972	(U84144) putative fimbrial chaperone [Escherichia coli]	4.9
498	2145678	B1549 C3 230 protein - Mycobacterium leprae	4.2
499	3182952	CGMP-INHIBITED 3',5'-CYCLIC PHOSPHODIESTERASE A (CYCLIC GMP INHIBITED PHOSPHODIESTERASE A) (CGI-PDE A) >gi 1145304 (U38179) cyclic nucleotide phosphodiesterase	4.2
500	4493738	(AL034358) predicted using hexExon; L4830.1, Hypothetical protein, len: 1107 [Leishmania major]	4.2
501	730336	PUTATIVE POLYKETIDE SYNTHASE PKSL 2.3.1.-) - Bacillus subtilis >gi 40058 emb CAA78479 subtilis] >gi 528996 (U11039) polyketide synthase polyketide synthase of type I [Bacillus subtilis]	4.2
502	188908	(M19720) L-myc protein [Homo sapiens]	4

Table 2B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)

SEQ ID	ACCESSION	DESCRIPTION1	P VALUE
503	4056436	(AC005990) EST gb AA650912 comes from this gene.	3.9
504	3874349	(Z81035) predicted using Genefinder; Similarity to Sheep vasopressin V1A receptor (SW:P48043)	3.9
505	3874067	(Z93374) similar to 7TM receptor elegans]	3.9
506	3979818	(Z49967) cDNA EST EMBL:T00743 comes from this gene; cDNA EST EMBL:D69356 comes from this gene; cDNA EST EMBL:D65790 comes from this gene; cDNA EST EMBL:D70463 comes from this gene; cDNA EST EMBL:D66620 comes from this	3.2
507	119462	ENVELOPE POLYPROTEIN GP160 PRECURSOR 2]	3.2
508	117657	>gi 225570 prf 1306388H gene env [Human immunodeficiency virus COLICIN V PRODUCTION PROTEIN (DEDE PROTEIN) (PUR REGULON 18 KD PROTEIN) colicin V production [Escherichia coli] dedE protein [Escherichia coli]	3.1
509	114441	ATP SYNTHASE A CHAIN (PROTEIN 6) 3.6.1.34) protein 6 - fruit fly (Drosophila yakuba) mitochondrion (SGC4)	3
510	1280094	>gi 12921 emb CAA25442 (X00924) ATPase subunit 6 [Drosophila (U55369) No definition line found [Caenorhabditis elegans]	3
511	226131	thyroid hormone receptor alpha 2 [Rattus norvegicus]	3
512	3860855	(AJ235271) GUANOSINE PENTAPHOSPHATE PHOSPHOHYDROLASE (gppA) [Rickettsia prowazekii]	2.9
513	584834	CELLULOSE SYNTHASE OPERON C PROTEIN xylinus]	2.4
514	629777	>gi 1090660 prf 2019362C acsC gene	2.2
515	2555183	chitinase (EC 3.2.1.14) - barley vulgare]	2.2
516	4503737	(AF026504) SPA-1 like protein p1294 [Rattus norvegicus] forkhead (Drosophila) homolog 1 HEAD DOMAIN PROTEIN FKHR >gi 631145 pir S40521 FKHR protein - human >gi 435423 (U02310) fork head domain protein [Homo sapiens]	1.8
517	3790719	>gi 737918 prf 1923399A FKHR gene [Homo sapiens]	1.8
518	1785942	(AF099916) contains similarity to C2H2-type zinc fingers	1.8
519	3877036	(U83412) CAG [Drosophila melanogaster]	1.4
520	281654	(Z81079) predicted using Genefinder; similar to collagen; cDNA EST EMBL:M88890 comes from this gene; cDNA EST EMBL:Z14325 comes from this gene; cDNA EST EMBL:D27520 comes from this gene; cDNA EST EMBL:D72240 comes from this	1.3
521	114972	hypothetical protein 24 - Agrobacterium tumefaciens plasmid pTi15955 >gi 39086 emb CAA25186 tumefaciens]	1.3
522	1707085	BETA-GLUCOSIDASE (GENTIOBIASE) Ruminococcus albus >gi 45968 emb CAA33461 (X15415) beta-glucosidase (AA 1 - 947) [Ruminococcus albus] albus]	1.3
523	483163	(U80451) Similar to collagen [Caenorhabditis elegans]	1.3
524	4455275	nonstructural protein - hepatitis E virus RNA-directed RNA polymerase [Hepatitis E virus]	0.99
525	4376875	(AL035527) putative protein [Arabidopsis thaliana]	0.45
526	2494911	(AE001642) CT465 hypothetical protein	0.44
527	4539280	HYPOTHETICAL PROTEIN KIAA0124 product is novel. [Homo	0.28
528	1842255	(AL049498) putative transcription factor	0.28
529	231977	(U74613) hepatocyte nuclear factor-3/fork head homolog 11B [Homo	0.073
530	987050	D(4) DOPAMINE RECEPTOR (D(2C) DOPAMINE RECEPTOR) >gi 203916 (M84009) dopamine receptor D4	0.042
531	2493416	(X65335) lacZ [Cloning vector pSV-beta-Galactosidase Control]	0.031
532	1778844	S100 CALCIUM-BINDING PROTEIN A13 calcium-binding protein A13 (S100A13) [Homo sapiens]	0.0006
533	3288470	(U83086) LimA [Dictyostelium discoideum]	5e-015
		(AJ224360) surf5c [Homo sapiens]	

Table 2B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)

SEQ ID	ACCESSION	DESCRIPTION1	P VALUE
534	3947614	(AL023828) cDNA EST yk491f8.5 comes from this gene [Caenorhabditis elegans]	1e-015
535	1086860	(U41272) Similar to man(9)-alpha-mannosidase.	3e-028
536	3875451	(Z66496) cDNA EST EMBL:D71941 comes from this gene; cDNA EST EMBL:D74691 comes from this gene; cDNA EST EMBL:D76330 comes from this gene; cDNA EST EMBL:D65192 comes from this gene; cDNA EST EMBL:D68540 comes from this	2e-030
537	3877493	(Z48583) similar to ATPases associated with various cellular activities (AAA); cDNA EST EMBL:Z14623 comes from this gene; cDNA EST EMBL:D75090 comes from this gene; cDNA EST EMBL:D72255 comes from this gene; cDNA EST yk200e4.5 ...	1e-035
538	3169010	(AJ006412) putative GTP-binding protein	2e-042
539	3877493	(Z48583) similar to ATPases associated with various cellular activities (AAA); cDNA EST EMBL:Z14623 comes from this gene; cDNA EST EMBL:D75090 comes from this gene; cDNA EST EMBL:D72255 comes from this gene; cDNA EST yk200e4.5 ...	4e-044
540	3877493	(Z48583) similar to ATPases associated with various cellular activities (AAA); cDNA EST EMBL:Z14623 comes from this gene; cDNA EST EMBL:D75090 comes from this gene; cDNA EST EMBL:D72255 comes from this gene; cDNA EST yk200e4.5 ...	3e-044
608	3882189	(AB018277) KIAA0734 protein [Homo sapiens]	9.9
609	3877937	(Z48716) similarity to a transmembranous region of ubiquinol-cytochrome-C reductase (PIR accession number S38960); cDNA EST EMBL:T00461 comes from this gene; cDNA EST EMBL:D27071 comes from this gene; cDNA EST EMBL:D27070	9.6
610	3643019	(AF064703) glucose transporter 1; CeGT1 [Drosophila	8.4
611	3219946	HYPOTHETICAL PROTEIN MJ1394 Methanococcus jannaschii >gi 1592041 (U67579) conserved hypothetical protein	8
612	3219946	HYPOTHETICAL PROTEIN MJ1394 Methanococcus jannaschii >gi 1592041 (U67579) conserved hypothetical protein	8
613	2833328	FIBRILLARIN	7.9
614	4505481	nucleoporin 88kD complex protein [Homo sapiens]	7.8
615	220578	(D00570) open reading frame (251 AA) [Mus musculus]	7.8
616	266810	NAD(P) TRANSHYDROGENASE SUBUNIT BETA transhydrogenase [Escherichia coli] transhydrogenase (B-specific) (EC 1.6.1.1) b chain NAD(P)+ transhydrogenase (B-specific) (EC 1.6.1.1) b chain [Escherichia coli] >gi 1787886 (AE000255) pyridine	7.6
617	807646	(M17294) unknown protein [Human herpesvirus 4]	7.6
618	829186	(X03879) rudimentary protein fragment	7.4
619	4322346	(AF081825) sodium-dependent high-affinity dicarboxylate transporter [Rattus norvegicus]	7.4
620	3334785	(AL031107) hypothetical protein SC5A7.04c	7.4
621	1346720	PHOSPHATIDYLINOSITOL-4-PHOSPHATE 5-KINASE TYPE II ALPHA (PIP5KII-ALPHA) KINASE) >gi 1079474 pir A55967 1-phosphatidylinositol-4-phosphate 5-kinase (EC 2.7.1.68) - human >gi 758697 (U14957) 53K isoform of Type II phosphatidylinositol-4-	7.3
622	4105819	(AF050175) Rab7 [Homo sapiens]	6.4
623	155865	(M93125) 80 kDa protein [Babesia bovis]	6.3
624	2133638	boule protein - fruit fly (Drosophila melanogaster) >gi 1395211 (U51858) boule protein	6.2
625	1788052	(AE000270) putative transport system permease protein	6.2
626	3875616	(Z77657) F08H9.9 [Caenorhabditis elegans]	6.2
627	2499150	HYPOTHETICAL PROTEIN IN CPS REGION	6.2

Table 2B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)

SEQ ID	ACCESSION	DESCRIPTION1	P VALUE
628	1170758	GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35)	6.1
629	2495335	HEAT SHOCK PROTEIN 42 (42 KD HEAT SHOCK PROTEIN) >gi 1077219 pir S49767 heat shock protein HSP42 - yeast (<i>Saccharomyces cerevisiae</i>)	6
630	1086677	(U41020) coded for by <i>C. elegans</i> cDNA yk64f5.3; coded for by <i>C. elegans</i> cDNA yk64f5.5; Similar to zinc finger. [<i>Caenorhabditis</i>	6
631	1170758	GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35)	6
632	440957	Achaete-Scute homolog Mash-1 gene product	6
633	1786037	(U72284) NADH dehydrogenase subunit 2 [<i>Apis mellifera</i>]	6
634	2495335	HEAT SHOCK PROTEIN 42 (42 KD HEAT SHOCK PROTEIN) >gi 1077219 pir S49767 heat shock protein HSP42 - yeast (<i>Saccharomyces cerevisiae</i>)	6
635	2662541	(AF036687) contains similarity to protease inhibitors, WAP-type four-disulfide core domains and thyroglobulin type-1 repeats	5.7
636	118249	DAUGHTERLESS PROTEIN fly (<i>Drosophila melanogaster</i>) >gi 7839 emb CAA68368 melanogaster] >gi 157174 (J03148) daughterless protein	5.6
637	2447066	(U42580) A570L [<i>Paramecium bursaria</i> Chlorella virus 1]	5.6
638	400927	RIBONUCLEOPROTEIN RB97D ribonucleoprotein [<i>Drosophila</i>	4.9
639	121189	GLUCOSE INHIBITED DIVISION PROTEIN A gidA (AC004238) putative phosphoribosylaminoimidazolecarboxamide formyltransferase [<i>Arabidopsis thaliana</i>]	4.8
640	3033398	POSSIBLE MALTASE PRECURSOR (LARVAL VISCERAL PROTEIN D) >gi 103222 pir S08597 hypothetical protein D - fruit fly (<i>Drosophila melanogaster</i>) melanogaster]	4.6
641	126691	RETROTRANSPOSABLE ELEMENT SLACS 132 KD PROTEIN (ORF2) >gi 84054 pir S14916 hypothetical protein 2 - <i>Trypanosoma brucei</i> gambiense transposon SLACS >gi 10535 emb CAA34931	4.5
642	134087	(L03172) This CDS feature is included to show the translation of the corresponding V_region. Presently translation qualifiers on V_region features are illegal.	4.3
643	567166	(Z14126) RhoNUC protein [<i>Saccharomyces cerevisiae</i>]	3.7
644	4355	MYOSIN IB HEAVY CHAIN heavy chain [<i>Dictyostelium</i>	3.7
645	462679	(U41508) similar to <i>C. elegans</i> proteins C26E6.9A and C26E6.9B; weakly similar to malate synthase G	3.6
646	1098989	(AF018261) EH domain binding protein Epsin [<i>Rattus norvegicus</i>]	2.1
647	3249559	(AF026212) No definition line found [<i>Caenorhabditis elegans</i>]	2
648	2435594	(U32240) Ig heavy chain [<i>Mus musculus</i>]	2
649	995808	(AL031004) putative protein [<i>Arabidopsis thaliana</i>]	1.8
650	3281870	!!!! ALU SUBFAMILY SQ WARNING ENTRY	1.6
651	728837	(Y08775) Men-3 [<i>Silene latifolia</i>]	1.2
652	1628461	hypothetical protein - Marek's disease virus gammaherpesvirus tumorigenicity associated mRNA, two complete cds's.], gene products [Gallid herpesvirus type 1] >gi 299459 bbs 129316 (S58431) CD4 precursor homolog to CD4 and IgM heavy chain [Gallid herpesvir	0.93
653	483165	hypothetical protein - Marek's disease virus gammaherpesvirus tumorigenicity associated mRNA, two complete cds's.], gene products [Gallid herpesvirus type 1] >gi 299459 bbs 129316 (S58431) CD4 precursor homolog to CD4 and IgM heavy chain [Gallid herpesvir	0.87
654	483165	RECOMBINASE FLP PROTEIN	0.71
655	120359		

Table 2B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)

SEQ ID	ACCESSION	DESCRIPTION1	P VALUE
656	1711563	STERYL-SULFATASE PRECURSOR (STEROID SULFATASE) (STERYL-SULFATE SULFOHYDROLASE) sulfatase [Mus	0.55
657	731849	HYPOTHETICAL 13.5 KD PROTEIN IN MOB1-SGA1 INTERGENIC REGION >gi 626376 pir S48473 probable membrane protein YIL100w - yeast (Saccharomyces cerevisiae) >gi 558707 emb CAA86281 (Z38125) orf, len: 117, CAI: 0.08, better	0.55
658	1669674	(X86819) Microtubule-associated protein 4	0.3
659	2493735	SKD3 PROTEIN SKD3 [Mus musculus]	0.25
660	110030	homeotic protein Hox 5.1 - mouse	0.19
661	1947160	(AF000298) weak similarity to collagens; glycine- and proline-rich [Caenorhabditis elegans]	0.012
662	4567275	(AC006841) hypothetical protein [Arabidopsis thaliana]	0.005
663	2677676	(AC002467) DRA protein (down-regulated in adenoma); sulfate transporter; match to P40879 (PID:g729367) [Homo sapiens]	4e-056
671	345474	hypothetical protein 2 - Mediterranean fruit fly >gi 5977 emb CAA49660 (X70053) unknown [Ceratitis capitata]	9.4
672	4538951	(AL049488) putative protein [Arabidopsis thaliana]	9.1
673	1749646	(D89219) unnamed protein product	7
674	320302	ORF X protein - human papillomavirus type 41	5.5
675	267288	REPLICATION PROTEIN E1 papillomavirus (type 1) >gi 61013 emb CAA44657 (X62844) E1 [Pygmy chimpanzee	5.4
676	3581899	(AL031543) hypothetical serine-rich protein [Schizosaccharomyces	4.2
677	3881119	(AL032653) predicted using Genefinder; cDNA EST EMBL:D36367 comes from this gene; cDNA EST yk408c12.5 comes from this gene [Caenorhabditis elegans]	4.2
678	1169663	TRANSCRIPTIONAL ACTIVATOR FE65 APP interacting protein [Rattus rattus]	4
679	1565257	(X57108) cerebroside sulfate activator	3.2
680	3093358	(AJ005559) SPR2A protein [Mus musculus]	1.1
681	1763113	(U71019) NADH dehydrogenase subunit F [Arrhenatherum elatius]	0.6
682	3548791	(AC005620) R33590_1 [Homo sapiens]	0.46
683	4567275	(AC006841) hypothetical protein [Arabidopsis thaliana]	0.025
684	3882311	(AB018338) KIAA0795 protein [Homo sapiens]	7e-017
687	2443342	(D88764) alpha 2 type I collagen [Rana catesbeiana]	5.1
688	220464	(D00232) E3 anti-[4-hydroxy-3-nitrophenyl(phenolate + phenolic form)] acetyl mAb V-L region [Mus musculus]	6.4
689	1351502	HYPOTHETICAL PROTEIN MG181 Mycoplasma genitalium (SGC3) >gi 3844777 (U39697) conserved hypothetical protein	2.1
693	250891	(S39392) protein tyrosine phosphatase, PTPase	4.6
695	3323042	(AE001245) sugar ABC transporter, periplasmic binding protein (msmE) [Treponema pallidum]	5.8
696	1001741	(D64004) hypothetical protein	2.7
697	1169288	DIHYDROXYACETONE KINASE (GLYCERONE KINASE) >gi 493083 (U09771) dihydroxyacetone kinase	3e-010
698	1169288	DIHYDROXYACETONE KINASE (GLYCERONE KINASE) >gi 493083 (U09771) dihydroxyacetone kinase	3e-010
699	3879530	(Z49130) cDNA EST yk486b9.3 comes from this gene; cDNA EST yk486b9.5 comes from this gene	7e-005
700	2191127	(AF007269) A_IG002N01.1 gene product [Arabidopsis thaliana]	0.0004
701	4504923	keratin, hair, acidic, 2 type I intermediate filament [Homo sapiens]	1.5
702	2633756	(Z99111) similar to heavy metal-transporting ATPase [Bacillus	7.4
703	3876796	(Z81531) F36D3.6 [Caenorhabditis elegans]	7.3
705	123299	HOMEODOMAIN PROTEIN HOX-D4 (HOX-4B) protein Hox D4 - human >gi 296652 emb CAA35237 (X17360) hox 5.1 protein [Homo	2.4

Table 2B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)

SEQ ID	ACCESSION	DESCRIPTION1	P VALUE
706	99899	DNA-directed RNA polymerase (EC 2.7.7.6) largest chain (isoform C) - soybean (fragment) polymerase [Glycine max]	0.83
707	4263788	(AC006068) hypothetical protein	0.28
708	500858	(D14168) 50kDa lectin [Bombyx mori]	4e-011
711	142283	(M30318) put. periplasmic receptor protein (chvE); putative [Agrobacterium tumefaciens]	9.2
712	4502949	collagen, type II, alpha 1 congenital >gi 115287 sp P02458 CA12_HUMAN PROCOLLAGEN ALPHA 1(II) CHAIN PRECURSOR [CONTAINS: CHONDROCALCIN] 1-	6.9
713	4539163	(AL049485) putative phytoene synthase	0.81
715	4056437	(AC005990) Strong similarity to PFAM PF00069 Eukaryotic protein kinase domain. [Arabidopsis thaliana]	2.3
716	119296	ELASTIN PRECURSOR (TROPOELASTIN) gallus]	1.3
717	4226073	(AF125443) contains similarity to S. pombe phosphatidyl synthase (GB:Z28295) [Caenorhabditis elegans]	8e-016
719	2498761	PEROXISOMAL MEMBRANE PROTEIN PMP30A protein - yeast (Candida boidinii) >gi 457391 (L27999) peroxisomal membrane protein 31 [Candida boidinii]	1.3
720	3914963	SECRETORY CARRIER-ASSOCIATED MEMBRANE PROTEIN 3 >gi 2232237 (AF005036) secretory carrier membrane protein [Mus	0.58
721	4457204	(AF108226) immunoglobulin mu heavy chain precursor [Monodelphis domestica]	0.15
722	3860573	(AJ235270) unknown [Rickettsia prowazekii]	4.9
723	2829912	(AC002291) Similar ATP-dependent RNA Helicase	0.0002
724	2130573	(U96771) putative polygalacturonase [Prevotella bryantii]	6.1
725	539244	hypothetical protein YKR028w - yeast	6.1
726	2633502	(Z99110) similar to hypothetical proteins from B. subtilis [Bacillus	4.7
728	1078087	hypothetical protein YLR424w - yeast	1.6
729	4240219	(AB020672) KIAA0865 protein [Homo sapiens]	2
732	3165370	(AB011874) alpha subunit of dinitrogenase reductase (Fe protein) [unidentified nitrogen-fixing bacteria]	9.3
733	3882195	(AB018280) KIAA0737 protein [Homo sapiens]	2e-061
735	3859938	(AF081101) reverse transcriptase [Lymantria dispar]	2.3
737	974143	(L42542) RLIP76 protein [Homo sapiens]	8.4
738	3877493	(Z48583) similar to ATPases associated with various cellular activities (AAA); cDNA EST EMBL:Z14623 comes from this gene; cDNA EST EMBL:D75090 comes from this gene; cDNA EST EMBL:D72255 comes from this gene; cDNA EST yk200e4.5 ...	3e-047
739	4240235	(AB020680) KIAA0873 protein [Homo sapiens]	3e-052
740	4191810	(AB006532) DNA helicase [Homo sapiens]	1e-065
741	4507851	reserved protease [Homo sapiens]	2e-071
742	3876797	(Z81531) cDNA EST EMBL:D66579 comes from this gene; cDNA EST EMBL:D70408 comes from this gene; cDNA EST yk263d3.5 comes from this gene; cDNA EST yk275c1.5 comes from this gene; cDNA EST EMBL:C10270 comes from this gene [Caenorh...	2.7
743	4376875	(AE001642) CT465 hypothetical protein	0.53
744	91305	sperm mitochondrial capsule selenoprotein - mouse	0.32
745	1938549	(U97016) similar to drosophila Rlc1 gene product ribosomal protein L4 (YML4) (NID:g459259)	9e-016
751	3882189	(AB018277) KIAA0734 protein [Homo sapiens]	7.8
752	505665	(U08023) novel cellular proto-oncogene [Homo sapiens]	7.8
753	3170498	(AF052872) APETALA3 homolog PcAP3 [Papaver californicum]	6
754	1082243	autotaxin precursor - human >gi 537906	2.6

Table 2B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)

SEQ ID	ACCESSION	DESCRIPTION1	P VALUE
755	4507721	titin >gi 1212992 emb CAA62188 via Swiss-Prot; available at present via e-mail from LBEIT@EMBL-Heidelberg.DE [Homo	1.5
756	3036883	(AL022374) putative ABC transporter	0.68
757	543593	hypothetical 39.8K protein (clone GV-B) - garlic virus B	0.06
758	79960	hypothetical 30.5K protein - Enterococcus faecalis plasmid pAM-beta-1 >gi 3023044 (AF007787) orfC	1e-024
759	3882195	(AB018280) KIAA0737 protein [Homo sapiens]	6e-060
766	1707719	(Y08256) orf c02007 [Sulfolobus solfataricus]	9.8
767	2133808	immunoglobulin heavy chain - nurse shark	7.6
768	1469880	(D63483) The KIAA0149 gene product is related to Notch3. [Homo	7.5
769	4454062	(AJ132911) NorD protein [Bradyrhizobium japonicum]	5.9
770	137532	PROTEIN C2 >gi 74386 pir WZVZB6 59K HindIII-C protein - vaccinia virus (strain WR)	4.4
771	1098985	(U41031) proline-rich [Caenorhabditis elegans]	3.4
772	4378891	(AF132481) EseiL protein [Mus musculus]	2.6
773	4557489	cone-rod homeobox PROTEIN >gi 2665534 (AF024711) cone rod homeobox protein	1.5
774	2135894	peripheral benzodiazepine receptor - human	0.52
775	477495	cell-fate determining gene Notch2 protein - rat	0.51
776	1945493	(U56965) Similar to NAD(P) transhydrogenase, mitochondrial; coded for by C. elegans cDNA yk27c1.5; coded for by C. elegans cDNA yk35b9.5; coded for by C. elegans cDNA yk35b9.3; coded for by C. elegans cDNA yk161c9.3; coded for by C. elegans ...	0.39
777	746516	(U23517) D1022.7 [Caenorhabditis elegans] >gi 3258651 elegans]	0.059
778	2498786	GLYCEROL-3-PHOSPHATE ACYLTRANSFERASE PRECURSOR (GPAT) (P90) acyltransferase homolog - mouse >gi 193367 (M77003) glycerol-3-phosphate acyltransferase [Mus	0.058
779	2134384	procKr2 - chicken (fragment) gallus]	0.015
780	4176500	(AL031177) dJ889M15.3 (novel protein)	0.001
781	500858	(D14168) 50kDa lectin [Bombyx mori]	5e-010
782	4204294	(AC003027) lcl prt seq No definition line found	3e-010
783	500858	(D14168) 50kDa lectin [Bombyx mori]	2e-010
784	3184082	(AL023781) N-terminal acetyltransferase 1	6e-014
785	3184082	(AL023781) N-terminal acetyltransferase 1	3e-014
786	1330401	(U58762) T27F7.1 gene product [Caenorhabditis elegans]	6e-030
787	1330401	(U58762) T27F7.1 gene product [Caenorhabditis elegans]	3e-030
788	3879850	(Z81592) predicted using Genefinder	8e-034
789	1072198	(U40942) No definition line found [Caenorhabditis elegans]	1e-037
790	3327160	(AB014573) KIAA0673 protein [Homo sapiens]	1e-062
791	3413886	(AB007931) KIAA0462 protein [Homo sapiens]	1e-073
800	1903264	(Y11824) hypothetical protein [Pisum sativum]	9.5
801	2739276	(AJ223176) Ser/Thr protein kinase	5.6
802	4521264	(AB015874) guanylate cyclase OlGC-R2	5.6
803	2144044	zinc finger protein AT-BP2 - black rat protein AT-BP2 [Rattus rattus]	5.5
804	4049682	(AF063866) ORF MSV092 hypothetical protein [Melanoplus sanguinipes entomopoxvirus]	4.3
805	2842704	HYPOTHETICAL 73.3 KD PROTEIN C6G9.14 IN CHROMOSOME I >gi 1644326 emb CAB03616.1 protein	3.2
806	1526981	(X99945) amino acid permease YeeF like protein [Salmonella	2.5
807	1082243	autotaxin precursor - human >gi 537906	2.5
808	3660667	(AF055079) inositol 1,4,5-trisphosphate receptor	2.4

Table 2B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)

SEQ ID	ACCESSION	DESCRIPTION1	P VALUE
809	2500002	PHOSPHORIBOSYLAMINE--GLYCINE LIGASE PHOSPHORIBOSYLFORMYLGLYCINAMIDINE CYCLO- LIGASE (AIRS) synthetase, aminoimidazole ribonucleotide synthetase, glycylamide ribonucleotide transformylase {EC 6.3.4.13, 6.3.3.1, 2.1.2.2} [Chironomus tentans, Peptide, 1371 aa]	2.4
810	4507721	titin >gi 1212992 emb CAA62188 via Swiss-Prot; available at present via e-mail from LABEIT@EMBL-Heidelberg.DE [Homo	1.5
811	4507721	titin >gi 1212992 emb CAA62188 via Swiss-Prot; available at present via e-mail from LABEIT@EMBL-Heidelberg.DE [Homo	1.4
812	2833215	INTERFERON-ACTIVATABLE PROTEIN 205 protein - mouse >gi 385703 bbs 133592 (S62227) D3=lipopolysaccharide-inducible [mice, macrophages, Peptide, 425 aa] [Mus sp.]	1.1
813	1262910	(U51645) cytidine triphosphate synthetase [Plasmodium falciparum]	0.64
814	1245061	(U46069) fertilin alpha subunit [Oryctolagus cuniculus]	0.005
815	4493746	(AL034358) predicted using hexExon; L4830.10, Hypothetical protein, len: 816 aa [Leishmania major]	0.003
816	3283350	(AF062378) calmodulin-binding protein SHA1 [Mus musculus]	0.003
817	4204294	(AC003027) lcl prt seq No definition line found	3e-006
818	4309681	(AC006930) R33423_1 [Homo sapiens]	4e-007
819	3293547	(AF072709) putative oxidoreductase [Streptomyces lividans]	5e-013
820	1086900	(U41278) contains similarity to G beta repeats	2e-028
821	3878739	(Z73428) similar to Zinc finger, C3HC4 type (RING finger); cDNA EST EMBL:D67323 comes from this gene [Caenorhabditis elegans] >gi 3881096 emb CAB16481 finger); cDNA EST EMBL:D67323 comes from this gene	6e-031
822	3882195	(AB018280) KIAA0737 protein [Homo sapiens]	1e-053
823	3095186	(AF057140) cargo selection protein TIP47 [Homo sapiens]	7e-060
841	1915885	(Y08370) alpha-amylase [Crassostrea gigas]	9.2
842	1621461	(U73103) laccase [Liriodendron tulipifera]	9.2
843	232620	(S41487) possible ribosomal protein=l(3)S12 Canton S wild type [Drosophila melanogaster, Peptide, 73 aa] [Drosophila melanogaster]	9.1
844	1731338	HYPOTHETICAL 73.6 KD PROTEIN CY49.21 >gi 1370248 emb CAA98194 (Z73966) hypothetical protein Rv2082	6.9
845	3873261	(AF096295) cytochrome oxidase subunit I [Naja siamensis]	6.9
846	4049727	(AF063866) ORF MSV173 putative serine/threonine protein kinase Swinpox virus C20L homolog (vaccinia F10L), similar to SW:P32216 [Melanoplus sanguinipes entomopoxvirus]	5.5
847	1175595	HYPOTHETICAL PROTEIN HI1265	4.1
848	446631	collagen:SUBUNIT=alpha2:ISOTYPE=IX [Homo sapiens]	4.1
849	627171	odz protein - fruit fly (Drosophila sp.) product=tenascin homolog [Drosophila melanogaster, 9- to 12-hour-old embryos, Peptide, 2406	3.2
850	3986440	(AF076785) serum amyloid A-activating factor SAF-5	3.1
851	91312	stem cell protein ERA-1-399, retinoic acid-induced - mouse >gi 387146 (M22115) ERA-1-399 protein [Mus musculus]	1.4
852	4102043	(AF008203) homeobox protein [Homo sapiens]	1.3
853	746516	(U23517) D1022.7 [Caenorhabditis elegans] >gi 3258651 elegans]	0.28
854	2935691	(AF032122) unknown [Streptococcus thermophilus bacteriophage	0.21
855	99972	nodule-specific (hydroxy)proline-rich protein	0.014
856	1169288	DIHYDROXYACETONE KINASE (GLYCERONE KINASE) >gi 493083 (U09771) dihydroxyacetone kinase	1e-005
857	3721912	(AB017156) gob-5 [Mus musculus]	1e-011
858	868241	(U29488) C56C10.3 gene product [Caenorhabditis elegans]	3e-012
859	3293547	(AF072709) putative oxidoreductase [Streptomyces lividans]	5e-013
860	2228750	(U93868) RNA polymerase III subunit [Homo sapiens]	1e-015

Table 2B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)

SEQ ID	ACCESSION	DESCRIPTION1	P VALUE
861	1175412	HYPOTHETICAL 24.2 KD PROTEIN C13A11.03 IN CHROMOSOME I >gi 984224 emb CAA90804	5e-021
883	4505413	non-metastatic cells 5, protein expressed in (nucleoside-diphosphate kinase) KINASE HOMOLOG 5 (NDK-H 5) (NDP KINASE HOMOLOG 5) nucleoside-diphosphate kinase [Homo sapiens]	9
884	3308984	(AB008516) mtprd [Mus musculus]	9
885	3273643	(AF042021) olfactory receptor [Sus scrofa]	9
886	1170338	HETEROCHROMATIN PROTEIN 1 HOMOLOG ALPHA (HP1 ALPHA) (ANTIGEN P25) >gi 184311 (L07515) complete cds., gene product [Homo sapiens] chromosomal autoantigen [human, (U42832) coded for by C. elegans cDNA yk107c8.5; coded for by C. elegans cDNA yk107c8.3; Similar to UDP-glucuronosyltransferase. [Caenorhabditis elegans]	9
887	1125745	(U42832) coded for by C. elegans cDNA yk107c8.5; coded for by C. elegans cDNA yk107c8.3; Similar to UDP-glucuronosyltransferase. [Caenorhabditis elegans]	6.9
888	2921102	(AF020337) P6 [rice ragged stunt virus]	6.9
889	1707199	(U80841) C13A10.1 gene product [Caenorhabditis elegans]	6.8
890	1125745	(U42832) coded for by C. elegans cDNA yk107c8.5; coded for by C. elegans cDNA yk107c8.3; Similar to UDP-glucuronosyltransferase. [Caenorhabditis elegans]	5.3
891	2493564	PUTATIVE RIBOFLAVIN BIOSYNTHESIS ENZYME >gi 1707704 emb CAA69508 (Y08256) riboflavin biosynthesis protein ribG [Sulfolobus solfataricus]	5.2
892	2276148	(Z81463) Similarity to C.elegans zinc finger proteins [Caenorhabditis]	5.2
893	1346425	L-LACTATE DEHYDROGENASE 1.1.1.27) - Mycoplasma genitalium (SGC3) >gi 1046180	5.2
894	4234795	(AF078135) unknown [Leptospira borgpetersenii]	5.2
895	3874963	(Z92780) cDNA EST EMBL:D75953 comes from this gene [Caenorhabditis elegans]	4
896	3875723	(Z54270) similar to membrane glycoprotein	3.9
897	1086593	(U41007) C33H5.15 gene product [Caenorhabditis elegans]	3.9
898	3289979	(AC005263) SP62 HUMAN; SAP 62; SF3A66 [Homo sapiens]	3.1
899	2208965	(Y10528) cyanide insensitive terminal oxidase [Pseudomonas]	3
900	4539386	(AL035526) extensin-like protein	1.8
901	2662561	(AF036692) Similar to seven transmembrane receptor	1.8
902	2129184	pheromone shutdown protein homolog - Methanococcus jannaschii >gi 1592009 (U67576) pheromone shutdown protein (traB) [Methanococcus jannaschii]	1.3
903	2317864	(U78289) tyactone synthase module 7 [Streptomyces fradiae]	0.61
904	3808242	(AF069669) pol protein [Human immunodeficiency virus type 1]	0.6
905	3327128	(AB014557) KIAA0657 protein [Homo sapiens]	0.46
906	294529	(L14933) convertase PC5 [Rattus norvegicus]	0.35
907	3005087	(AF044924) hook2 protein [Homo sapiens]	0.12
908	3297817	(AL031032) putative protein [Arabidopsis thaliana]	0.025
909	3941342	(AF043250) mitochondrial outer membrane protein [Homo sapiens] >gi 3941347 (AF043253) mitochondrial outer membrane protein [Homo sapiens] >gi 4105703 gb AAD02504	0.01
910	480989	finger protein rfp - mouse (fragment)	5e-006
911	2842526	(AL021746) hypothetical anaphase promoting factor component [Schizosaccharomyces pombe] anaphase promoting complex	3e-018
912	4226073	(AF125443) contains similarity to S. pombe phosphatidyl synthase (GB:Z28295) [Caenorhabditis elegans]	4e-022
913	3551821	(AF058803) mucin 4 [Homo sapiens]	3e-038
914	3882195	(AB018280) KIAA0737 protein [Homo sapiens]	4e-051
940	279539	RNA-directed RNA polymerase (EC 2.7.7.48) - Marburg virus (strain Musoke) >gi 332179 (M92834) L Protein [Marburg virus]	8.7

Table 2B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)

SEQ ID	ACCESSION	DESCRIPTION1	P VALUE
941	117865	CYTOCHROME B >gi 2144288 pir H22848 ubiquinol--cytochrome-c reductase (EC 1.10.2.2) cytochrome b - <i>Sauroleishmania tarentolae</i> (AL008970) predicted using hexExon; MAL3P4.10 (PFC0515c),	8.6
942	3764008	Hypothetical protein, len: 1237 aa (Z98547) predicted using hexExon; MAL3P3.11 (PFC0380w), Dual-specificity protein phosphatase, len: 581 aa; Similarity to protein phosphatases. <i>S.cerevisiae</i> protein-tyrosine phosphatase YVH1 (SW:PVH1_YEAST) BLAST Score: 123, s...	8.6
943	3649770	(U42832) coded for by <i>C. elegans</i> cDNA yk107c8.5; coded for by <i>C. elegans</i> cDNA yk107c8.3; Similar to UDP-glucuronosyltransferase. [<i>Caenorhabditis elegans</i>]	6.5
944	1125745	(Y10528) cyanide insensitive terminal oxidase [<i>Pseudomonas</i> .	5.1
945	2208965	L-selectin precursor - rabbit >gi 847788	5
946	2146997	ALANYL-TRNA SYNTHETASE (ALANINE--TRNA LIGASE) (ALARS) >gi 95227 pir S16897 alanine--tRNA ligase (EC 6.1.1.7) - <i>Rhizobium leguminosarum</i> bv. <i>viciae</i> synthetase [<i>Rhizobium</i>	3.8
947	135091	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 >gi 102585 pir S26021 NADH dehydrogenase mitochondrion (SGC4) >gi 559495 emb CAA38170 (X54253) ND4 protein [<i>Ascaris</i>	3.8
948	1171815	glycoprotein B homolog precursor - feline herpesvirus 1 >gi 261095 bbs 120003 (S49775) glycoprotein B homolog [feline herpesvirus type 1 FHV-1, Peptide, 948 aa] [<i>Feline herpesvirus 1</i>]	1.7
949	2120034	UNKNOWN >gi 2587054 (AF027204) putative tetraspan transmembrane protein L6H [<i>Homo sapiens</i>]	0.99
950	4507539	CHEMOTAXIS LAFT PROTEIN parahaemolyticus >gi 677909 (U20541) Laft [<i>Vibrio parahaemolyticus</i>] >gi 1518953 (U52957) (AF082100) FK506 polyketide synthase [<i>Streptomyces</i> sp. MA6548]	0.26
951	417237	(AL034358) predicted using hexExon; L4830.10, Hypothetical protein, len: 816 aa [<i>Leishmania major</i>]	0.12
952	3798624	HYPOTHETICAL 24.2 KD PROTEIN C13A11.03 IN CHROMOSOME I >gi 984224 emb CAA90804 (AB020680) KIAA0873 protein [<i>Homo sapiens</i>]	0.003
953	4493746	RIBONUCLEOSIDE-DIPHOSPHATE REDUCTASE ALPHA CHAIN (RIBONUCLEOTIDE REDUCTASE) reductase (EC 1.17.4.1) - <i>Mycoplasma genitalium</i> (SGC3) reductase, alpha chain	6e-014
954	1175412	HYPOTHETICAL 23.9 KD PROTEIN IN SGA1-KTR7 INTERGENIC REGION >gi 1077785 pir S49791 probable membrane protein YIL089w - yeast (<i>Saccharomyces cerevisiae</i>) >gi 577125 emb CAA86705.1 (Z46728) YI9910.07, unknown orf,	8e-044
955	4240235	probable membrane protein YDL118w - yeast	
976	1350599	60S RIBOSOMAL PROTEIN L22 homologue to human L22 (AF041468) rbcR homolog [<i>Guillardia theta</i>]	8.2
977	731840	L-selectin precursor - rabbit >gi 847788	6.4
978	2132436	(AL023838) predicted using Genefinder; similar to Helix-hairpin-helix motif; cDNA EST yk241d12.5 comes from this gene; cDNA EST yk401c3.5 comes from this gene; cDNA EST CEMSE47F comes from this gene [<i>Caenorhabditis elegans</i>]	6.3
979	1710518	(AL032632) predicted using Genefinder	6.3
980	3602956	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 2 >gi 2147757 pir S62766 NADH dehydrogenase caldarium) mitochondrion (fragment) subunit 2 [<i>Cyanidium caldarium</i>]	4.9
981	2146997	(AF071879) capsid protein [<i>Porcine circovirus</i>]	4.8
982	3880890	(AF068139) S5 ribosomal protein/maturase fusion protein [<i>Cryphonectria parasitica</i>]	2.8
983	3880727		
984	1352547		2.2
985	3551845		2.1
986	3249009		2.1

Table 2B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)

SEQ ID	ACCESSION	DESCRIPTION1	P VALUE
987	1707126	(U80454) T16A1.2 [Caenorhabditis elegans]	2.1
988	1497971	(U55797) VP6 [Bluetongue virus]	1.7
989	3877568	(Z70208) similar to collagen	0.97
990	3309543	(AF036382) MLL [Fugu rubripes]	1e-005
991	4240235	(AB020680) KIAA0873 protein [Homo sapiens]	2e-039
1015	3257605	(AP000005) 484aa long hypothetical protein	8.2
		(X57019) unnamed protein product [Homo sapiens]	
1016	37593	>gi 238775 bbs 65126 (S65125) putative tyrosine kinase receptor=UFO [human, NIH3T3, Peptide, 894 aa]	8.1
1017	746533	(U23520) similar to cuticular collagen [Caenorhabditis elegans]	8
1018	729045	BETA CASEIN PRECURSOR scrofa]	7.9
		INTERLEUKIN-1 BETA CONVERTASE PRECURSOR (IL-1BC)	
1019	1170463	(IL-1 BETA CONVERTING ENZYME) (ICE) converting enzyme	7.8
1020	1197641	(U46859) DdhB [Yersinia enterocolitica (type 0:8)]	6
1021	2104691	(U92794) alpha glucosidase II, beta subunit [Mus musculus]	4.7
1022	1139577	(D63706) Orf5 [Streptomyces griseus]	4.7
		EARLY GLYCOPROTEIN GP48 PRECURSOR glycoprotein (18)	
1023	136785	[human herpesvirus 5]	3.5
1024	1314757	(U54761) phosphoglucose isomerase [Erwinia amylovora]	2.6
		PUTATIVE TRANSPOSASE FOR INSERTION SEQUENCE IS408	
1025	2497383	>gi 309869 (L09108) IS408 transposase; putative [Pseudomonas cepacia] >gi 1097384 prf 2113421C transposase [Burkholderia	1.6
		CHITOOLIGOSACCHARIDOLYTIC BETA-N-	
1026	1346281	ACETYLGLUCOSAMINIDASE PRECURSOR (BETA-GLCNACASE) 3.2.1.-) - silkworm >gi 998377 bbs 165703 (S77548) chitooligosaccharidolytic beta-N-acetylglucosaminidase, beta-	0.7
		ALPHA-1D ADRENERGIC RECEPTOR (ALPHA 1D-	
1027	3121722	ADRENOCEPTOR) (ALPHA-1A ADRENERGIC RECEPTOR) receptor [mice, brain, Peptide, 562 aa] [Mus sp.]	0.18
1028	4071321	(AF073954) Y-box protein MSY2 [Mus musculus]	0.14
1029	1293835	(U56965) C15H9.5 gene product [Caenorhabditis elegans]	0.11
		(AC004084) similar to GTPase-activating proteins; 35% similar to	
1030	2822157	JC5047 (PID:g2136083) [Homo sapiens]	2e-013
1040	1877301	(Z92774) hypothetical protein Rv3570c	9.7
		GAMMA-SOLUBLE NSF ATTACHMENT PROTEIN (SNAP-	
1041	3024629	GAMMA) >gi 423252 pir S32369 gamma-SNAP protein - bovine >gi 298669 bbs 127528 gamma soluble NSF attachment protein, gamma SNAP=N-ethyl-maleimide-sensitive fusion protein attachment	7.8
		UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 7	
1042	731044	(UBIQUITIN THIOLESTERASE 7) probable membrane protein YIL156w - yeast (Saccharomyces cerevisiae) >gi 557767 emb CAA86122 (Z38059) orf, len: 1071, CAI: 0.13,	7.6
1043	2190592	(U78315) Hermansky-Pudlak syndrome protein homolog [Mus	4.3
1044	2627435	(AF013614) No definition line found [Fugu rubripes]	3.5
1045	3881166	(AL032641) Y5F2A.3 [Caenorhabditis elegans]	2
		LA PROTEIN HOMOLOG (LA RIBONUCLEOPROTEIN) (LA	
1046	729918	AUTOANTIGEN HOMOLOG)	0.009
		(Z83819) dJ146H21.2 (similar to CYTOCHROME B-245 HEAVY	
1047	4106562	CHAIN) [Homo sapiens]	3e-017
		down-regulated in adenoma protein down-regulated in adenoma	
1048	4557535	(DRA) - human >gi 291964 576-580, 579-583; acidic transcr. activ. domain 620-640.; homeobox motif 653-676 [Homo sapiens]	4e-026
1049	4240235	(AB020680) KIAA0873 protein [Homo sapiens]	1e-037
1050	4240235	(AB020680) KIAA0873 protein [Homo sapiens]	2e-056

Table 2B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)

SEQ ID	ACCESSION	DESCRIPTION1	P VALUE
1065	586240	VITAMIN K-DEPENDENT GAMMA-CARBOXYLASE (GAMMA-GLUTAMYL CARBOXYLASE) 4.1.1.-) - bovine >gi 289399 (L09726) gamma-carboxylase	9.6
1066	3413410	(AL031231) 30S ribosomal protein S15	7.4
1067	1170758	GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35)	7.4
1068	867985	(L39002) S1 gene product [Avian orthoreovirus] orthoreovirus]	7.4
1069	127494	METALLOTHIONEIN (MT) lucius] >gi 62783 emb CAA49636 (X70042) Metallothioein	7.3
1070	3150259	(AL023634) palmitoyl-protein thioesterase precursor [Schizosaccharomyces pombe]	5.7
1071	328647	(M81729) tat [Human immunodeficiency virus type 1]	4.3
1072	2605979	(AF030027) 35 [Equine herpesvirus 4]	3.3
1073	137532	PROTEIN C2 >gi 74386 pir WZVZB6 59K HindIII-C protein - vaccinia virus (strain WR)	3.3
1074	3769620	(AF091563) olfactory receptor [Rattus norvegicus]	3.3
1075	687367	(U15829) envelope glycoprotein V3-V5 loop region [Human immunodeficiency virus type 1]	1.4
1076	3915901	TRANSCRIPTION INITIATION FACTOR TFIID 60 KD SUBUNIT (TAFII-60) (TAFII60)	0.48
1077	2317934	(U97553) unknown [murine herpesvirus 68]	0.37
1080	3878966	(Z68009) R09A8.1 [Caenorhabditis elegans]	9.1
1081	2341037	(AC000104) F19P19.17 [Arabidopsis thaliana]	2.3
1084	4508019	zinc finger protein 231 protein [Homo sapiens]	8.9
1085	3877198	(Z69903) predicted using Genefinder; Similarity to Rat casein kinase I (SW:KC1D_RAT); cDNA EST EMBL:D65322 comes from this gene; cDNA EST EMBL:D68704 comes from this gene; cDNA EST yk475f2.5 comes from this gene [Caenorhabditis...	4
1086	171998	(J02691) mitochondrial phenylalanyl-tRNA synthetase alpha subunit precursor [Saccharomyces cerevisiae]	2.3
1087	135574	LARGE TEGUMENT PROTEIN BPLF1 reading frame, 1 NXT/S, analogous to VZV RF22 BPLF1 [Human herpesvirus 4]	0.77
1091	1718312	(U75698) ORF K10 [Kaposi's sarcoma-associated herpesvirus]	9.8
1092	1076012	stress-sensitive restriction system protein 2 - Corynebacterium glutamicum (ATCC 13032) >gi 549844 restriction endonuclease which is stress-sensitive and ATP-dependent. It contains a typical	7.5
1093	882341	(U24702) LRP1 [Arabidopsis thaliana]	0.71
1094	3955011	(AJ005438) beta adrenoreceptor B	0.54
1095	1086900	(U41278) contains similarity to G beta repeats	1e-028
1096	4519908	(AB018106) HrSmad1/5 [Halocynthia roretzi]	6
1097	3043868	(U95835) extracellular protein Exp5 precursor	5.9
1098	2494294	NEUROGENIC LOCUS NOTCH 3 PROTEIN	3.5
1099	3879748	(Z72514) predicted using Genefinder; similar to collagen; cDNA EST EMBL:M89258 comes from this gene; cDNA EST EMBL:D68856 comes from this gene; cDNA EST yk232e11.3 comes from this gene; cDNA EST yk232e11.5 comes from this gene;...	0.079
1100	1123087	(U42436) C49H3.3 gene product [Caenorhabditis elegans]	5e-006
1101	3880809	(AL021483) similar to Probable rabGAP domains; cDNA EST EMBL:D34945 comes from this gene; cDNA EST EMBL:D27313 comes from this gene; cDNA EST EMBL:D34829 comes from this gene; cDNA EST EMBL:D27312 comes from this gene; cDNA	3e-011
1105	1772652	(U70664) 2-keto-3-deoxygluconate kinase [Haloferax alicantei]	5.8
1106	113000	ACTIN BINDING PROTEIN	5.5

Table 2B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)

SEQ ID	ACCESSION	DESCRIPTION1	P VALUE
1107	2702276	(AC003033) putative beta-glucosidase [Arabidopsis thaliana]	4.2
1108	1504006	(D86966) similarto human ZFY protein. [Homo sapiens]	4.2
1109	2337833	(Z98604) hypothetical protein MLCB2052.27	1.8
1110	3122952	TIPD PROTEIN >gi 2407788 (AF019236) TipD [Dictyostelium	6e-019
1112	4049344	(AL034567) putative protein [Arabidopsis thaliana]	6.8
1113	2143767	glycoprotein - rat >gi 986943 (L08134) glycoprotein [Rattus norvegicus] norvegicus]	0.018
1116	200135	(M63849) 2'-5' oligoadenylate synthetase [Mus musculus]	7.9
1119	133135	MITOCHONDRIAL RIBOSOMAL PROTEIN VAR1 1-339)	9.7
1120	1580768	(X92688) NADH dehydrogenase [Pecten maximus]	4.4
1121	4587868	(AF069302) Orf2 [Pediococcus pentosaceus]	1.5
1123	3851496	(AF051933) cyclin T; positive elongation transcription factor b cyclin subunit [Drosophila melanogaster]	3.4
1131	3877133	(Z83109) predicted using Genefinder	6
1132	118864	DNA POLYMERASE (A PROTEIN) 2.7.7.7) - ground squirrel hepatitis virus >gi 325402	4.6
1133	415638	(U03388) cyclooxygenase 1 [Rattus rattus]	4.5
1134	4100099	(U93502) hypothetical protein 256 [Secale cereale]	2.7
1135	2130154	hypothetical protein 241 - maize chloroplast	1.2
1136	4521280	(AB011832) cytochrome c oxidase subunit I [Dicyema misakiense]	0.94
1137	2706875	(D85084) NCAM-180 [Cynops pyrrhogaster]	0.68
1138	746516	(U23517) D1022.7 [Caenorhabditis elegans] >gi 3258651 elegans]	0.061
1139	746516	(U23517) D1022.7 [Caenorhabditis elegans] >gi 3258651 elegans]	0.061
1140	1938549	(U97016) similar to drosophila Rlc1 gene product ribosomal protein L4 (YML4) (NID:g459259)	5e-017
1141	1938549	(U97016) similar to drosophila Rlc1 gene product ribosomal protein L4 (YML4) (NID:g459259)	3e-017
1142	3851703	(AF100421) p80 [Rattus norvegicus]	1e-056
1143	4191810	(AB006532) DNA helicase [Homo sapiens]	8e-066
1144	3851703	(AF100421) p80 [Rattus norvegicus]	8e-070
1163	82620	probable serine-type carboxypeptidase (EC 3.4.16.1) - wheat	9.7
1164	3879471	(Z69885) predicted using Genefinder	9.6
1165	1075011	mercury resistance regulatory protein KW20)	9.5
1166	4490715	(AL035680) putative protein [Arabidopsis thaliana]	9.3
1167	487418	(L20303) actin filament-associated protein [Gallus gallus]	7.6
1168	560610	trypsin inhibitor, WTI [Triticum aestivum=wheat, variety San Pastore, endosperm, Peptide, 71 aa]	7.5
1169	3322954	(AE001240) spermidine/putrescine ABC transporter, permease protein (potB) [Treponema pallidum]	7.5
1170	1707179	(U80839) ZC204.15 gene product [Caenorhabditis elegans]	7.4
1171	209619	(J01901) major coat protein A [Adeno associated virus 2]	7.3
1172	1657233	(D88529) serine acetyltransferase serine acetyltransferase [Spinacia	7.3
1173	722375	(U23139) similar to phospholipase ADRAB-B precursor	7.2
1174	138018	TAIL FIBER PROTEIN GP37 (RECEPTOR RECOGNIZING PROTEIN) >gi 76090 pir TLBP74 tail fiber protein gp37 - phage T4 >gi 15374 emb CAA24228 (V00863) gene 37 [coliphage T4] >gi 215887 (J02509) tail fiber protein 37 [Bacteriophage T4]	5.5
1175	1001217	(D64003) hypothetical protein	4.4
1176	1175410	HYPOTHETICAL 126.5 KD PROTEIN C31A2.16 IN CHROMOSOME I >gi 2130427 pir S58108 hypothetical protein	4.4
1177	2829216	(AF044287) delta adaptin subunit of AP-3 [Drosophila melanogaster]	4.2
1178	1084374	histone-lysine N-methyltransferase (EC 2.1.1.43) large chain N-methyltransferase - garden pea carboxylase large subunit N-methyltransferase [Pisum sativum]	4.1

Table 2B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)

SEQ ID	ACCESSION	DESCRIPTION1	P VALUE
1179	567166	(L03172) This CDS feature is included to show the translation of the corresponding V_region. Presently translation qualifiers on V_region features are illegal.	3.8
1180	2492625	HYPOTHETICAL 49.3 KD PROTEIN C09G5.1 IN CHROMOSOME II >gi 3874104 emb CAA86760	3.2
1181	1065455	(U40410) coded for by C. elegans cDNA yk9e10.5; coded for by C. elegans cDNA yk9e10.3; multiple regions of similarity to EGF-like repeats and cysteine-rich repeats	2.6
1182	3406753	(AF068182) B cell linker protein BLNK [Mus musculus]	2.6
1183	1065455	(U40410) coded for by C. elegans cDNA yk9e10.5; coded for by C. elegans cDNA yk9e10.3; multiple regions of similarity to EGF-like repeats and cysteine-rich repeats	2.5
1184	4539761	(AF118391) salivary peroxidase	2.5
1185	101919	mating-type locus protein b3 - smut fungus	2.1
1186	329876	(M32084) polyprotein [Hepatitis C virus]	1.5
1187	3881059	(AL023844) similar to Ion transport proteins [Caenorhabditis]	1.4
1188	2981221	(AF053091) eyelid [Drosophila melanogaster]	1.4
1189	4566750	(AF115773) basic helix-loop-helix transcription factor Ndr1b [Danio]	1.4
1190	552072	(M13235) abl-like putative oncogene; putative	0.62
1191	1438951	(U61842) cutinase negative acting protein [Fusarium solani f. sp. (Z70207) predicted using Genefinder; similar to collagen; cDNA EST EMBL:D65905 comes from this gene; cDNA EST EMBL:D65858 comes from this gene; cDNA EST EMBL:D69306 comes from this gene; cDNA EST EMBL:D65755 comes from this	0.025
1192	3875904	(AF067217) contains similarity to myosin head (motor) domains (Pfam: myosin_head.hmm score: 602.72, 40.38 and 128.290) and phorbol esters/diacylglycerol binding domains (Pfam: DAG_PE-bind.hmm, score: 21.52 and 36.32)	0.002
1193	3150503	proline-rich protein - mouse proline-rich protein [Mus musculus]	5e-005
1194	110849	(AF049910) TACC1 [Homo sapiens]	7e-011
1195	3435157	(AF014903) NADH dehydrogenase subunit 2 [Pan troglodytes]	5e-011
1196	3287336	>gi 3287338 (AF014904) NADH dehydrogenase subunit 2 [Pan (AF125443) contains similarity to S. pombe phosphatidyl synthase (GB:Z28295) [Caenorhabditis elegans]	2e-011
1197	4226073	(U29488) C56C10.3 gene product [Caenorhabditis elegans]	2e-011
1198	868241	(AB020063) Keap1 [Mus musculus]	5e-012
1199	3894323	PUTATIVE AMINOPEPTIDASE ZK353.6 IN CHROMOSOME III >gi 1078908 pir S44657 ZK353.6 protein - Caenorhabditis elegans >gi 289760 (L15313) homology with leucine aminopeptidase; coded for by C. elegans cDNAs CE2F12 (GenBank: Z14714) and CE15D11	3e-014
1200	466102	(AF053768) brain specific cortactin-binding protein CBP90 [Rattus	2e-016
1201	3608372	(AF072709) putative oxidoreductase [Streptomyces lividans]	2e-019
1202	3293547	(AF125568) tumor suppressing STF cDNA 4 [Homo sapiens]	3e-031
1203	4567068	reserved >gi 3928762 dbj BAA34703	1e-048
1204	4507851	(AF081788) putative spliceosome associated protein [Homo sapiens]	4e-051
1205	3746791	>gi 3985930 dbj BAA34863 (AB020623) DAM1 [Homo sapiens]	2e-064
1206	3851703	(AF100421) p80 [Rattus norvegicus]	3e-071
1207	4519883	(AB017970) dipeptidyl peptidase III (Z98763) putative Inositol polyphosphate phosphatase [Schizosaccharomyces pombe]	9.1
1245	2370558	NADH dehydrogenase subunit I - maize	8.3
1246	1076815	(L25658) ORF [Blueberry scorch virus]	8.3
1247	409711	(AF098293) pyruvate decarboxylase	8.3
1248	4323053		

Table 2B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)

SEQ ID	ACCESSION	DESCRIPTION1	P VALUE
		C4B-BINDING PROTEIN BETA CHAIN PRECURSOR	
1249	2493794	>gi 2143627 pir S57960 C4BP protein beta chain precursor - rat	8.2
1250	1703342	>gi 899382 emb CAA90392 (Z50052) C4BP beta chain, leader	6.8
		APOLIPOPROTEIN D PRECURSOR	
1251	133652	PROBABLE RNA-DIRECTED RNA POLYMERASE polymerase (EC 2.7.7.48) - southern bean mosaic virus mosaic virus]	6.6
1252	2128472	hypothetical protein MJ0749 - Methanococcus jannaschii	6.5
		>gi 1591462 (U67520) conserved hypothetical protein	
1253	2499265	NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4	6.4
1254	1098322	>gi 1182022 emb CAA56534 (X80245) ND4 [Locusta migratoria]	5.3
		Ran/TC4-binding nucleopore protein [Homo sapiens]	
1255	283518	homeotic protein smox-5 - fluke (Schistosoma mansoni) >gi 161110 (M85304) homeodomain protein	5.2
1256	119714	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN) >gi 82169 pir S06733 hydroxyproline-rich glycoprotein precursor - common tobacco >gi 19867 emb CAA32090 (X13885) extensin (AA 1-620) [Nicotiana tabacum]	4.9
1257	1176529	HYPOTHETICAL 100.9 KD PROTEIN C34E10.3 IN CHROMOSOME III >gi 500726 (U10402) C34E10.3 gene product	4.8
1258	116922	COPPER RESISTANCE PROTEIN B PRECURSOR	3.8
		>gi 77826 pir B32018 copper resistance protein B precursor -	
		HYPOTHETICAL 19.0 KD PROTEIN IN NNF1-STE24 INTERGENIC REGION >gi 1077909 pir S57138 hypothetical protein YJR115w - yeast (Saccharomyces cerevisiae)	
1259	1352916	>gi 1015833 emb CAA89645 (Z49615) ORF YJR115w	3.7
1260	184111	(M20677) Kruppel-related protein (AA at 172) [Homo sapiens]	3.7
1261	122137	BOLA CLASS I HISTOCOMPATIBILITY ANTIGEN, ALPHA CHAIN BL3-6 PRECURSOR antigen alpha chain precursor (BL3-6)	3.6
1262	1086822	(U41263) this gene lies in the intron of T19D12.4 and on the opposite strand; strong similarity to casein kinases and to C. elegans proteins C03C10.2, F41G3.5 and ZK507.1	3
1263	3257206	(AP000003) 338aa long hypothetical protein	3
1264	4493896	(AL034558) predicted using hexExon; MAL3P2.18 (PFC0245c), Hypothetical protein, len: 3934 aa	2.8
1265	732330	GENERAL STRESS PROTEIN A Bacillus subtilis	2.2
1266	4155225	>gi 580866 emb CAA51568 (X73124) ipa-12d [Bacillus subtilis]	2.1
1267	2224448	(AE001499) putative ROD SHAPE-DETERMINING PROTEIN	1.4
1268	3406654	(AB001684) ORF54c [Chlorella vulgaris]	1.4
1269	3335561	(AF079369) transcriptional repressor TUP1 [Dictyostelium]	1.3
1270	2326171	(AF069736) PCAF associated factor 65 beta [Homo sapiens]	1.3
1271	3406654	(U62794) CDC42 GAP-related protein [Homo sapiens]	1.2
		(AF079369) transcriptional repressor TUP1 [Dictyostelium]	
1272	2145956	probable phosphomannomutase (EC 5.4.2.8) - Mycobacterium leprae	1
1273	2649256	>gi 467178 (U00022) u0308b; L308_F1_13 [Mycobacterium leprae]	1
1274	3451437	(AE001012) GMP synthase (guaA-2) [Archaeoglobus fulgidus]	0.76
1275	1653006	(AL031350) putative secreted protein	0.21
1276	1001821	(D90910) hypothetical protein	0.14
1277	1123087	(D64005) nickel resistance [Synechocystis sp.]	0.013
1278	1123087	(U42436) C49H3.3 gene product [Caenorhabditis elegans]	0.0004
1279	183894	(U42436) C49H3.3 gene product [Caenorhabditis elegans]	7e-005
1280	3608372	(M69054) insulin-like growth factor binding protein 6	9e-011
1281	3114818	(AF053768) brain specific cortactin-binding protein CBP90 [Rattus]	5e-011
1282	3608372	(AJ005891) JM2 [Homo sapiens]	7e-016
		(AF053768) brain specific cortactin-binding protein CBP90 [Rattus]	

Table 2B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)

SEQ ID	ACCESSION	DESCRIPTION1	P VALUE
1283	3608372	(AF053768) brain specific cortactin-binding protein CBP90 [Rattus	2e-016
1284	3649741	(AJ000281) mucin [Homo sapiens]	2e-031
1285	4240307	(AB020716) KIAA0909 protein [Homo sapiens]	1e-043
1286	4240307	(AB020716) KIAA0909 protein [Homo sapiens]	1e-043
1287	3649741	(AJ000281) mucin [Homo sapiens]	1e-047
1288	4557535	down-regulated in adenoma protein down-regulated in adenoma (DRA) - human >gi 291964 576-580, 579-583; acidic transcr. activ. domain 620-640.; homeobox motif 653-676 [Homo sapiens]	1e-060
1324	3879589	(Z50875) Proline rich domain; cDNA EST EMBL:D35637 comes from this gene; cDNA EST yk322a3.5 comes from this gene; cDNA EST yk397b2.5 comes from this gene; cDNA EST yk348b11.5 comes from this gene; cDNA EST yk397b2.3 comes from ...	9.9
1325	3879505	(AL023816) T05G11.4 [Caenorhabditis elegans]	9.4
1326	1346035	FOS-RELATED ANTIGEN-1 >gi 998348	8
1327	2648784	(AE000981) dipeptide ABC transporter, dipeptide-binding protein (dppA) [Archaeoglobus fulgidus]	7.9
1328	142774	(L07023) delta-endotoxin [Bacillus thuringiensis]	7.9
1329	2648784	(AE000981) dipeptide ABC transporter, dipeptide-binding protein (dppA) [Archaeoglobus fulgidus]	7.9
1330	3874201	(Z81015) predicted using Genefinder	7.7
1331	2358287	(AF010404) ALR [Homo sapiens]	7.7
1332	3881262	(AL021175) Y6E2A.6 [Caenorhabditis elegans]	6
1333	974143	(L42542) RLIP76 protein [Homo sapiens]	6
1334	3287188	(Y10601) ankyrin-like protein [Homo sapiens]	6
1335	730684	UBIQUITIN--PROTEIN LIGASE RSP5 yeast (Saccharomyces cerevisiae) >gi 603364 (U18916) Rsp5p [Saccharomyces cerevisiae]	4.6
1336	1255865	(U53340) coded for by C. elegans cDNA yk39e8.5; weakly similar to C. elegans proteins F09G8.4 and F02E8.6	3.6
1337	2687999	(AE001123) B. burgdorferi predicted coding region BB0110	3.3
1338	623044	(L38896) This CDS feature is included to show the translation of the corresponding V_region. Presently translation qualifiers on V_region features are illegal	3.1
1339	987050	(X65335) lacZ [Cloning vector pSV-beta-Galactosidase Control]	2.7
1340	1136390	(D79986) similar to human DNA-binding protein 5. [Homo sapiens]	2.6
1341	3599395	(AF083072) histone H1 DNA binding protein [Cenarchaeum	1.4
1342	1144514	(U34781) Antho-LWamidII preprohormone [Anthopleura elegantissima] >gi 1586846 prf 2204411A prepro-hormone	1.2
1343	3406654	(AF079369) transcriptional repressor TUP1 [Dictyostelium	0.98
1344	3132825	(AF063403) putative cytosine-5 DNA methyltransferase [Zea mays]	0.89
1345	1754989	(U47661) proline-rich protein PRP2 precursor [Lupinus luteus]	0.078
1346	728834	!!!! ALU SUBFAMILY SB2 WARNING ENTRY	0.025
1347	1123087	(U42436) C49H3.3 gene product [Caenorhabditis elegans]	0.021
1348	3608372	(AF053768) brain specific cortactin-binding protein CBP90 [Rattus	1e-009
1349	4507029	sodium bicarbonate cotransporter 2 >gi 3097316 dbj BAA25898 (AB012130) sodium bicarbonate cotransporter2 [Homo sapiens]	5e-016
1350	2781381	(AC004013) Similar to rabbit A-kinase-anchoring protein sapiens]	1e-029
1351	4584423	(AJ131693) AKAP450 protein [Homo sapiens]	3e-052
1359	1518135	(U66260) multidrug resistance related protein 1	5.2
1362	3450974	(AF082496) interleukin-2 [Marmota monax]	6.8
1363	1123087	(U42436) C49H3.3 gene product [Caenorhabditis elegans]	0.001
1364	119760	COAGULATION FACTOR X PRECURSOR 3.4.21.6) precursor - chicken >gi 222870 dbj BAA00724	2
1367	3861111	(AJ235272) unknown [Rickettsia prowazekii]	5.5

Table 2B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)

SEQ ID	ACCESSION	DESCRIPTION1	P VALUE
1370	117143	CYTOCHROME P450 1A1 (CYP1A1) rainbow trout >gi 213780 (M21310) cytochrome P4501A1	7.1
1371	3915910	HYPOTHETICAL 36.3 KD PROTEIN IN NRDC-MOBD INTERGENIC REGION >gi 1667570 (U76612) unknown	5.4
1372	1708230	HOMEBOX PROTEIN ABDOMINAL-A	4.1
1373	3024292	RHODOPSIN >gi 2290717 (AF000947) rhodopsin [Sepia officinalis] (AF053723) region 2 capsular polysaccharide biosynthesis protein	5.3
1374	2996206	[Actinobacillus pleuropneumoniae]	2.3
1375	2228750	(U93868) RNA polymerase III subunit [Homo sapiens]	5e-011
1379	79960	hypothetical 30.5K protein - Enterococcus faecalis plasmid pAM-beta-1 >gi 3023044 (AF007787) orfC	2e-025
1380	465532	HYPOTHETICAL 14.2 KD PROTEIN IN BLAB 3'REGION >gi 282541 pir C41855 orf3 - Streptomyces cacaoi >gi 217001 dbj BAA00776 (D00937) regulatory protein for beta-	5.7
1381	3913279	COAT PROTEIN PRECURSOR (CAPSID PROTEIN) >gi 535774 (L09205) capsid protein [Tobacco ringspot virus]	0.66
1389	4493762	(AL034368) predicted using hexExon; L779.1, Serine/threonine protein kinase, len: 1359 aa; Similarity to protein kinases. A.thaliana NPK1-related protein kinase (TR:O22041) BLAST score: 303, sum	4.6
1390	131002	PROLINE-RICH PROTEIN MP-3 >gi 200549	0.1
1391	632098	isp3 protein - fission yeast	4.5
1392	2496862	HYPOTHETICAL 6.1 KD PROTEIN C03B1.10 IN CHROMOSOME X >gi 1072242 (U40952) C03B1.10 gene product	6e-006
1393	3851703	(AF100421) p80 [Rattus norvegicus]	4e-056
1399	4493762	(AL034368) predicted using hexExon; L779.1, Serine/threonine protein kinase, len: 1359 aa; Similarity to protein kinases. A.thaliana NPK1-related protein kinase (TR:O22041) BLAST score: 303, sum	4.3
1400	129648	PAIRED BOX PROTEIN PAX-1	4.3
1401	4115789	(D89861) cytochrome C-type biogenesis protein CCMF [Cyanidioschyzon merolae]	1.9
1402	135514	T-CELL RECEPTOR BETA CHAIN PRECURSOR precursor (ANA (U41264) coded for by C. elegans cDNA CEESN26F; coded for by C. elegans cDNA CEESI89F; similar to 60S acidic ribosomal protein	0.034
1403	1086833	Po (L10) [Caenorhabditis elegans]	3e-009
1404	4104168	(AF033339) UNC-45 [Caenorhabditis briggsae]	7e-013
1410	1175805	HYPOTHETICAL PROTEIN HI1452 Haemophilus influenzae (strain Rd KW20) >gi 1574290	7.3
1411	1708230	HOMEBOX PROTEIN ABDOMINAL-A	4.2
1412	127774	MYOSIN II HEAVY CHAIN, NON MUSCLE heavy chain [Dictyostelium discoideum]	0.56
1413	728833	!!!! ALU SUBFAMILY SB1 WARNING ENTRY	0.48
1414	3080645	(AC004611) Hsp27 ERE-TATA-binding protein [Homo sapiens]	3e-008
1415	3687476	(AL031786) putative atp dependent rna helicase [Schizosaccharomyces pombe]	1e-014
1416	4557535	down-regulated in adenoma protein down-regulated in adenoma (DRA) - human >gi 291964 576-580, 579-583; acidic transcr. activ. domain 620-640.; homeobox motif 653-676 [Homo sapiens]	5e-060
1421	2088648	(AF002109) hypothetical protein [Arabidopsis thaliana]	6.9
1422	1707768	(Y08256) orf c01038 [Sulfolobus solfataricus]	5.3
1423	3370996	(AB008674) mBlm [Mus musculus]	4
1424	3878128	(Z69663) Weak similarity to Cotton isocitrate lyase (SW:ACEA_GOSHI); cDNA EST EMBL:D33259 comes from this gene; cDNA EST EMBL:D35346 comes from this gene; cDNA EST EMBL:D36032 comes from this gene; cDNA EST EMBL:D73253	1.8

Table 2B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)

SEQ ID	ACCESSION	DESCRIPTION1	P VALUE
1425	83996	hypothetical protein 1 (CYb-COII intergenic region) - Sauroleishmania tarentolae mitochondrion uncertain [Leishmania	1.8
1426	1322210	(U26347) immunoglobulin kappa, VJ region [Homo sapiens]	1.4
1427	3043810	(U88273) NADH dehydrogenase subunit 4 [Sceloporus aeneus]	0.46
1428	3080645	(AC004611) Hsp27 ERE-TATA-binding protein [Homo sapiens]	0.0007
1429	4506223	proteasome (prosome, macropain) 26S subunit, non-ATPase, 13 >gi 3618343 dbj BAA33214	1e-066
1438	2944430	(AF050157) butyrophilin-like [Mus musculus]	8.9
1439	1652823	(D90908) hypothetical protein	3
1440	119714	EXTENSIN PRECURSOR (CELL WALL HYDROXYPROLINE-RICH GLYCOPROTEIN) >gi 82169 pir S06733 hydroxyproline-rich glycoprotein precursor - common tobacco >gi 19867 emb CAA32090 (X13885) extensin (AA 1-620) [Nicotiana tabacum]	0.9
1441	509813	(L29010) ORFB [Cryphonectria hypovirus]	0.78
1442	238617	(S64572) nonfibrillar collagen Partial, 907 aa [Strongylocentrotus	0.2
1443	3522970	(U42390) Trio [Homo sapiens]	0.12
1449	3328726	(AE001303) ATP Synthase Subunit E [Chlamydia trachomatis]	8.6
1450	501174	(L33965) MHC class II protein [Morone saxatilis]	8.5
1451	2661685	(AL009199) hypothetical protein SC7B7.10	8.5
1452	1575684	(U70316) Iona [Dictyostelium discoideum]	8.4
1453	2128472	hypothetical protein MJ0749 - Methanococcus jannaschii >gi 1591462 (U67520) conserved hypothetical protein	5
1454	1549329	(U52845) class IV chitinase EP3-1/H5 [Daucus carota]	4.9
1455	3845167	(AE001390) hypothetical protein [Plasmodium falciparum]	2.9
1456	2833306	PUTATIVE IMPORTIN ALPHA SUBUNIT for by C. elegans cDNA yk117h8.5; coded for by C. elegans cDNA yk8f10.5; coded for by C. elegans cDNA yk134a4.5; coded for by C. elegans cDNA yk53c4.5; coded for by C. elegans cDNA yk8f10.3; coded for by C.	1.7
1463	1731097	HYPOTHETICAL 34.2 KD PROTEIN F07F6.2 IN CHROMOSOME III >gi 746449 (U23486) No definition line found	8.3
1464	4321805	(AF063232) variant 1 major surface glycoprotein [Pneumocystis	8.3
1465	4557059	(AC007154) hypothetical protein	4.8
1466	139372	ENDOPROTEASE (LATE L3 23 KD PROTEIN) adenovirus type 7]	4.8
1467	8509	(X04813) CAD protein (AA 1 - 2236) [Drosophila melanogaster]	3.6
1468	422690	myosin-binding protein H - chicken	2e-005
1472	265108	(S54379) sucrose-phosphate synthase, SPS oleracea]	2.1
1473	2842704	HYPOTHETICAL 73.3 KD PROTEIN C6G9.14 IN CHROMOSOME I >gi 1644326 emb CAB03616.1 pr otein	1.6
1474	113109	NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, NON-ALPHA-3 CHAIN PRECURSOR (GFN-ALPHA-3) non-alpha-3 chain precursor - goldfish >gi 212956 auratus]	0.7
1475	4557535	down-regulated in adenoma protein down-regulated in adenoma (DRA) - human >gi 291964 576-580, 579-583; acidic transcr. activ. domain 620-640;; homeobox motif 653-676 [Homo sapiens]	1e-051
1485	2315339	(AF016438) contains similarity to C4-type zinc fingers	9.9
1486	549664	HYPOTHETICAL 23.0 KD PROTEIN IN IXR1-TFA1 INTERGENIC REGION >gi 539152 pir S37847 hypothetical protein YKL030w - yeast (Saccharomyces cerevisiae)	4.4
1487	4204234	>gi 486029 emb CAA81864 (Z28029) ORF YKL030w (AF035379) MADS-box protein 2 [Lolium temulentum]	0.51
1488	126390	LORICRIN >gi 110649 pir A35628 loricrin - mouse >gi 198871 (M34398) loricrin [Mus musculus] >gi 520480 (U09189) loricrin	0.14

Table 2B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)

SEQ ID	ACCESSION	DESCRIPTION1	P VALUE
1489	4557535	down-regulated in adenoma protein down-regulated in adenoma (DRA) - human >gi 291964 576-580, 579-583; acidic transcr. activ. domain 620-640,; homeobox motif 653-676 [Homo sapiens]	4e-050
1492	1707768	(Y08256) orf c01038 [Sulfolobus solfataricus]	4.3
1493	4376203	(U35226) putative cytochrome P-450	4.3
1494	3721884	(AB016248) sterol-C5-desaturase [Mus musculus]	4.2
1495	131000	ACIDIC PROLINE-RICH PROTEIN PRECURSOR salivary protein [Rattus norvegicus]	3.3
1496	3123638	(AJ223069) TCF-3 protein [Mus musculus]	0.49
1497	854065	(X83413) U88 [Human herpesvirus 6]	5e-010
1501	126679	GALECTIN-3 (GALACTOSE-SPECIFIC LECTIN 3) (MAC-2 ANTIGEN) (IGE-BINDING PROTEIN) (35 KD LECTIN) (CARBOHYDRATE BINDING PROTEIN 35) (CBP 35) GALACTOSIDE-BINDING LECTIN) >gi 1072481 pir A28651	0.21
1502	4106562	(Z83819) dJ146H21.2 (similar to CYTOCHROME B-245 HEAVY CHAIN) [Homo sapiens]	1e-011
1504	265108	(S54379) sucrose-phosphate synthase, SPS oleracea]	1.6
1505	1177322	(X95466) CPG2 protein [Rattus norvegicus]	0.0002
1507	3878057	(Z99942) similar to von Willebrand factor type A domain; cDNA EST yk412d4.5 comes from this gene; cDNA EST yk412d4.3 comes from this gene [Caenorhabditis elegans]	0.039
1509	2394509	(AF024503) No definition line found [Caenorhabditis elegans]	6.1
1510	2827872	(U79229) NADH dehydrogenase subunit F [Tradescantia zebrina]	4.6
1511	3004653	(AF017777) tweety [Drosophila melanogaster]	3.7
1512	3873773	(Z83316) Similarity to S.pombe hypothetical protein C2F7.02C	1.6
1513	586295	HYPOTHETICAL 33.8 KD PROTEIN IN YSW1-RIB7 INTERGENIC REGION >gi 626526 pir S46023 hypothetical protein YBR152w - yeast (Saccharomyces cerevisiae)	0.081
1519	3882147	>gi 536480 emb CAA85111 (Z36021) ORF YBR152w	9.9
1520	2117181	(AB018256) KIAA0713 protein [Homo sapiens]	7.3
1521	1169862	(Z95584) mcr [Mycobacterium tuberculosis]	6
1522	3257950	G-BOX BINDING FACTOR 3 >gi 600863 thaliana]	6
1523	4138677	(AP000006) 236aa long hypothetical protein	5.9
1524	2736413	(AJ009814) polymerase [Viral hemorrhagic septicemia virus]	5.7
1525	2058691	(AF039044) No definition line found [Caenorhabditis elegans]	2.7
1526	347124	(U94836) ERROT 213-21 [Homo sapiens]	2
1527	3913674	(L20967) phosphodiesterase [Homo sapiens]	2
1528	1086636	FERRIC REDUCTASE TRANSMEMBRANE COMPONENT 3 PRECURSOR >gi 2132959 pir S67293 probable membrane protein YOR381w - yeast (Saccharomyces cerevisiae)	0.9
1529	2495706	>gi 1420821 emb CAA99713 (Z75289) ORF YOR381w	0.86
1530	4007775	(U41013) similar to phosphoribosylaminoimidazolecarboxamide formyltransferase [Caenorhabditis elegans]	0.65
1531	113671	HYPOTHETICAL PROTEIN KIAA0136 product is novel. [Homo	0.39
1532	4098124	(AL034486) hypothetical fungal binuclear cluster domain protein [Schizosaccharomyces pombe]	8e-008
1533	1174546	!!!! ALU CLASS F WARNING ENTRY !!!!	5e-010
1534	4139228	(U73522) AMSH [Homo sapiens]	5e-044
1535	2564328	SYNAPTOTAGMIN II	3e-050
1536	3668141	(AF109134) 7-60 [Homo sapiens] >gi 4139272 (AF112980) 7-60	3e-057
1544	3256484	(AB006628) KIAA0290 [Homo sapiens]	9.1
1545	2735945	(AJ007398) PBK1 protein [Homo sapiens]	7.5
		(AP000001) 158aa long hypothetical protein [Pyrococcus horikoshii]	
		(AF015193) NADH dehydrogenase subunit 3 [Onchocerca volvulus]	

Table 2B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)

SEQ ID	ACCESSION	DESCRIPTION1	P VALUE
1546	3983015	(AF096056) antigen receptor [Ginglymostoma cirratum]	3.2
1547	1552169	(D42138) PIG-B [Homo sapiens]	3
1548	2440180	(Z99531) ubiquitin system protein	2.4
1549	3882159	(AB018262) KIAA0719 protein [Homo sapiens]	1.8
1550	3004653	(AF017777) tweety [Drosophila melanogaster]	1.3
1551	77657	hypothetical 30.1K protein - Pseudomonas aeruginosa	0.26
1552	4098124	(U73522) AMSH [Homo sapiens]	0.002
1553	3979818	(Z49967) cDNA EST EMBL:T00743 comes from this gene; cDNA EST EMBL:D69356 comes from this gene; cDNA EST EMBL:D65790 comes from this gene; cDNA EST EMBL:D70463 comes from this gene; cDNA EST EMBL:D66620 comes from this	0.001
1554	3550295	(AJ009947) putative ATPase [Homo sapiens]	1e-008
1555	4507507	UNKNOWN >gi 3929583 (AF098162) timeless homolog [Homo	1e-035
1562	3152567	(AC002986) Contains similarity to membrane associated salt-inducible protein gb AF007269 from A. thaliana.	8.4
1563	4493978	(AL034559) predicted using hexExon; MAL3P7.21 (PFC0960c), Hypothetical protein, len: 1929 aa	5
1564	1169862	G-BOX BINDING FACTOR 3 >gi 600863 thaliana]	4.7
1565	140550	HYPOTHETICAL 259 KD PROTEIN (ORF 2136) >gi 81341 pir A05037 hypothetical protein 2136 - liverwort (Marchantia polymorpha) chloroplast polymorpha]	3.7
1566	2224354	(AB001684) ORF104 [Chlorella vulgaris]	0.76
1567	106322	hypothetical protein (L1H 3' region) - human	0.53
1568	3522937	(AC004411) unknown protein [Arabidopsis thaliana]	0.4
1569	4097433	(U61084) phorbol 3 [Homo sapiens]	4e-017
1578	1944122	(AB002531) SSU1p [Saccharomyces cerevisiae]	9.7
1579	4127662	(Y11176) fructosidase [Cichorium intybus]	5.3
1580	119515	EPENDYMIN I PRECURSOR (EPD-I) rainbow trout >gi 213412 (M93697) ependymin	4.4
1581	1439625	(U64598) weakly similar to S. cerevisiae PTM1 precursor	2.6
1582	2183261	(AF002133) MAV264 [Mycobacterium avium]	2.3
1583	2388564	(AC000098) ESTs gb AA042402,gb ATTS1380 come from this gene. [Arabidopsis thaliana]	1.9
1584	1381091	(U51723) V-SERA 1 [Plasmodium vivax]	9.8
1587	2496317	HYPOTHETICAL PROTEIN MG144 HOMOLOG Mycoplasma pneumoniae (SGC3) (ATCC 29342) >gi 1674380 genitalium	0.65
1588	2496317	HYPOTHETICAL PROTEIN MG144 HOMOLOG Mycoplasma pneumoniae (SGC3) (ATCC 29342) >gi 1674380 genitalium	0.64
1589	3184073	(AL023779) hypothetical protein	8e-009
1590	3560165	(AL031525) hypothetical protein	3.7
1612	133594	RNA-DIRECTED RNA POLYMERASE (ORF1B) 2.7.7.48) - avian infectious bronchitis virus (strain Beaudette) >gi 292953 (M95169) pol protein [Avian infectious bronchitis virus] >gi 331173 (M94356) ORF 1b encodes a polypeptide of potential mol. wt. 300,000.	9.7
1613	3043622	(AB011121) KIAA0549 protein [Homo sapiens]	6.8
1614	72870	translation elongation factor eEF-1 alpha chain factor 1-alpha (AA 1 - 461) [Mus musculus]	5.6
1615	2315365	(AF016441) No definition line found [Caenorhabditis elegans]	5.3
1616	586120	TRICHOHYALIN >gi 539701 pir A45973 trichohyalin - human >gi 292836 (L09190) trichohyalin	4.9
1617	281206	nuclear antigen EBNA-3B - human herpesvirus 4	3.9
1618	2146731	FK506-binding protein - Arabidopsis thaliana	3.5
1619	3876045	(Z81506) similar to Lectin C-type domain short and long forms, CUB domain [Caenorhabditis elegans]	3.5

Table 2B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)

SEQ ID	ACCESSION	DESCRIPTION1	P VALUE
1620	2833191	LACCASE 4 PRECURSOR precursor - Rhizoctonia solani >gi 1150568 emb CAA91042	3.3
1621	2981221	(AF053091) eyelid [Drosophila melanogaster]	3.2
1622	1118179	(U42304) chitin synthase [Phytophthora capsici]	2.9
1623	1351576	HYPOTHETICAL PROTEIN MG419 Mycoplasma genitalium	2.9
1624	320309	AL2 protein - beet curly top virus >gi 210683	2.5
1625	1523997	(X99510) CDK4/6 kinase [Drosophila melanogaster]	2.1
1626	3646450	(AL031603) conserved hypothetical protein.	2
1627	3599342	(AF081112) ORF2 [Mus musculus domesticus]	1.9
1628	2114473	(U96963) p140mDia [Mus musculus]	1.5
1629	3638957	(AC004877) sco-spondin-mucin-like; similar to P98167 uncertain [Homo sapiens]	1
1630	2558942	(AF024714) interferon-inducible protein [Homo sapiens]	0.93
1631	3257709	(AP000005) 115aa long hypothetical protein	0.69
1632	346430	adenylylcyclase type V-alpha - dog >gi 290082	0.46
1633	4263788	(AC006068) hypothetical protein	0.3
1634	2134199	myosin I beta - bullfrog >gi 602138 (U14549) myosin I beta [Rana catesbeiana] >gi 603692 (U14382) myosin I beta [Rana catesbeiana]	0.044
1635	2134199	myosin I beta - bullfrog >gi 602138 (U14549) myosin I beta [Rana catesbeiana] >gi 603692 (U14382) myosin I beta [Rana catesbeiana]	0.036
1636	3776027	(AJ010475) RNA helicase [Arabidopsis thaliana]	2e-006
1637	134787	ATP-DEPENDENT RRNA HELICASE SPB4 cerevisiae] >gi 836754 dbj BAA09238 (D50617) rRNA helicase [Saccharomyces cerevisiae] SPB4 [Saccharomyces cerevisiae]	1e-015
1638	134787	ATP-DEPENDENT RRNA HELICASE SPB4 cerevisiae] >gi 836754 dbj BAA09238 (D50617) rRNA helicase [Saccharomyces cerevisiae] SPB4 [Saccharomyces cerevisiae]	4e-016
1639	4454698	(AF070661) HSPC005 [Homo sapiens]	2e-016
1640	4185892	(AL033125) 1-evidence=predicted by content; 1- method=genefinder;084; 1-evidence_end; 2-evidence=predicted by match; 2-match accession=SWISS-PROT:P38205; 2- match description=HYPOTHETICAL 77.9 KD PROTEIN IN	6e-021
1641	3043548	(AB011084) KIAA0512 protein [Homo sapiens]	9e-041
1643	2435574	(AF026209) similar to C. elegans olfactory receptor ODR-10 (NID:g1235900) [Caenorhabditis elegans]	7.3
1644	3880252	(Z82055) similar to Zinc finger, C4 type	5.7
1645	3023744	PUTATIVE FLAGELLA-RELATED PROTEIN C	4.5
1646	267478	HYPOTHETICAL 64.3 KD PROTEIN IN RPS3 3'REGION (ORF516) >gi 419731 pir S34525 hypothetical protein 516 (rps3 3' region) - Euglena gracilis chloroplast >gi 2673852 emb CAA50104 (X70810) orf516; ttg start [Euglena gracilis]	2
1647	82551	hypothetical 237 protein (psbA 5' region) - rye chloroplast (fragment)	0.49
1648	1255792	(U51993) similar drosophila lethal (2) giant larvae protien (SP:Q08470) [Caenorhabditis elegans]	0.09
1663	627837	All-1 protein +GTE form - mouse (fragment)	9.6
1664	4115789	(D89861) cytochrome C-type biogenesis protein CCMF [Cyanidioschyzon merolae]	6.3
1665	942618	(U31081) MnxB [Bacillus sp.]	6
1666	220579	(D00570) open reading frame (196 AA) [Mus musculus]	5.8
1667	2120082	hypothetical protein II (retroposon LINE-1)	4.9
1668	2120082	hypothetical protein II (retroposon LINE-1)	4.8
1669	862343	(L10908) Gcap1 gene product [Mus musculus] marker protein [Mus	4.6
1670	1168540	ARGININOSUCCINATE SYNTHASE argininosuccinate synthetase (argG) homolog - Haemophilus influenzae (strain Rd KW20)	4.5

Table 2B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)

SEQ ID	ACCESSION	DESCRIPTION1	P VALUE
1671	160385	(M63277) malaria antigen [Plasmodium falciparum]	4
1672	1177607	(X92485) pva1 [Plasmodium vivax]	3.8
1673	2497678	ZYXIN >gi 1430883 emb CAA67510	2.5
1674	4049518	(AL031852) conserved hypothetical protein	2.1
1675	135514	T-CELL RECEPTOR BETA CHAIN PRECURSOR precursor (ANA	0.55
1676	729942	LIPASE 1 PRECURSOR (TRIACYLGLYCEROL LIPASE) >gi 538817 pir A47081 triacylglycerol lipase	0.45
1677	4503629	coagulation factor XII (Hageman factor) >gi 119763 sp P00748 FA12_HUMAN COAGULATION FACTOR XII PRECURSOR (HAGEMAN FACTOR) (HAF) 3.4.21.38) precursor - human >gi 180357 (M17466) coagulation factor XII	0.27
1678	1708392	CASPASE-5 PRECURSOR (ICH-3 PROTEASE) (TY PROTEASE) (ICE(REL)-III) enzyme ICERel-III - human >gi 903936 (U28015) cysteine protease [Homo sapiens]	4e-006
1679	3550295	(AJ009947) putative ATPase [Homo sapiens]	1e-008
1680	3875400	(Z73906) cDNA EST EMBL:M88866 comes from this gene [Caenorhabditis elegans]	1e-009
1681	3874685	(Z78539) Similarity to S.pombe hypothetical protein C4G8.04 (SW:YAD4_SCHPO); cDNA EST EMBL:D27846 comes from this gene; cDNA EST EMBL:D27845 comes from this gene; cDNA EST yk202h7.3 comes from this gene; cDNA EST yk202h7.5 come...	6e-010
1682	3979818	(Z49967) cDNA EST EMBL:T00743 comes from this gene; cDNA EST EMBL:D69356 comes from this gene; cDNA EST EMBL:D65790 comes from this gene; cDNA EST EMBL:D70463 comes from this gene; cDNA EST EMBL:D66620 comes from this	2e-015
1683	4584877	(AF068302) choline/ethanolaminephosphotransferase [Homo	5e-020
1685	3914503	ASPARTATE CARBAMOYLTRANSFERASE 2 PRECURSOR (ASPARTATE TRANSCARBAMYLASE 2) (ATCASE 2) sativum]	9.9
1686	1845893	(U69426) envelope glycoprotein [Human immunodeficiency virus	9.7
1687	1730629	HYPOTHETICAL 43.0 KD PROTEIN B0361.6 IN CHROMOSOME III >gi 458954 (U00031) similar to H. marismortui hypothetical 23.1 kd protein in HMAL3 5' region [Caenorhabditis	5e-014
1690	2133580	gag polyprotein - red flour beetle retrotransposon Woot >gi 805076 (U09586) ORF 1	1.1
1695	126296	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG protein [Nycticebus coucang]	6
1696	111816	probable pol polyprotein-related protein 4 - rat >gi 56590 emb CAA37647 (X53581) ORF4 [Rattus norvegicus]	5.3
1697	1517923	(U51117) ascospore maturation 1 protein [Neurospora crassa]	5.3
1698	2924552	(AL022018) 1-evidence=predicted by content; 1- method=genefinder;084; 1-method_score=165.48; 1-evidence_end; 2- evidence=predicted by match; 2-match_accession=AA264666; 2- match_description=LD08351.5prime LD Drosophila melanogaste...	6e-012
1699	1663706	(D87685) similar to human transcription factor TFIIS (S34159).	2e-014
1700	3879850	(Z81592) predicted using Genefinder	3e-034
1707	3184085	(AL023781) cytochrome c oxidase polypeptide v precursor [Schizosaccharomyces pombe]	8.7
1708	3845206	(AE001400) novel protein kinase [Plasmodium falciparum]	3.9
1709	283435	hypothetical protein DGF-1 - Trypanosoma cruzi cruzi]	3
1710	3329623	(AF078790) No definition line found [Caenorhabditis elegans]	1.3
1711	2459999	(AF013108) tubulin Uni3 [Chlamydomonas reinhardtii]	0.32
1712	1705447	BACTENECIN 7 PRECURSOR (BAC7) aries]	0.26
1713	3043596	(AB011108) KIAA0536 protein [Homo sapiens]	4e-022
1714	3879850	(Z81592) predicted using Genefinder	3e-033

Table 2B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)

SEQ ID	ACCESSION	DESCRIPTION1	P VALUE
1724	987050	(X65335) lacZ [Cloning vector pSV-beta-Galactosidase Control]	7.6
1725	1334582	(X55026) ORF16; no ATG start codon	6.8
1726	2981631	(AB012223) ORF2 [Canis familiaris]	5.2
1727	628300	gene F protein - rinderpest virus virus]	4.8
1728	4008417	(Z77669) Similarity to Human aminopeptidase N (SW:AMPN_HUMAN); cDNA EST EMBL:D36412 comes from this gene; cDNA EST EMBL:D37688 comes from this gene; cDNA EST EMBL:D34550 comes from this gene; cDNA EST EMBL:D33568	3.9
1729	1170083	PROBABLE GLOBAL TRANSACTIVATOR transactivator-like protein [Autographa californica nucleopolyhedrovirus]	3.4
1730	3757727	(AL022727) dJ80I19.7 (olfactory receptor-like protein (hs6M1-3)) [Homo sapiens]	3.3
1731	126296	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG protein [Nycticebus coucang]	1.2
1732	130702	LARGE STRUCTURAL PHOSPHOPROTEIN PHOSPHOPROTEIN) (BPP) >gi 73955 pir XPBEA9 large structural phosphoprotein pp150 - human cytomegalovirus phosphoprotein 150	0.97
1733	1706571	EPITHELIAL CHLORIDE CHANNEL PROTEIN calcium-activated chloride channel [Bos taurus]	0.87
1734	2981631	(AB012223) ORF2 [Canis familiaris]	0.56
1735	1280072	(U55366) coded for by C. elegans cDNA yk85a2.5; coded for by C. elegans cDNA yk85a2.3; Similar to cuticlin	0.44
1736	2496862	HYPOTHETICAL 6.1 KD PROTEIN C03B1.10 IN CHROMOSOME X >gi 1072242 (U40952) C03B1.10 gene product	0.001
1737	2228750	(U93868) RNA polymerase III subunit [Homo sapiens]	1e-007
1738	4503511	UNKNOWN >gi 3264861 (U97670) eukaryotic translation initiation factor eIF3, p35 subunit [Homo sapiens]	4e-031
1739	4503511	UNKNOWN >gi 3264861 (U97670) eukaryotic translation initiation factor eIF3, p35 subunit [Homo sapiens]	1e-032
1740	113667	!!!! ALU CLASS B WARNING ENTRY !!!!	5.3
1742	2736375	(AF039040) No definition line found [Caenorhabditis elegans]	6
1743	2736375	(AF039040) No definition line found [Caenorhabditis elegans]	3.4
1744	1002672	(U30261) G protein beta subunit-like; Method: conceptual translation supplied by author [Schistosoma mansoni]	5e-024
1752	4200151	(AJ011538) hypothetical protein virus]	3.9
1753	134528	SLP1 PROTEIN (VACUOLAR PROTEIN SORTING PROTEIN 33) >gi 101624 pir A34708 SLP1 protein SLP1 protein [Saccharomyces cerevisiae] >gi 173185	1.6
1754	1175386	HYPOTHETICAL 37.7 KD PROTEIN C18B11.06 IN CHROMOSOME I >gi 2130289 pir S58305 hypothetical protein SPAC18B11.06 - fission yeast pombe]	0.13
1756	2909528	(AL021932) PPE [Mycobacterium tuberculosis]	4.9
1760	3876797	(Z81531) cDNA EST EMBL:D66579 comes from this gene; cDNA EST EMBL:D70408 comes from this gene; cDNA EST yk263d3.5 comes from this gene; cDNA EST yk275c1.5 comes from this gene; cDNA EST EMBL:C10270 comes from this gene [Caenorh...	3.9
1770	3608418	(AF086634) cyclin B [Dreissena polymorpha]	8.9
1771	416868	CYTOKINE RECEPTOR COMMON BETA CHAIN PRECURSOR >gi 110595 pir A35782 cytokine receptor common beta chain precursor - mouse >gi 309101 (M34397) interleukin 3 receptor-like	4.3
1772	126296	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG protein [Nycticebus coucang]	2.9
1773	728834	!!!! ALU SUBFAMILY SB2 WARNING ENTRY	1.9
1774	728836	!!!! ALU SUBFAMILY SP WARNING ENTRY	0.3

Table 2B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)

SEQ ID	ACCESSION	DESCRIPTION1	P VALUE
1775	126296	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG protein [Nycticebus coucang]	0.001
1776	3879850	(Z81592) predicted using Genefinder	2e-037
1777	4155993	(AE001560) putative [Helicobacter pylori J99]	1.4
1782	225047	reverse transcriptase related protein [Homo sapiens]	2.2
1790	3785977	(AC005560) putative growth regulator protein (AP000005) 617aa long hypothetical prolyl endopeptidase [Pyrococcus horikoshii]	9.4
1791	3257681	(U97553) capsid protein [murine herpesvirus 68]	7.8
1792	2317972	cytochrome-c oxidase (EC 1.9.3.1) chain I - Trypanoplasma borreli mitochondrion (SGC6) >gi 563140 borreli]	1.5
1793	1085738	(AL034559) predicted using hexExon; MAL3P7.14 (PFC0925w), Hypothetical protein, len: 489 aa	0.014
1794	4493973	CYTOCHROME C OXIDASE POLYPEPTIDE III honeybee mitochondrion (SGC4) >gi 552443 (L06178) cytochrome oxidase subunit 3 [Apis mellifera ligustica]	0.002
1800	461796	(U88295) carnitine palmitoyltransferase II [Rattus norvegicus]	9.1
1801	1850592	(M35837) alpha-amylase/alpha-galactosidase fusion protein	9
1802	207854	Ksp-cadherin - rabbit >gi 902886 (U28945) Ksp-cadherin [Oryctolagus cuniculus] cuniculus]	8.7
1803	2136989	(X06487) bcl2-Ig fusion gene [Homo sapiens]	3.4
1804	288448	(U62325) FE65-like protein [Homo sapiens]	3.4
1805	1657752	(AB012223) ORF2 [Canis familiaris]	2.1
1806	2981631	annexin 31 XXXI [Homo sapiens]	5e-007
1807	4502103	(U92864) maturase [Quercus rubra]	1e-043
1808	2149830	(AB012223) ORF2 [Canis familiaris]	9.6
1809	2981631	!!!! ALU SUBFAMILY SB WARNING ENTRY	0.046
1810	728832	(Z98547) predicted using hexExon; MAL3P3.17 (PFC0420w), Calcium-dependent protein kinase, len: 591 aa; Similarity to calcium-dependent protein kinases. P.falciparum calcium-dependent protein kinase CDPK2 (TR:O15865) BLAST Sco...	0.035
1813	3649769	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG protein [Nycticebus coucang]	2.1
1814	126296	(M26361) LINE/Ig H-chain fusion protein [Mus musculus]	1.6
1815	197968	HYPOTHETICAL 6.1 KD PROTEIN C03B1.10 IN CHROMOSOME X >gi 1072242 (U40952) C03B1.10 gene product	0.036
1816	2496862	T-CELL RECEPTOR BETA CHAIN PRECURSOR precursor (ANA	0.001
1817	135514	(AB011108) KIAA0536 protein [Homo sapiens]	0.0006
1818	3043596	!!!! ALU SUBFAMILY SX WARNING ENTRY	4e-016
1821	728838	(X92485) pva1 [Plasmodium vivax]	7
1822	1177607	hypothetical protein (LIH 5' region) - human	0.23
1823	106323	(AB012223) ORF2 [Canis familiaris]	0.071
1824	2981631	(U41272) Similar to man(9)-alpha-mannosidase.	2e-009
1825	1086860	(AF007261) SecY-type transporter protein [Reclinomonas	1e-032
1829	2258350	FMRFAMIDE-RELATED NEUROPEPTIDES PRECURSOR >gi 416208 (U03137) neuropeptide precursor FMRFamide-related	2.9
1830	1169643	LIPOATE-PROTEIN LIGASE A 6.3.4.-) A - Escherichia coli >gi 504496 (L27665) lipoate-protein ligase A [Escherichia coli]	0.026
1834	585424	(AB012223) ORF2 [Canis familiaris]	7.1
1835	2981631	(AL049608) putative protein [Arabidopsis thaliana]	0.044
1841	4584540	(AL034559) predicted using hexExon; MAL3P7.17 (PFC0940c), Hypothetical protein, len: 807 aa	7.3
1842	4493975	(M14820) NADH dehydrogenase subunit 4 [Trypanosoma brucei]	3
1843	343539	(AF047441) RNA polymerase I 40kD subunit [Homo sapiens]	1.7
1844	3335138		1

Table 2B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)

SEQ ID	ACCESSION	DESCRIPTION1	P VALUE
1852	2612897	(AF015825) hypothetical ABC transporter [Bacillus subtilis] >gi 2633579 emb CAB13082 (Z99110) similar to amino acid ABC transporter (ATP-binding protein)	5.9
1853	728836	!!!! ALU SUBFAMILY SP WARNING ENTRY	1.2
1854	113668	!!!! ALU CLASS C WARNING ENTRY !!!!	0.17
1855	728836	!!!! ALU SUBFAMILY SP WARNING ENTRY	0.05
1856	106323	hypothetical protein (L1H 5' region) - human	0.048
1857	2981631	(AB012223) ORF2 [Canis familiaris]	0.0002
1859	729785	HEXOSE TRANSPORTER HXT8 YJL214w - yeast (Saccharomyces cerevisiae) cerevisiae] >gi 1015600 emb CAA89511 (Z49489) ORF YJL214w [Saccharomyces cerevisiae]	0.12
1861	1791243	(U83119) ORF2 consensus sequence encoding endonuclease and reverse transcriptase minus RNaseH [Rattus norvegicus]	4e-006
1862	854065	(X83413) U88 [Human herpesvirus 6]	2e-006
1863	1707274	(U80931) strong similarity to class-III of pyridoxal-phosphate-dependent aminotransferases	3e-032
1871	4049828	(AF063866) ORF MSV145 hypothetical protein [Melanoplus sanguinipes entomopoxvirus]	5.6
1872	1109853	(U41538) weak similarity to the S. cerevisiae activator 1 05 KD subunit (replication factor C 95 KD subunit)	4.5
1873	113668	!!!! ALU CLASS C WARNING ENTRY !!!!	3.6
1874	1684995	(U20663) NADH dehydrogenase subunit [Encyclia tampensis]	1.6
1875	3599325	(AF081106) ORF1 [Mus musculus domesticus]	0.36
1876	160379	(M63274) malaria antigen [Plasmodium falciparum]	0.16
1877	728837	!!!! ALU SUBFAMILY SQ WARNING ENTRY	0.12
1878	2134199	myosin I beta - bullfrog >gi 602138 (U14549) myosin I beta [Rana catesbeiana] >gi 603692 (U14382) myosin I beta [Rana catesbeiana]	0.036
1879	1872200	(U22376) alternatively spliced product using exon 13A	0.009
1880	1938524	(U97012) contains similarity to a ground domain, also weakly similar to drosophila fork head domain transcription factor SLP1 (SP:P32030) [Caenorhabditis elegans]	0.17
1882	3510507	(AF032382) metalloprotease-disintegrin [Xenopus laevis]	0.77
1883	728837	!!!! ALU SUBFAMILY SQ WARNING ENTRY	0.33
1884	854065	(X83413) U88 [Human herpesvirus 6]	1e-007
1886	728833	!!!! ALU SUBFAMILY SBI WARNING ENTRY	7.4
1887	1353178	PUTATIVE SERINE/THREONINE PROTEIN PHOSPHATASE C27B7.6 IN CHROMOSOME IV serine/threonine protein phosphatase [Caenorhabditis elegans]	7.2
1888	728837	!!!! ALU SUBFAMILY SQ WARNING ENTRY	7e-009
1890	435942	(U04295) DNA-binding factor of bZIP class [Oryza sativa]	1
1891	728832	!!!! ALU SUBFAMILY SB WARNING ENTRY	0.94
1892	3599347	(AF081114) ORF2 [Mus musculus domesticus]	0.55
1893	728837	!!!! ALU SUBFAMILY SQ WARNING ENTRY	0.056
1894	1196432	(M22333) unknown protein [Homo sapiens]	0.002
1895	728838	!!!! ALU SUBFAMILY SX WARNING ENTRY	0.004
1901	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	8
1902	3646450	(AL031603) conserved hypothetical protein.	7e-028
1903	2213560	(Z97052) hypothetical protein	5e-026
1905	3002527	(AF010144) neuronal thread protein AD7c-NTP [Homo sapiens]	0.066
1906	2072977	(U93574) putative p150 [Homo sapiens]	0.022
1907	728835	!!!! ALU SUBFAMILY SC WARNING ENTRY	0.019
1908	4153886	(AB013357) 49 kDa zinc finger protein [Mus musculus]	2e-005
1910	2072974	(U93573) p40 [Homo sapiens]	2
1911	728837	!!!! ALU SUBFAMILY SQ WARNING ENTRY	0.011

Table 2B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)

SEQ ID	ACCESSION	DESCRIPTION1	P VALUE
1914	4572297	(AF071799) T-cell surface glycoprotein CD4 precursor	6
1915	1350904	RIBOSOME RECYCLING FACTOR (RIBOSOME RELEASING FACTOR) (RRF) >gi 1361841 pir A64248 ribosome releasing factor Mycoplasma genitalium (SGC3) releasing factor (frr) [Mycoplasma	3.7
1916	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	1.4
1917	728832	!!!! ALU SUBFAMILY SB WARNING ENTRY	0.0006
1918	126296	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG protein [Nycticebus coucang]	4e-005
1919	1791243	(U83119) ORF2 consensus sequence encoding endonuclease and reverse transcriptase minus RNaseH [Rattus norvegicus]	4e-009
1920	126295	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG	0.006
1921	348317	ATPase 6 - Sauroleishmania tarentolae	7.7
1923	1723547	HYPOTHETICAL 61.8 KD PROTEIN C12B10.03 IN CHROMOSOME I >gi 1262416 emb CAA94693	8.6
1924	1177607	(X92485) pva1 [Plasmodium vivax]	4.9
1925	3068583	(AF000580) Rep-like [Dictyostelium discoideum]	2.4
1926	2120082	hypothetical protein II (retroponon LINE-1)	0.21
1927	1335198	(X03145) pot. ORF III [Homo sapiens]	0.0003
1930	2134328	ECH - chicken >gi 1037160 dbj BAA08364	8.3
1931	4502377	B-cell growth factor 1 (12kD)	0.094
1932	3417289	(U95740) Unknown gene product [Homo sapiens]	0.065
1933	565080	(U14550) SThM [Homo sapiens]	0.006
1934	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	7e-006
1935	3649741	(AJ000281) mucin [Homo sapiens]	5e-020
1936	3551821	(AF058803) mucin 4 [Homo sapiens]	8e-021
1937	4519443	(AB017430) kinesin-like DNA binding protein [Homo sapiens]	3e-029
1939	1710216	(U79260) unknown [Homo sapiens]	1e-005
1940	728837	!!!! ALU SUBFAMILY SQ WARNING ENTRY	5e-008
1942	4494012	(AL034559) predicted using hexExon; MAL3P7.32 (PFC1010w), Hypothetical protein, len: 1322 aa	4.5
1943	220578	(D00570) open reading frame (251 AA) [Mus musculus]	0.077
1944	2731377	(U28739) similar to alcohol dehydrogenase/ribitol dehydrogenase [Caenorhabditis elegans]	1e-028
1945	4587207	(AB020527) Na/PO4 cotransporter homolog	4e-034
1948	728832	!!!! ALU SUBFAMILY SB WARNING ENTRY	0.21
1949	929913	(V01442) ribosomal protein S8 [Xenopus laevis]	0.066
1950	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	2e-006
1951	1125754	(U42833) coded for by C. elegans cDNA cml16f6; coded for by C. elegans cDNA CEESU63F; similar to S. cerevisiae SOF1 protein (SP:P33750) [Caenorhabditis elegans]	1e-028
1952	4587207	(AB020527) Na/PO4 cotransporter homolog	6e-047
1953	4587207	(AB020527) Na/PO4 cotransporter homolog	2e-051
1955	2981631	(AB012223) ORF2 [Canis familiaris]	0.027
1956	4138064	(Y18301) reverse transcriptase [Ovine pulmonary adenocarcinoma	0.0002
1961	4507991	zinc finger protein 140 (clone pHZ-39) >gi 1731416 sp P52738 Z140_HUMAN ZINC FINGER PROTEIN 140 >gi 2136409 pir C57785 zinc finger protein ZNF140 - human >gi 487787 (U09368) zinc finger protein ZNF140 [Homo sapiens]	8.6
1962	1711541	SERINE/THREONINE PROTEIN KINASE SSK2 (SUPPRESSOR OF SENSOR KINASE 2) SSK2 gene product [Saccharomyces	5.9
1963	3236252	(AC004684) CER1-like protein [Arabidopsis thaliana]	3
1964	728836	!!!! ALU SUBFAMILY SP WARNING ENTRY	0.001
1965	4138070	(Y18303) reverse transcriptase [Ovine pulmonary adenocarcinoma	0.0002
1966	114128	ADP-RIBOSYLATION FACTOR 6 1-175 [Gallus gallus]	9e-011

Table 2B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)

SEQ ID	ACCESSION	DESCRIPTION1	P VALUE
1967	2293566	(AF012896) ADP-ribosylation factor 1 [Oryza sativa]	2e-012
1969	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	0.091
1970	59977	(Z14310) tripartite fusion transcript PLA2L	2e-005
1971	126296	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG protein [Nycticebus coucang]	9
1972	4155181	(AE001495) putative TYPE II RESTRICTION ENZYME	4.8
1973	2239204	(Z97209) vacuolar carboxypeptidase	0.008
1974	3342107	(AF075269) nef protein [Simian immunodeficiency virus]	6.9
1978	423149	X-linked retinopathy protein (C-terminal, clone XEH.8c) - human (fragment) >gi 299471 bbs 129340 XEH.8c} [human, Peptide Partial,	0.66
1979	1791243	(U83119) ORF2 consensus sequence encoding endonuclease and reverse transcriptase minus RNaseH [Rattus norvegicus]	0.025
1980	126296	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG protein [Nycticebus coucang]	0.011
1981	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	0.0009
1982	1791243	(U83119) ORF2 consensus sequence encoding endonuclease and reverse transcriptase minus RNaseH [Rattus norvegicus]	4e-006
1984	1903379	(U52073) differentially repressed by testosterone and dihydrotestosterone [Mus musculus]	3.2
1985	1903379	(U52073) differentially repressed by testosterone and dihydrotestosterone [Mus musculus]	3.1
1986	3599339	(AF081111) ORF2 [Mus musculus domesticus]	2e-007
1990	728835	!!!! ALU SUBFAMILY SC WARNING ENTRY	5.9
1991	729093	CCAAT DISPLACEMENT PROTEIN (HOMEBOX PROTEIN CLOX) (CLOX-1) >gi 423173 pir S33121 homeotic protein Clox - dog (fragment) >gi 2202 emb CAA48782	0.018
1992	126295	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG	0.004
1993	1125754	(U42833) coded for by C. elegans cDNA cml6f6; coded for by C. elegans cDNA CEESU63F; similar to S. cerevisiae SOF1 protein (SP:P33750) [Caenorhabditis elegans]	1e-030
1994	3789771	(AF055386) MHC class I related protein precursor	1.9
1995	728832	!!!! ALU SUBFAMILY SB WARNING ENTRY	3.1
1996	3023729	FRUCTOSE-1,6-BISPHOSPHATASE fructose-1,6-bisphosphatase [Mus musculus]	0.21
1997	3182916	ADP-RIBOSYLATION FACTOR factor [Plasmodium falciparum] >gi 1932731 (U57370) ADP-ribosylation factor [Plasmodium	2e-015
2000	113668	!!!! ALU CLASS C WARNING ENTRY !!!!	1
2001	728836	!!!! ALU SUBFAMILY SP WARNING ENTRY	0.0003
2002	59977	(Z14310) tripartite fusion transcript PLA2L	7e-007
2003	91035	laminin receptor homolog - mouse 295) [Mus musculus] >gi 228997 prf 1815216A laminin receptor [Cricetinae gen. sp.]	0.12
2005	4506545	regulator of mitotic spindle assembly 1 >gi 1350799 sp P49646 RMS1 HUMAN REGULATOR OF	3.7
2006	1619936	(U70935) reverse transcriptase [Peromyscus maniculatus]	0.015
2007	728837	!!!! ALU SUBFAMILY SQ WARNING ENTRY	0.007
2008	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	0.0002
2009	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	5e-006
2010	3157938	(AC002131) Similar to seryl-tRNA synthetase gb U10400 from S cerevisiae. EST gb N96627 comes from this gene.	5e-029
2011	2496862	HYPOTHETICAL 6.1 KD PROTEIN C03B1.10 IN CHROMOSOME X >gi 1072242 (U40952) C03B1.10 gene product	0.17
2012	2443342	(D88764) alpha 2 type I collagen [Rana catesbeiana]	1.2

Table 2B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)

SEQ ID	ACCESSION	DESCRIPTION1	P VALUE
2013	1546035	(U64570) myelin/oligodendrocyte glycoprotein-16.3kD(a) precursor [Homo sapiens] >gi 1546037 (U64571) myelin/oligodendrocyte glycoprotein-16.3kD(b) precursor	0.15
2014	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	0.006
2015	113668	!!!! ALU CLASS C WARNING ENTRY !!!!	0.003
2016	728838	!!!! ALU SUBFAMILY SX WARNING ENTRY	0.0003
2017	728837	!!!! ALU SUBFAMILY SQ WARNING ENTRY	1e-005
2019	3002527	(AF010144) neuronal thread protein AD7c-NTP [Homo sapiens]	1e-005
2021	728838	!!!! ALU SUBFAMILY SX WARNING ENTRY	3e-005
2022	2879805	(AL021813) hypothetical protein	0.6
2023	1711659	TCP1-CHAPERONIN COFACTOR A taurus]	0.003
2024	113667	!!!! ALU CLASS B WARNING ENTRY !!!!	0.0007
2025	113667	!!!! ALU CLASS B WARNING ENTRY !!!!	0.0007
2026	87765	hypothetical L1 protein (third intron of gene TS) - human >gi 364964 prf 1510254A L1 repetitive element ORF [Homo	0.0003
2027	4009460	(AF039401) calcium-dependent chloride channel-1 [Homo sapiens]	2e-011
2028	1730840	PUTATIVE CYSTEINYL-TRNA SYNTHETASE C29E6.06C (CYSTEINE--TRNA LIGASE) (CYSRS) YNL247w - yeast	2e-035
2030	4200165	(Y16262) neutral invertase [Daucus carota]	5.7
2031	1150834	(U42471) Wiscott-Aldrich Syndrome protein homolog [Mus	0.032
2032	113669	!!!! ALU CLASS D WARNING ENTRY !!!!	0.002
2033	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	0.0008
2034	1657758	(U66707) densin-180 [Rattus norvegicus]	1e-024
2035	4165313	(AB022083) SOX30 protein [Homo sapiens]	0.42
2036	1657758	(U66707) densin-180 [Rattus norvegicus]	1e-024
2037	3193336	(AF069301) DBI-related protein [Homo sapiens]	7e-055
2038	126296	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG protein [Nycticebus coucang]	8e-008
2039	2981631	(AB012223) ORF2 [Canis familiaris]	6e-008
2040	4098124	(U73522) AMSH [Homo sapiens]	3e-018
2042	113668	!!!! ALU CLASS C WARNING ENTRY !!!!	9e-006
2043	728837	!!!! ALU SUBFAMILY SQ WARNING ENTRY	5e-009
2044	3123312	ZINC FINGER PROTEIN 142 (KIAA0236) Human zinc finger protein(ZNF142) [Homo sapiens]	0.7
2045	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	0.13
2046	1710216	(U79260) unknown [Homo sapiens]	0.005
2047	558401	(Z38113) incomplete orf, len: 160, CAI: 0.09 similar to MRP_ECOLI P21590 39.9 KD PROTEIN	1e-035
2048	224398	ORF [Simian virus 40]	1.6
2049	728838	!!!! ALU SUBFAMILY SX WARNING ENTRY	0.001
2050	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	3e-005
2051	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	3e-005
2052	2981631	(AB012223) ORF2 [Canis familiaris]	6e-007
2053	2981631	(AB012223) ORF2 [Canis familiaris]	3e-007
2054	2052393	(U86758) netrin-2 like protein [Homo sapiens] sapiens]	5e-012
2055	3023928	PROBABLE HISTONE DEACETYLASE 1-2	6e-031
2056	2500285	60S RIBOSOMAL PROTEIN L5	0.015
2057	728836	!!!! ALU SUBFAMILY SP WARNING ENTRY	0.0003
2058	113668	!!!! ALU CLASS C WARNING ENTRY !!!!	0.001
2059	1546035	(U64570) myelin/oligodendrocyte glycoprotein-16.3kD(a) precursor [Homo sapiens] >gi 1546037 (U64571) myelin/oligodendrocyte glycoprotein-16.3kD(b) precursor	0.0006
2060	543944	CBID PROTEIN >gi 154423 (L12006) putative [Salmonella	5.9
2064	728836	!!!! ALU SUBFAMILY SP WARNING ENTRY	0.002

Table 2B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)

SEQ ID	ACCESSION	DESCRIPTION1	P VALUE
2065	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	6e-006
2068	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	0.013
2069	2072977	(U93574) putative p150 [Homo sapiens]	0.001
2070	2072972	(U93572) putative p150 [Homo sapiens]	8e-005
2071	130402	RETROVIRUS-RELATED POL POLYPROTEIN	4e-013
2072	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	0.002
2073	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	0.007
2074	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	4e-006
2075	987050	(X65335) lacZ [Cloning vector pSV-beta-Galactosidase Control]	0.017
2076	106322	hypothetical protein (L1H 3' region) - human	7e-006
2078	804808	(M13100) unknown protein [Rattus norvegicus]	0.11
2079	347964	(L22453) TARBP-b gene product [Homo sapiens]	0.001
2080	1196432	(M22333) unknown protein [Homo sapiens]	4e-005
2081	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	8e-006
2082	3023928	PROBABLE HISTONE DEACETYLASE 1-2	5e-037
2083	4505895	pleiotropic regulator 1 (PRL1, Arabidopsis homolog) >gi 2832296 (AF044333) pleiotropic regulator 1 [Homo sapiens]	6e-071
2086	728836	!!!! ALU SUBFAMILY SP WARNING ENTRY	2e-005
2087	126296	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG protein [Nycticebus coucang]	6e-008
2088	126296	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG protein [Nycticebus coucang]	7e-006
2089	106322	hypothetical protein (L1H 3' region) - human	2e-006
2090	2981631	(AB012223) ORF2 [Canis familiaris]	1e-014
2091	3336903	(Y10809) bZIP DNA-binding protein	2.1
2092	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	0.01
2093	126296	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG protein [Nycticebus coucang]	0.002
2094	728837	!!!! ALU SUBFAMILY SQ WARNING ENTRY	4e-008
2095	113671	!!!! ALU CLASS F WARNING ENTRY !!!!	0.0001
2096	386786	(J04988) 90 kD heat shock protein [Homo sapiens]	3e-009
2097	106322	hypothetical protein (L1H 3' region) - human	7e-005
2099	126296	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG protein [Nycticebus coucang]	0.1
2100	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	1e-005
2101	2981631	(AB012223) ORF2 [Canis familiaris]	1e-006
2102	2500367	60S RIBOSOMAL PROTEIN L21 musculus]	4e-007
2103	4106562	(Z83819) dJ146H21.2 (similar to CYTOCHROME B-245 HEAVY CHAIN) [Homo sapiens]	2e-061
2104	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	8e-006
2106	1869835	(Z86099) protein kinase [human herpesvirus 2]	8.9
2107	1754989	(U47661) proline-rich protein PRP2 precursor [Lupinus luteus]	6.7
2108	2580578	(AF000996) ubiquitous TPR motif, Y isoform [Homo sapiens]	0.0004
2109	1173220	40S RIBOSOMAL PROTEIN S15A	0.0003
2110	3646139	(AJ011081) mader-drop8 [Homo sapiens]	2e-006
2111	3192897	(AF066071) SP85; PsB [Dictyostelium discoideum]	1e-008
2112	126295	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG	8e-009
2113	3599336	(AF081110) ORF2 [Mus musculus domesticus]	5e-012
2115	4185943	(Y17833) pol protein [Human endogenous retrovirus K]	2e-022
2118	53912	(X57960) ribosomal protein L7 [Mus musculus]	3e-027
2120	2506605	HYPOTHETICAL 65.0 KD PROTEIN IN HUPB-COF INTERGENIC REGION >gi 1580716 dbj BAA11649 hypothetical	4.5
2121	2642222	(AF030885) telomere-associated recQ-like helicase	0.001

Table 2B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)

SEQ ID	ACCESSION	DESCRIPTION1	P VALUE
2125	1085573	microtubule-associated protein MAP2 - rat molecular weight	
2126	3192899	microtubule-associated protein cell line, Peptide Partial, 381 aa]	1.9
2127	106322	(AF066072) SP85; PsB [Dictyostelium discoideum]	0.024
2128	2981631	hypothetical protein (L1H 3' region) - human	1e-005
2129	403460	(AB012223) ORF2 [Canis familiaris]	2e-010
		(L24521) transformation-related protein [Homo sapiens]	0.003
2130	1082633	Nascent polypeptide associated complex alpha chain - human >gi 556642 emb CAA56869 (X80909) Nascent polypeptide associated complex alpha subunit [Homo sapiens] >gi 4092060 (AF054187) alpha NAC [Homo sapiens]	3e-006
2132	1669472	(U53757) pol polyprotein [Feline immunodeficiency virus]	6.2
2133	1127036	(D26178) serine/threonine protein kinase	0.81
2134	728835	!!!! ALU SUBFAMILY SC WARNING ENTRY	2e-007
2136	728837	!!!! ALU SUBFAMILY SQ WARNING ENTRY	5e-008
2137	730246	OX-2 MEMBRANE GLYCOPROTEIN PRECURSOR precursor - human (fragment) >gi 1335216 emb CAA28943	3e-008
2138	3341992	(AF054174) histone macroH2A1.2 [Homo sapiens]	6e-033
2139	1363325	RNA helicase HEL117 - rat >gi 897915	9.9
2140	3892705	(AL033545) putative protein [Arabidopsis thaliana]	0.14
2141	2565196	(AF000381) non-functional folate binding protein [Homo sapiens]	0.007
2142	106322	hypothetical protein (L1H 3' region) - human	5e-007
2143	106322	hypothetical protein (L1H 3' region) - human	0.033
2144	133902	40S RIBOSOMAL PROTEIN S27 ribosomal protein S27 isoform [Homo sapiens]	0.0004
2145	111814	hypothetical protein 3 - rat norvegicus]	2e-011
2146	1669454	(U53748) pol polyprotein [Feline immunodeficiency virus]	8.6
2147	126296	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG protein [Nycticebus coucang]	6e-005
2148	4506701	ribosomal protein S23 S23 >gi 543449 pir S41955 ribosomal protein S23 - rat protein [Homo sapiens] >gi 453281 emb CAA54584 (X77398) ribosomal protein S23 [Rattus norvegicus]	3e-009
2149	126296	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG protein [Nycticebus coucang]	3e-011
2152	1353390	(U34998) Rad9 [Coprinus cinereus]	8
2153	2134082	hepatocyte growth factor receptor - African clawed frog	4.8
2154	1196432	(M22333) unknown protein [Homo sapiens]	3e-006
2155	730451	60S RIBOSOMAL PROTEIN L13A (23 KD HIGHLY BASIC PROTEIN) >gi 345897 pir S29539 basic protein, 23K - human >gi 23691 emb CAA40254 (X56932) 23 kD highly basic protein	2e-008
2156	2072964	(U93569) putative p150 [Homo sapiens]	3e-009
2157	1791243	(U83119) ORF2 consensus sequence encoding endonuclease and reverse transcriptase minus RNaseH [Rattus norvegicus]	4e-012
2158	4506437	retinoblastoma-binding protein 1; RBP1 >gi 1710030 sp P29374 RBB1_HUMAN RETINOBLASTOMA BINDING PROTEIN 1 (RBBP-1) >gi 2136103 pir I58383 retinoblastoma binding protein 1 - human protein 1, RBP1 [human,	5e-008
2160	2981631	(AB012223) ORF2 [Canis familiaris]	0.0008
2161	126296	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG protein [Nycticebus coucang]	0.0005
2162	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	2e-007
2163	114977	MEMBRANE-ASSOCIATED PROTEIN HEM-2 H19 protein - mouse (fragment) >gi 51136 emb CAA43693	2e-012
2165	126296	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG protein [Nycticebus coucang]	6e-005

Table 2B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)

SEQ ID	ACCESSION	DESCRIPTION1	P VALUE
2166	126296	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG protein [Nycticebus coucang]	1e-012
2172	106323	hypothetical protein (L1H 5' region) - human	9e-010
2173	126296	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG protein [Nycticebus coucang]	2e-013
2174	126296	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG protein [Nycticebus coucang]	2e-013
2175	695802	(L39061) transcription factor SL1 [Homo sapiens]	4e-014
2177	2072964	(U93569) putative p150 [Homo sapiens]	5e-007
2180	1085573	microtubule-associated protein MAP2 - rat molecular weight microtubule-associated protein cell line, Peptide Partial, 381 aa]	3.8
2181	104623	collagen, corneal - chicken (fragment)	0.097
2182	2981631	(AB012223) ORF2 [Canis familiaris]	1e-010
2183	2493820	CYTOCHROME C OXIDASE POLYPEPTIDE I ornatipinnis]	3e-011
2184	2494737	HYPOTHETICAL 71.7 KD PROTEIN F52H3.2 IN CHROMOSOME II >gi 3877390 emb CAA91322	3e-046
2185	1709997	DNA REPAIR PROTEIN RAD18 pombe]	0.64
2186	59977	(Z14310) tripartite fusion transcript PLA2L	1e-006
2187	2072967	(U93570) putative p150 [Homo sapiens]	5e-007
2188	1800307	(U83883) p105 coactivator [Rattus norvegicus]	4e-010
2189	728831	!!!! ALU SUBFAMILY J WARNING ENTRY	4e-009
2190	2245560	(AF004339) cytochrome c oxidase subunit II [Homo sapiens]	9e-007
2191	3875269	(Z77655) Weak similarity to Human calcium-dependent proetase (SW:CANS_HUMAN)	0.2
2192	728835	!!!! ALU SUBFAMILY SC WARNING ENTRY	2e-010
2193	106322	hypothetical protein (L1H 3' region) - human	3e-013
2194	2072967	(U93570) putative p150 [Homo sapiens]	1e-015
2196	189086	(M18728) ORF1 [Homo sapiens]	0.0005
2197	2605776	(AF027404) signal recognition particle 14a [Macaca radiata]	0.0003
2202	339777	(M80344) ORF2 contains a reverse transcriptase domain.	5e-017
2203	4539386	(AL035526) extensin-like protein	1
2204	3043654	(AB011137) KIAA0565 protein [Homo sapiens]	3e-020
2206	3929396	HYPOTHETICAL 47.8 KD PROTEIN F57B9.5 IN CHROMOSOME III >gi 532824 (U13876) F57B9.5 gene product	0.1
2207	1769472	(U15780) p82 [Homo sapiens]	9e-037
2208	728837	!!!! ALU SUBFAMILY SQ WARNING ENTRY	8e-015
2209	2506089	26S PROTEASE REGULATORY SUBUNIT 7	1e-016
2210	1073466	aldehyde dehydrogenase (EC 1.2.1.-) aldB - Escherichia coli >gi 912476 (U00039) No definition line found [Escherichia coli] >gi 1790014 (AE000436) aldehyde dehydrogenase B (lactaldehyde	1.4
2211	2072960	(U93568) p40 [Homo sapiens]	3e-005
2212	4009460	(AF039401) calcium-dependent chloride channel-1 [Homo sapiens]	2e-020
2214	100687	hydroxyproline-rich glycoprotein - rice glycoprotein [Oryza sativa]	8.7
2215	3043616	(AB011118) KIAA0546 protein [Homo sapiens]	2e-010
2216	126296	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG protein [Nycticebus coucang]	6e-014
2218	91043	LINE-1 hypothetical protein - mouse (fragment) musculus]	3e-005
2220	4106562	(Z83819) dJ146H21.2 (similar to CYTOCHROME B-245 HEAVY CHAIN) [Homo sapiens]	5e-061
2221	631507	zinc-containing protein - human	0.0001
2223	2072972	(U93572) putative p150 [Homo sapiens]	3e-009
2224	3123174	HYPOTHETICAL PROTEIN	1e-012
2226	126296	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG protein [Nycticebus coucang]	1e-007

Table 2B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)

SEQ ID	ACCESSION	DESCRIPTION1	P VALUE
2227	2981631	(AB012223) ORF2 [Canis familiaris]	3e-013
2228	109930	GTP-binding protein rah - mouse (fragment) G-protein=low-molecular-weight GTP-binding protein GTP-binding protein [Mus	4e-020
2229	2981631	(AB012223) ORF2 [Canis familiaris]	5e-007
2230	1698455	(U49974) mariner transposase [Homo sapiens]	5e-007
2231	2289235	(U95016) myocyte nuclear factor-beta [Mus musculus]	8e-015
2232	2827495	(AL009196) 1-evidence=predicted by content; 1-method=genefinder;084; 1-evidence_end; 2-evidence=predicted by match; 2-match_accession=AA391048; 2-match_description=LD09991.5prime LD Drosophila melanogaster	1.9
2233	2465330	(U92818) unnamed HERV-H protein [Homo sapiens]	1e-011
2234	2135837	nuclear protein H731 - human >gi 1825562	4e-014
2235	4164448	(AF044958) NADH:ubiquinone oxidoreductase ASH1 subunit	2e-025
2236	4506077	protein kinase C substrate 80K-H >gi 120629 sp P14314 G19P_HUMAN PROTEIN KINASE C SUBSTRATE, 80 KD-PROTEIN, HEAVY CHAIN (PKCSH) (80K-H PROTEIN) >gi 105167 pir A32469 80K protein H precursor 80K-	4e-031
2237	2981631	(AB012223) ORF2 [Canis familiaris]	0.007
2238	1176422	(U43194) rhophilin [Mus musculus]	0.81
2239	4263743	(AC004923) similar to UNC-93; similar to U89424 (PID:g3642687) [Homo sapiens]	3e-041
2240	106322	hypothetical protein (L1H 3' region) - human	2e-018
2241	2352427	(AF004161) peroxisomal Ca-dependent solute carrier	1e-044
2242	4104400	(AF035401) exocellobiohydrolase precursor [Piromyces rhizinflata]	4.2
2243	158154	(M81959) POU domain protein [Drosophila melanogaster]	3
2244	114858	MAGNESIUM-PROTOPORPHYRIN IX MONOMETHYL ESTER OXIDATIVE CYCLASE 66 KD SUBUNIT Rhodobacter capsulatus >gi 46113 emb CAA77530 (Z11165) 575 aa (66 kD) oxidative	2.2
2245	2352427	(AF004161) peroxisomal Ca-dependent solute carrier	3e-044
2246	116746	PROBABLE COAT PROTEIN virus >gi 58812 emb CAA29526 (X06166) ORF IV (AA 1-489)	4.3
2247	2072967	(U93570) putative p150 [Homo sapiens]	6e-008
2248	2137494	M-sema F protein precursor - mouse homolog=M-Sema F [mice, neonatal brain, Peptide, 834 aa]	5.5
2249	1709971	60S RIBOSOMAL PROTEIN L10A (CSA-19)	1e-015
2250	1498225	(Y07569) PHAPI2a protein [Homo sapiens]	4e-012
2251	1711550	TRANSLOCON-ASSOCIATED PROTEIN, DELTA SUBUNIT PRECURSOR (TRAP-DELTA) (SIGNAL SEQUENCE RECEPTOR DELTA SUBUNIT) (SSR-DELTA) unnamed protein product [Homo sapiens] >gi 1302656 sapiens] >gi 1673433 emb CAA92215	3e-012
2252	126296	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG protein [Nycticebus coucang]	1e-013
2253	4502643	chaperonin containing T-complex subunit 6 >gi 730922 sp P40227 TCPZ_HUMAN T-COMPLEX PROTEIN 1, ZETA SUBUNIT (TCP-1-ZETA) (CCT-ZETA) (TCP20) sapiens]	1e-014
2254	2737894	(U59151) Cbf5p homolog [Homo sapiens]	4e-070
2255	1076557	extensin-like protein - cowpea (fragment) (Z69664) Similarity to Yeast cell division control protein cdc25 (SW:CC@%_SACKL); cDNA EST EMBL:D32475 comes from this gene; cDNA EST EMBL:D34376 comes from this gene; cDNA EST EMBL:D35124 comes from this gene; cDNA EST EMBL:D37...	0.6
2257	3878245	MAD2 (mitotic arrest deficient, yeast, homolog)-like 1 >gi 950199	9.2
2258	4505067	(U31278) mitotic feedback control protein Madp2 homolog [Homo	2e-009

Table 2B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)

SEQ ID	ACCESSION	DESCRIPTION1	P VALUE
2259	126296	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG protein [Nycticebus coucang]	4e-018
2260	4507669	tumor protein, translationally-controlled 1 CONTROLLED TUMOR PROTEIN (TCTP) (P23) factor - human >gi 37496 emb CAA34200 (X16064) tumor protein (AA 1 - 172) [Homo sapiens]	0.043
2261	66499	arylamine N-acetyltransferase (EC 2.3.1.5), monomorph - rabbit >gi 217728 dbj BAA00989 (D10108) arylamine N-acetyltransferase [Oryctolagus cuniculus]	1.8
2262	733532	(U23420) unknown [Drosophila melanogaster]	0.51
2263	3041664	DEOXYURIDINE 5'-TRIPHOSPHATE NUCLEOTIDOHYDROLASE PRECURSOR (DUTPASE) (DUTP PYROPHOSPHATASE) >gi 2443580 (AF018432) dUTPase [Homo sapiens] >gi 2735292 (U90223) deoxyuridine triphosphate	2e-029
2264	2136246	tastin - human >gi 905356 (U04810) tastin	1.1
2266	126295	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG	0.0002
2267	825671	(X16934) B23 nucleophosmin (280 AA) [Homo sapiens]	4e-013
2268	2231019	(Z97207) B-IND1 protein [Mus musculus]	2e-023
2269	4502189	aquaporin 8 sapiens]	1e-014
2270	126296	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG protein [Nycticebus coucang]	5e-015
2271	126296	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG protein [Nycticebus coucang]	5e-015
2272	218564	(D90358) HB-SOD [Schizosaccharomyces pombe]	4e-024
2274	1352736	PELOTA PROTEIN >gi 973224 (U27197) pelota [Drosophila	3e-038
2275	102177	hypothetical protein (ribosomal RNA repeat region) - Giardia lamblia	1.3
2276	113668	!!!! ALU CLASS C WARNING ENTRY !!!!	0.13
2277	961444	(D63876) KIAA0154 gene product is related to mouse gamma adaptin. [Homo sapiens]	7e-026
2278	3183217	HYPOTHETICAL PROTEIN KIAA0103 sapiens]	5e-017
2282	2072972	(U93572) putative p150 [Homo sapiens]	4e-017
2283	961444	(D63876) KIAA0154 gene product is related to mouse gamma adaptin. [Homo sapiens]	6e-028
2285	4586287	(AB004794) DUF140 [Xenopus laevis]	0.005
2286	3879684	(Z74042) predicted using Genefinder; Similarity to Haemophilus 3- oxoacyl-(acyl-carrier protein) reductase (SW:FABG_HAEIN); cDNA EST yk470b2.3 comes from this gene; cDNA EST yk470b2.5 comes from this gene [Caenorhabditis elegans]	0.0002
2287	131786	RAS-RELATED PROTEIN RAB-1A protein ypt1 - mouse >gi 2144599 pir TVHUYP GTP-binding protein Rab1 - human >gi 2144600 pir TVDGYP GTP-binding protein Rab1 - dog >gi 55457 emb CAA68284 (Y00094) Ypt1 protein (AA 1-205) [Mus musculus] >gi 550060 (M28209) GTP	1e-017
2288	4115532	(AB012043) NBR13 [Homo sapiens]	0.69
2289	4586287	(AB004794) DUF140 [Xenopus laevis]	1e-007
2290	126296	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG protein [Nycticebus coucang]	9e-020
2293	2981950	Pathogenesis-Related Protein 5d From Nicotiana Tabacum	7.8
2294	482300	cell surface antigen CD34 precursor - human	1e-019
2295	104623	collagen, corneal - chicken (fragment)	0.14
2296	4191746	(L30113) alcohol dehydrogenase; ADH [Papio hamadryas]	2e-018
2297	1518609	(U57715) FGF receptor activating protein FRAG1 [Rattus	1e-020
2298	4502953	collagen, type IV, alpha 4 CHAIN PRECURSOR >gi 1360674 pir CGHU1B collagen alpha 4(IV) chain precursor - human >gi 574806 emb CAA56943 IV [Homo sapiens]	0.025

Table 2B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)

SEQ ID	ACCESSION	DESCRIPTION1	P VALUE
2299	2565196	(AF000381) non-functional folate binding protein [Homo sapiens]	1e-006
2300	2492620	NEURONAL ACETYLCHOLINE RECEPTOR PROTEIN, ALPHA-6 CHAIN PRECURSOR >gi 1458118 (U62435) nicotinic acetylcholine receptor alpha6 subunit precursor [Homo sapiens] >gi 2815225 emb CAA76155 precursor [Homo sapiens]	1e-009
2301	95095	hypothetical protein 2 - Agrobacterium tumefaciens >gi 39102 emb CAA37890.1 (X53945) ORF2	3.3
2302	1765938	(U47077) DNA-dependent protein kinase catalytic subunit	6e-021
2303	2493783	COLLAGEN ALPHA 4(IV) CHAIN bovine (fragment)	3
2304	2645205	(U63648) p160 myb-binding protein [Mus musculus]	3e-029
2305	2645205	(U63648) p160 myb-binding protein [Mus musculus]	9e-030
2306	2495322	HOMEODOMAIN PROTEIN HOX-A9	8e-014
2307	116509	CALCYCLIN (PROLACTIN RECEPTOR ASSOCIATED PROTEIN) (PRA) (GROWTH FACTOR-INDUCIBLE PROTEIN 2A9) (S100 CALCIUM-BINDING PROTEIN A6) put. calcyclin;	4e-006
2308	4502991	cytochrome c oxidase subunit VIIb >gi 461804 sp P24311 COXM_HUMAN CYTOCHROME C OXIDASE POLYPEPTIDE VIIb PRECURSOR 1.9.3.1) chain VIIb - human >gi 30151 emb CAA78613 sapiens]	0.002
2309	4507669	tumor protein, translationally-controlled 1 CONTROLLED TUMOR PROTEIN (TCTP) (P23) factor - human >gi 37496 emb CAA34200 (X16064) tumor protein (AA 1 - 172) [Homo sapiens]	6e-020
2311	4507207	sorcin sorcin [Homo sapiens] >gi 1094394 prf 2106141A sorcin	2e-018
2312	117061	CYTOCHROME C OXIDASE POLYPEPTIDE III chain III - human mitochondrion (SGC1) oxidase III [Homo sapiens]	3e-017
2313	1709972	60S RIBOSOMAL PROTEIN L10A (CSA-19)	5e-013
2314	4454698	(AF070661) HSPC005 [Homo sapiens]	3e-014
2315	1885381	(U77665) RNaseP protein P30 [Homo sapiens]	1e-020
2316	209383	(M27786) MS-2 pol-stefin B fusion protein [Artificial gene]	7e-008
2318	631507	zinc-containing protein - human	0.03
2319	4502991	cytochrome c oxidase subunit VIIb >gi 461804 sp P24311 COXM_HUMAN CYTOCHROME C OXIDASE POLYPEPTIDE VIIb PRECURSOR 1.9.3.1) chain VIIb - human >gi 30151 emb CAA78613 sapiens]	5e-013
2320	87765	hypothetical L1 protein (third intron of gene TS) - human >gi 364964 prf 1510254A L1 repetitive element ORF [Homo	2e-015
2321	129379	MITOCHONDRIAL MATRIX PROTEIN P1 PRECURSOR (P60 LYMPHOCYTE PROTEIN) (60 KD CHAPERONIN) PROTEIN) (HUCHA60) >gi 107086 pir A32800 heat shock protein 60 precursor - human >gi 190127 (M22382) mitochondrial matrix protein [Homo	8e-016
2322	2231019	(Z97207) B-IND1 protein [Mus musculus]	6e-022
2323	4154176	(U96639) ATPase subunit 6 [Canis familiaris]	0.007
2324	2575807	(D49692) adenylate cyclase [Spirulina platensis]	4.4
2325	4502991	cytochrome c oxidase subunit VIIb >gi 461804 sp P24311 COXM_HUMAN CYTOCHROME C OXIDASE POLYPEPTIDE VIIb PRECURSOR 1.9.3.1) chain VIIb - human >gi 30151 emb CAA78613 sapiens]	5e-007
2326	2119918	P43 - human >gi 833999 bbs 160014 (S75463) P43=mitochondrial elongation factor homolog [human, liver, Peptide, 452 aa] [Homo	3e-020
2327	4503145	cathepsin E precursor - human >gi 181194 (J05036) cathepsin E precursor [Homo sapiens] >gi 181205 (M84424) cathepsin E	1e-041
2328	4502189	aquaporin 8 sapiens]	2e-023
2329	4502189	aquaporin 8 sapiens]	2e-026
2330	2306969	(AF007860) xl-Mago [Xenopus laevis]	2e-037

Table 2B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)

SEQ ID	ACCESSION	DESCRIPTION1	P VALUE
2333	3970731	(AJ006480) SBT4B protein [Lycopersicon esculentum]	9
2334	2736524	(AF039052) Similar to inosine monophosphate dehydrogenase; coded for by C. elegans cDNA CEMSF04F; coded for by C. elegans cDNA yk247b12.3; coded for by C. elegans cDNA cm20d8; coded for by C. elegans cDNA yk247b12.5; coded for by C. elegans ...	2.7
2335	1085957	hypothetical protein Y - Streptomyces nogalater	1.1
2336	3183217	>gi 2147591 pir S69232 hypothetical protein Y	3e-021
2337	2494312	HYPOTHETICAL PROTEIN KIAA0103 sapiens]	3e-037
2338	337930	TRANSLATION INITIATION FACTOR EIF-2B GAMMA SUBUNIT (EIF-2B GDP-GTP EXCHANGE FACTOR) subunit	1e-024
2339	68891	(M22146) scar protein [Homo sapiens]	2e-007
2340	126296	transforming protein ets - chicken >gi 211753	9e-017
2341	4507517	LINE-1 REVERSE TRANSCRIPTASE HOMOLOG protein [Nycticebus coucang]	9e-023
2343	106851	tight junction protein 1 (zona occludens 1) >gi 585098 sp Q07157 ZO1_HUMAN TIGHT JUNCTION PROTEIN ZO-1 (TIGHT JUNCTION PROTEIN 1) human	4e-023
2344	1723438	>gi 292938 (L14837) tight junction (zonula occludens) protein ZO-1	7.5
2345	2231019	keratin 18, cytoskeletal - human (fragment) sapiens]	7e-022
2346	2047300	HYPOTHETICAL 52.3 KD PROTEIN C56F8.06C IN CHROMOSOME I PRECURSOR	0.48
2347	129383	(Z97207) B-IND1 protein [Mus musculus]	2e-023
2351	4502411	(L40459) latent transforming growth factor-beta binding protein [Mus musculus]	3e-025
2352	2072961	PROBABLE RNA-DEPENDENT HELICASE P68 human >gi 35220 emb CAA36324 (X52104) p68 protein (AA 1-614) [Homo sapiens] >gi 38318 emb CAA33751 (X15729) protein p68 (AA 1-614) [Homo sapiens] >gi 2599360	2e-014
2354	2306969	BCL2-interacting killer BCL-2 INTERACTING KILLER (APOPTOSIS INDUCER NBK) (BP4) sapiens] >gi 1235989	3e-041
2355	1872498	(U93568) putative p150 [Homo sapiens]	2e-033
2356	1783123	(AF007860) xl-Mago [Xenopus laevis]	1e-029
2357	2306969	(U74297) PiUS [Oryctolagus cuniculus]	2e-041
2358	1872498	(AB000170) endopeptidase 24.16 type M3 endopeptidase 24.16 type M3 [Sus scrofa] type M3 [Sus scrofa] >gi 1783130 dbj BAA19065 type M3 [Sus scrofa] >gi 1783134 dbj BAA19067 type M3 [Sus	6e-034
2359	4519602	(AF007860) xl-Mago [Xenopus laevis]	3e-041
2360	1944330	(U74297) PiUS [Oryctolagus cuniculus]	2e-019
2361	4502189	(AB017563) IGSF4 [Homo sapiens]	6e-040
2362	4502189	(D49545) KIFC2 [Mus musculus]	2e-041
2363	1537070	aquaporin 8 sapiens]	2e-040
2364	3024124	aquaporin 8 sapiens]	8e-030
2365	107215	(U63840) nucleoporin p54 [Rattus norvegicus]	5e-040
2366	2306969	HOMEODOMAIN PROTEIN MEIS3	7e-054
2367	2306969	notch protein homolog TAN-1 precursor - human	2e-054
2368	4464284	(AF007860) xl-Mago [Xenopus laevis]	7e-045
2369	4502741	(AF007860) xl-Mago [Xenopus laevis]	1e-060

Table 2B Nearest Neighbor (BlastX vs. Non-Redundant Proteins)

SEQ ID	ACCESSION	DESCRIPTION1	P VALUE
2371	2496815	HYPOTHETICAL 68.1 KD PROTEIN B0304.7 IN CHROMOSOME II >gi 1041881 (U39472) similar to f44f4.5	0.59
2372	2496815	HYPOTHETICAL 68.1 KD PROTEIN B0304.7 IN CHROMOSOME II >gi 1041881 (U39472) similar to f44f4.5	0.56
2373	3327226	(AB014606) KIAA0706 protein [Homo sapiens]	1e-031
2374	3327226	(AB014606) KIAA0706 protein [Homo sapiens]	2e-034
2375	3327226	(AB014606) KIAA0706 protein [Homo sapiens]	2e-038
2376	2231019	(Z97207) B-IND1 protein [Mus musculus]	2e-039
2377	3327226	(AB014606) KIAA0706 protein [Homo sapiens]	4e-043
2378	417743	NEUROLYSIN PRECURSOR (NEUROTENSIN ENDOPEPTIDASE) (MITOCHONDRIAL OLIGOPEPTIDASE M) ANGIOTENSIN-BINDING PROTEIN) (SABP) protein - pig >gi 217709 dbj BAA01949 (D11336) soluble angiotensin-binding protein [Sus scrofa] type M1 [Sus scrofa] >gi 1871389 dbj BAA1	1e-047
2379	1783127	(AB000172) endopeptidase 24.16 type M2 endopeptidase 24.16 type M2 [Sus scrofa]	7e-050
2380	2494312	TRANSLATION INITIATION FACTOR EIF-2B GAMMA SUBUNIT (EIF-2B GDP-GTP EXCHANGE FACTOR) subunit	7e-056
2381	1085499	CDC4 repeat unit-containing protein - mouse	4e-056
2382	4092846	(AB019987) chromosome-associated polypeptide-C [Homo sapiens]	4e-058
2383	4103446	(AF023265) NAD ⁺ -specific isocitrate dehydrogenase beta subunit isoform A [Homo sapiens]	5e-059
2384	1353709	(U42385) FIN16 gene product [Mus musculus]	8e-061
2385	4106818	(AF083395) phospholipase A2-activating protein [Homo sapiens]	5e-061
2386	473407	(U08215) NST-1 [Mus musculus]	2e-061
2387	4103446	(AF023265) NAD ⁺ -specific isocitrate dehydrogenase beta subunit isoform A [Homo sapiens]	6e-062
2388	1537070	(U63840) nucleoporin p54 [Rattus norvegicus]	2e-062
2389	3851584	(AF092563) chromosome-associated protein-E [Homo sapiens]	7e-063
2390	3851584	(AF092563) chromosome-associated protein-E [Homo sapiens]	6e-063
2391	3493209	(AF052577) aldo-keto reductase [Homo sapiens]	3e-064
2392	4502741	cyclin-dependent kinase 6 KINASE 6 (KINASE PLSTIRE) >gi 107662 pir S23387 protein kinase (EC 2.7.1.37) cdk6 - human >gi 4389286 pdb 1BI8 A Chain A, Mechanism Of G1 Cyclin Dependent Kinase Inhibition From The Structures Cdk6-P19ink4d	5e-065
2393	3493209	(AF052577) aldo-keto reductase [Homo sapiens]	7e-066
2394	4165018	(D89053) Acyl-CoA synthetase 3 [Homo sapiens]	3e-068
2395	4106818	(AF083395) phospholipase A2-activating protein [Homo sapiens]	1e-068
2396	4165018	(D89053) Acyl-CoA synthetase 3 [Homo sapiens]	1e-070

Table 2A Nearest Neighbor (BlastN vs. GenBank)

SEQ ID	ACCESSION	DESCRIPTION	P VALUE
101	U73106	Liriodendron tulipifera high-pI laccase (LAC2-4) mRNA,	4.9
102	M63897	Bacillus thuringiensis insecticidal crystal protein (CryIF) gene, complete cds.	4.8
103	X75014	M.musculus Phox2 mRNA for homeodomain protein	4.4
104	X77320	A.officinalis L. unknown mRNA	4.1
105	M64982	Human fibrinogen alpha chain gene, complete mRNAs.	4.1
106	U28241	Gallus gallus collapsin-3 mRNA, partial cds.	4.1
107	M36860	Human elastin mRNA, complete cds.	4.1
108	X99641	M.musculus mRNA for HP1 alpha protein	4.1
109	X92557	S.erythraea pccB, bcpA2, and orfX genes	4
110	M21514	Rinderpest virus fusion protein mRNA, complete cds.	4
111	M64982	Human fibrinogen alpha chain gene, complete mRNAs.	4
112	D87218	Trypanosoma cruzi mRNA, partial cds, clone:TcEST002	4
113	M27273	E.coli rafA, rafB, and rafD genes encoding alpha-D-galactosidase, raf-permease, and raf-invertase, complete cds.	3.9
114	U50065	Caenorhabditis elegans cosmid T23A7.	3.9
115	X76186	Rinderpest virus (RBOK vaccine) mRNA for matrix protein	3.9
116	L05165	Gorilla gorilla glycophorin-gene related sequence.	3.9
117	M77212	Apis koschevnikovi mitochondrial cytochrome oxidase II gene, complete cds.	3.9
118	U64453	Human ELK1 pseudogene (ELK2) and immunoglobulin heavy chain gamma pseudogene (IGHGP)	3.9
119	M87502	Rotavirus SA114F nonstructural protein 34 (NS34) mRNA, complete cds.	3.9
120	L24376	Bacillus subtilis ribosomal protein L7/12 (rplL) gene, beta subunit of RNA polymerase (rpoBC) gene, 3' end, complete	3.9
121	U97143	Rattus norvegicus RET ligand 2 (RETL2) mRNA, complete	3.9
122	M95610	Human alpha 2 type IX collagen (COL9A2) mRNA, partial	3.9
123	M21890	Human alpha-1-antitrypsin like (PIL) pseudogene, exon 2.	3.9
124	NM_002205.1	Homo sapiens integrin, alpha 5 (fibronectin receptor, alpha polypeptide) (ITGA5) mRNA > :: emb X06256.1 HSFNRA Human mRNA for integrin alpha 5 subunit	3.9
125	U38949	Gallus gallus cardiac C-protein mRNA, complete cds.	3.9
126	U04985	Simian immunodeficiency virus clone SIVsm62J vpx gene, partial cds, env, nef, tat and rev genes, complete cds.	3.9
127	U05237	Human fetal Alz-50-reactive clone 1 (FAC1) mRNA,	3.9
128	X96616	P.primaurelia gene encoding 156D surface antigen	3.8
129	U31929	Human orphan nuclear receptor (DAX1) gene, complete cds	3.8
130	X13523	Yeast CBS2 gene for cytochrome b translational activator	3.8
131	M57769	Chinese vaccinia virus I segment DNA fragment.	3.8
132	U08443	HIV-1 isolate 652 clone 11 from Haiti, envelope glycoprotein (env) gene, partial cds.	3.8
133	L39876	Caldicellulosiruptor saccharolyticus alpha-dextrin 6-glucanohydrolase (pula) and pepX genes, complete cds and	3.8
134	M20363	Soybean heat-shock protein (Gmhsp26-A) gene, complete	3.8
135	J02836	Mouse beta-glucuronidase gene, complete cds..	3.8
136	U64880	Eubacterium thermomarinus ribonuclease P RNA	3.8
137	X93520	E.caballus microsatellite DNA marker (clone ASB6)	3.8
138	Z83151	H.sapiens Fanconi anaemia group A gene, exon 6	3.8
139	D28484	Aspergillus oryzae pgkA gene for phosphoglycerate kinase, complete cds > :: dbj E04898 E04898 gDNA encoding	3.8
140	Z28091	S.cerevisiae chromosome XI reading frame ORF YKL091c	3.8
141	V01291	Yeast gene for alcohol dehydrogenase	3.8

Table 2A Nearest Neighbor (BlastN vs. GenBank)

SEQ ID	ACCESSION	DESCRIPTION	P VALUE
142	U44843	Lactococcus lactis plasmid pND324, complete sequence	3.8
143	M13496	Chicken type X collagen gene.	3.8
144	Y14946	Homo sapiens mRNA for SPIN protein	3.8
145	U94776	Human muscle glycogen phosphorylase (PYGM) gene, exons 6 through 17	3.8
146	U43844	Mus musculus cyclin D3 gene, complete cds	3.8
147	X03431	Drosophila melanogaster transposable element 297	3.8
148	U05237	Human fetal Alz-50-reactive clone 1 (FAC1) mRNA,	3.8
149	U92856	Comptonia peregrina maturase (matK) gene, chloroplast gene encoding chloroplast protein, complete cds	3.8
150	X94165	Human papillomavirus type 73 E6, E7, E1, E2, E4, L2, and	3.7
151	U47875	Drosophila azteca NDSSC 14012-0171.6 glycerolphosphate dehydrogenase (Gpd) gene, partial cds	3.7
152	X02882	Human HLA class II alpha chain gene DZ-alpha	3.7
153	AF005932	Clavispora opuntiae Spt3 (SPT3) gene, complete cds	3.7
154	Z11840	D.melanogaster hedgehog gene DNA	3.7
155	U06745	Arabidopsis thaliana ecotype Landsberg K+ transport system AKT1 gene, complete cds.	3.7
156	U63362	Unidentified crenarchaeote 16S ribosomal RNA gene, 5' partial sequence	3.7
157	D30810	Wheat gene for transcription factor HBP-1b(c38), final exon, partial cds	3.7
158	X56089	X. laevis mRNA for alpha-subunit of G-protein, type G-	3.7
159	X07701	Chironomus tentans Balbiani ring mRNA BR 2.1 3'-end	3.7
160	X64649	G.gallus mRNA for restrictin	3.7
161	Y13426	Homo sapiens TCRDV2 gene, partial	3.7
162	Y14443	Homo sapiens mRNA for zinc finger protein	3.7
163	U92794	Mus musculus alpha glucosidase II beta subunit mRNA,	3.7
164	Y09480	A.europaeus genes encoding dehydrogenase and cytochrome	3.7
165	NM_001659.1	Homo sapiens ADP-ribosylation factor 3 (ARF3) mRNA > :: gb M74491 HUMADPRF3A Human ADP-ribosylation factor 3 mRNA, complete cds.	3.7
166	L20893	Rice yellow mottle virus complete genome.	3.7
167	AF019759	Canis familiaris beta-glucuronidase (GUSB) mRNA,	3.7
168	U62587	Cricetulus griseus beta-1,6-N-acetylglucosaminyltransferase Lec4A cell line point mutant mRNA, complete cds	3.7
169	D50085	Cucumis sativus mRNA for NADPH-protochlorophyllide oxidoreductase, complete cds	3.7
170	M81890	Human interleukin 11 (IL11) gene, complete mRNA.	3.7
171	M57765	Human interleukin 11 mRNA, complete cds.	3.7
172	X55880	T. reesei ura3 (OMPdecase) gene for orotidine-5'-phosphate decarboxylase (EC 4.1.1.23)	3.6
173	J03028	P.falciparum dihydrofolate reductase-thymidylate synthase gene, complete cds.	3.6
174	AF000949	Canis familiaris keratin (KRT9) gene, complete cds	3.6
175	U78718	Dugesia tigrina 26S ribosomal RNA gene, partial sequence	3.6
176	D16471	Human mRNA, Xq terminal portion	3.6
177	X69838	H.sapiens mRNA for G9a	3.6
178	M24685	Human angiotensinogen (AGT) gene, exon 1.	3.6
179	L05468	Trichomonas vaginalis beta-tubulin (btub1) gene, complete	3.6
180	Y08926	P.falciparum mRNA for AARP1 protein, partial	3.6
181	M59743	Rabbit cardiac muscle Ca-2+ release channel	3.6
182	X51952	Human UCP gene for uncoupling protein exons 1 and 2	3.6

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SEQ ID	ACCESSION	DESCRIPTION	P VALUE
183	U25180	<i>Candida albicans</i> phosphoglycerate kinase (PGK1) gene, complete cds.	3.6
184	X58080	Maize chloroplast ORF170 and <i>psaA</i> gene	3.6
185	Z24609	<i>H. sapiens</i> (D1S502) DNA segment containing (CA) repeat; clone AFM361td9; single read	3.6
186	M24936	<i>Mus musculus</i> (BALB/c) L1 repeat insertion in the kappa chain 5' flank.	3.6
187	U50951	<i>Thermoanaerobacterium thermosulfurigenes</i> <i>orfA</i> gene, partial cds, polygalacturonase precursor (<i>pglA</i>), <i>abcA</i> , <i>abcB</i> and sigma factor (<i>sigA</i>) genes, complete cds	3.6
188	U57999	<i>Mus musculus</i> <i>prosaposin</i> (<i>psap/SGP-1</i>) gene, complete cds.	3.6
189	AF000949	<i>Canis familiaris</i> keratin (<i>KRT9</i>) gene, complete cds	3.6
190	S54325	nucleoprotein [tomato chlorotic spot virus, isolate BR-03, Genomic RNA, 929 nt]	3.6
191	S70572	{endogenous retrovirus SY-3, provirus} [human, lymphocytes, Genomic, 2189 nt]	3.6
192	AE000092	<i>Rhizobium</i> sp. NGR234 plasmid pNGR234a, section 29 of 46 of the complete plasmid sequence	3.6
193	U75285	<i>Homo sapiens</i> apoptosis inhibitor survivin gene, complete	3.6
194	X91404	<i>W.mirabilis</i> mRNA for phosphoenolpyruvate carboxylase	3.6
195	M17376	Mouse alpha-1-acid glycoprotein I (<i>AGP-1</i>) gene, complete	3.6
196	Z73360	Human DNA sequence from cosmid 92M18, <i>BRCA2</i> gene region chromosome 13q12-13	3.6
197	L05364	<i>Arabidopsis thaliana</i> polyubiquitin (<i>ubq7</i>) gene sequence.	3.6
198	J04353	Human papillomavirus type 31 (HPV-31) complete genome.	3.6
199	X03882	<i>Paramecium primaurelia</i> gene for G surface protein	3.6
200	U53152	<i>Caenorhabditis elegans</i> cosmid K11D5.	3.6
201	M65126	Human snRNP E protein pseudogene EB.	3.6
202	J04186	Yeast (<i>S.cerevisiae</i>) lysyl-tRNA synthetase (<i>KRS1</i>) alpha-2 subunit gene, complete cds.	3.6
203	L35281	<i>Mus musculus</i> (clone MKT6) morphogenetic protein 1 (<i>BMP-1/His</i>), alternative splice	3.6
204	D83390	<i>Gallus gallus</i> mRNA for connectin/titin, partial cds	3.6
205	U22103	Glycine max partial SIRE-1 sequence gag-protease polyprotein mRNA, complete cds	3.6
206	U82705	Human interferon alpha2 upstream scaffold associated region 3 (<i>SAR3</i>) and non- <i>SAR</i> region DNA	3.6
207	U39389	<i>Rhagoletis cerasi</i> 16S ribosomal RNA gene, mitochondrial gene encoding mitochondrial RNA, partial sequence	3.5
208	X13287	<i>Medicago sativa</i> nodulin-25 gene	3.5
209	X91337	<i>H.sapiens</i> La/SS-B pseudogene 2	3.5
210	M19684	Human alpha-1-antitrypsin-related protein gene, exons 3, 4	3.5
211	M35296	Human tyrosine kinase <i>arg</i> gene mRNA.	3.5
212	X88000	<i>S.tenacellus</i> mRNA for ubiquinol:cytochrome c	3.5
213	M61906	Human P13-kinase associated p85 mRNA sequence.	3.5
214	Z29084	<i>C.butyricum</i> transposon containing <i>tbcC</i> gene	3.5
215	M92039	<i>Gallus gallus</i> violet sensitive cone opsin mRNA, complete	3.5
216	D86478	<i>Schizosaccharomyces pombe</i> DNA for <i>Crb2</i> , complete cds	3.5
217	U35737	<i>Saccharomyces cerevisiae</i> nuclear polyadenylated RNA-binding protein (<i>NAB4</i>) gene, complete cds.	3.5
218	M22860	<i>B.thuringiensis</i> 20 and 67 kd mosquitocidal protein genes, complete cds and IS231-like transposase, 3' end.	3.5

Table 2A Nearest Neighbor (BlastN vs. GenBank)

SEQ ID	ACCESSION	DESCRIPTION	P VALUE
219	Z57857	H.sapiens CpG island DNA genomic MseI fragment, clone 1d10, forward read cpg1d10.fla	3.5
220	U07059	Pneumocystis carinii clone PC14103 major surface glycoprotein mRNA, complete cds.	3.5
221	X52978	H.sapiens gene for lipoprotein lipase	3.5
222	M24566	Dictyostelium discoideum tRNA-Glu-GAA gene, clone	3.5
223	U11058	Homo sapiens calcium dependent potassium channel alpha subunit (MaxiK) mRNA, complete cds	3.5
224	M21514	Rinderpest virus fusion protein mRNA, complete cds.	3.5
225	X80454	HIV type 1 (CA7) env-gene	3.5
226	X98695	Bacteriophage T4 modA and modB genes	3.5
227	X76186	Rinderpest virus (RBOK vaccine) mRNA for matrix protein	3.5
228	S82456	PGHS-2=prostaglandin endoperoxide H synthase-2	3.5
229	D85194	Arabidopsis thaliana mRNA, partial cds	3.5
230	L35661	Homo sapiens (subclone H8 4 b9 from P1 35 H5 C8) DNA	3.5
231	L76205	Colletotrichum gloeosporioides non-LTR retrotransposon	3.5
232	NM_000464.1	Homo sapiens xeroderma pigmentosum, complementation group F (XPF) mRNA > :: gb U64315 HSU64315 Human DNA repair endonuclease subunit	3.5
233	X02155	Bovine mRNA fragment for thyroglobulin N-terminal region	3.5
234	D16437	Synechococcus sp. DNA for PacS, complete cds	3.5
235	X97570	Z.mays dek34 gene	3.5
236	S65225	PEP-19=neuron-specific [mice, Genomic, 1358 nt, segment	3.5
237	U33099	Human immunodeficiency virus type 1 isolate GM4, envelope glycoprotein (env) gene, V1-V5 region, partial cds	3.5
238	X71604	H.sapiens son-pseudogene	3.5
239	L47357	Homo sapiens TIMP1 gene, exon 1.	3.5
240	AF015490	Bos taurus immunoglobulin variable region mRNA, partial cds > :: gb AF015492 AF015492 Bos taurus immunoglobulin variable region mRNA, partial cds	3.4
241	U93308	Arabidopsis thaliana decoy (DECOY) gene, complete cds and valyl tRNA synthetase (valRS) gene, partial cds	3.4
242	Y12576	Arabidopsis thaliana mRNA for histone H2B	3.4
243	X07977	Aspergillus amstelodami mtDNA with ARS element	3.4
244	X70276	Yeast centromere-containing shuttle vector YCp50	3.4
245	J03268	Yeast (S.cerevisiae) polymerase I gene, complete cds.	3.4
246	AF013168	Homo sapiens hamartin (TSC1) mRNA, complete cds	3.4
247	M32476	Rat carcinoembryonic antigen-related protein	3.4
248	X83390	Albinaria coerulea complete mitochondria DNA	3.4
249	U63337	Mus musculus cyclin-dependent kinase-2 alpha	3.4
250	D85530	Human CpG island sequence, clone G0310	3.4
251	M92423	Human FK506-binding protein 12 (FKBP12) mRNA, exons 3 and 4, complete FKBP12A mRNA and complete cds.	3.4
252	AB002693	Mouse mRNA for ISBT, complete cds	3.4
253	L01057	Human (clone TRI-6) satellite I repeat region.	3.4
254	U11270	Human antithrombin III gene, exon 1 and partial cds.	3.4
255	AB000280	Rattus norvegicus mRNA for peptide/histidine transporter, complete cds	3.4
256	J03886	Rat skeletal muscle myosin light chain kinase, complete cds.	3.4
257	M16809	Yeast (S.cerevisiae) CLS4 gene encoding a Ca regulatory protein, complete cds.	3.4
258	X58286	Drosophila genes z600, gdl, Eip28/29 and mex1	3.4
259	X07267	Rat gene 33 5'-region	3.4

Table 2A

Table 2A Nearest Neighbor (BlastN vs. GenBank)

SEQ ID	ACCESSION	DESCRIPTION	P VALUE
260	Z68129	H.sapiens IDH gamma gene and TRAP delta gene	3.4
261	X87241	H.sapiens mRNA for hFat protein	3.4
262	Z93650	O.bellus 28S rRNA gene, D2 variable region	3.4
263	D87471	Mus musculus mRNA for gsg3, complete cds	3.4
264	L34193	Ipomopsis aggregata chloroplast maturase	3.4
265	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	3.4
266	X17318	Zea mays chloroplast trnC gene, rpoB gene, rpoC1 gene, rpoC2 gene and rps2 gene for transfer RNA-Cys, RNA polymerase subunits beta, beta-1, beta-2 and ribosomal	3.4
267	L35661	Homo sapiens (subclone H8 4_b9 from P1 35 H5 C8) DNA	3.4
268	U25236	Human immunodeficiency virus type 1 clone XSH159D1D envelope glycoprotein (env) pseudogene, v1-v5 region,	3.4
269	L81392	Homo sapiens (subclone 1_c12 from P1 H39) DNA	3.4
270	M60172	G.domesticus novel collagen protein mRNA, 3' end.	3.4
271	M15263	E.coli araBAD operon encoding L-ribulokinase, L-arabinose isomerase, and L-ribulose 5-phosphate 4-epimerase.	3.4
272	S53273	OMP=olfactory marker protein {promoter} [mice, Genomic,	3.4
273	U22056	Mus musculus fertilin alpha precursor (ADAM 1) mRNA,	3.3
274	X63382	Antithamnion sp. rhodoplast genes atpI, atpH, atpG, atpF, atpD, atpA, orf1, orf2 and orf3	3.3
275	U67462	Methanococcus jannaschii section 4 of 150 of the complete	3.3
276	M24566	Dictyostelium discoideum tRNA-Glu-GAA gene, clone	3.3
277	L13609	Human catalase (CAT) gene, exon 1, 5' end.	3.3
278	Z11486	Pinus strobus L. mRNA for pine globulin-1	3.3
279	X03366	Bovine spleen trypsin inhibitor II (SI) gene	3.3
280	D49558	Human DNA for gastric inhibitory polypeptide receptor, exon 5, 6, 7, 8, 9, 10, 11 and 12	3.3
281	U52110	Sulfolobus solfataricus putative ribokinase and Dbh genes, complete cds, and putative ATPase gene, partial cds	3.3
282	M34663	Human chaperonin (HSP60) non-functional pseudogene 4.	3.3
283	X82303	P.groenlandica mitochondrial cytochrome b gene	3.3
284	D78174	Mouse cerebellum mRNA for Zic4 protein, complete cds	3.3
285	D86966	Human mRNA for KIAA0211 gene, complete cds	3.3
286	L13198	Clortridium perfringens type B beta-toxin gene, complete	3.3
287	J05516	E.coli leucine-specific transport (LS-BP; LIV-BP) system (livHMGF) genes, complete cds.	3.3
288	M58318	Homo sapiens ala gene.	3.3
289	X57297	A. majus TAM1 gene for TNP1 and TNP2	3.3
290	U33099	Human immunodeficiency virus type 1 isolate GM4, envelope glycoprotein (env) gene, V1-V5 region, partial cds	3.3
291	D29809	Coptis japonica mRNA for S-adenosyl-L-methionine:scoulerine 9-O-methyltransferase, complete cds	3.3
292	M12727	Human T-cell surface antigen T3 delta-chain gene, exons 2,3,4 and 5, clone pKR-1.	3.3
293	X54601	Human MFD72 dinucleotide repeat DNA > :: gb I31132 I31132 Sequence 44 from patent US 5582979	3.2
294	Y11740	H.sapiens whn gene, exon 1a and 1b	3.2
295	M24566	Dictyostelium discoideum tRNA-Glu-GAA gene, clone	3.2
296	S83358	focal adhesion kinase/pp125FAK/FAK + {alternatively spliced} [rats, striatum, mRNA, 4575 nt]	3.2
297	M68519	Human pulmonary surfactant-associated protein SP-A (SFTP1) gene, complete cds.	3.2

Table 2A Nearest Neighbor (BlastN vs. GenBank)

SEQ ID	ACCESSION	DESCRIPTION	P VALUE
298	U22056	Mus musculus fertilin alpha precursor (ADAM 1) mRNA,	3.2
299	AB005803.1	Homo sapiens DNA for histidine-rich glycoprotein,	3.2
300	M24566	Dictyostelium discoideum tRNA-Glu-GAA gene, clone	3.2
301	X66139	M.fascicularis mRNA for epididymal apical protein I	3.2
302	U16955	Plasmodium falciparum ATPase 2 gene, complete cds.	3.2
303	M87108	Human immunodeficiency virus type 2 (FOPOLC4) polymerase fragment.	3.2
304	U67585	Methanococcus jannaschii section 127 of 150 of the	3.2
305	U70559	Saccharomyces cerevisiae DNA repair/transcription protein Mms19p (MMS19) gene, complete cds	3.2
306	D88191	Chlorella Virus vChta-1 gene, complete cds	3.2
307	M32352	Mouse renin (Ren-1-d) gene, complete cds.	3.2
308	X64406	Marburg Virus RNA for ORF-2 and ORF-3	3.2
309	NM_002763.1	Homo sapiens prospero-related homeobox 1 protein (Prox 1) mRNA, complete cds	3.2
310	Y11681	Homo sapiens mRNA for mitochondrial ribosomal protein svp[40]=svp-related nuclear receptor/retinoid signaling modulator [zebrafishes, mRNA, 3876 nt]	3.2
311	S80986	R.norvegicus mRNA for J1-160/180 neural recognition	3.2
312	Z18630	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	3.2
313	AF012899	Filamentous Bacteriophage I2-2 genome	3.1
314	X14336	Mus musculus SH3-containing protein SH3P7 mRNA, complete cds. similar to Human Drebrin	3.1
315	U58884	M.fascicularis mRNA for epididymal apical protein I	3.1
316	X66139	E.coli genomic DNA, Kohara clone #328(39.4-39.8 min.)	3.1
317	D90819	Mus musculus spasmodic polypeptide (mSP) gene,	3.1
318	U78770	Human N-acetylgalactosamine 6-sulphatase	3.1
319	U06083	Plasmodium falciparum 5.8S ribosomal RNA gene, partial sequence, internal transcribed spacer 2, and large subunit ribosomal RNA gene, complete sequence	3
320	U48228	R.norvegicus mRNA for Pristanoyl-CoA Oxidase	3
321	X95188	S.scrofa mRNA for protein phosphatase 2A 55 kDa regulatory subunit, alpha isoform (partial)	3
322	Z34932	Ovine adenovirus terminal protein gene, partial cds, 52/55K, pIIIa, III, pVII, pX, pVI, II, endopeptidase and DNA binding protein genes, complete cds, and 100K hexon	3
323	U40837	L.esculentum (de Ruiter 83G38) Adh2 gene	2.9
324	X77233	Plasmodium falciparum cysteine proteinase gene, complete	2.8
325	M81341	H.sapiens CLN3 gene, complete CDS	2.7
326	X99832	N.crassa valyl-tRNA synthetase (cyt-20/un-3) gene.	2.1
327	M64703	Homo sapiens DNA for cGMP-binding cGMP-specific phosphodiesterase (PDE5), exon 21 and complete cds	1.9
328	AB001635.1	H.sapiens gene for arginase exon 8 and 3'-flanking region	1.8
329	X12669	Yeast (S.cerevisiae) ribosomal protein L44' gene, complete	1.8
330	M19238	Chlamydia pneumoniae section 81 of 103 of the complete	1.8
331	AE001665	Human elastin gene, exon 1	1.8
332	X15603	Helicobacter pylori 26695 section 31 of 134 of the complete	1.8
333	AE000553.1	obligately oligotrophic bacteria POC-111 DNA for 16S rRNA, partial sequence	1.8
334	AB022333	S.cerevisiae DNA for SEC62 gene	1.8
335	X51666	B. nigra repeat DNA (clone pBN 35)	1.8
336	X16588	Xenopus laevis/gilli complement component C3 mRNA,	1.8
337	U19253		

Table 2A Nearest Neighbor (BlastN vs. GenBank)

SEQ ID	ACCESSION	DESCRIPTION	P VALUE
338	U32770	Haemophilus influenzae Rd section 85 of 163 of the	1.7
339	U64618	Propithecus verreauxi epsilon globin gene, 5' flanking region and exons 1-3, complete cds	1.7
340	U39700	Mycoplasma genitalium section 22 of 51 of the complete	1.7
341	Z82656	R.prowazekii genomic DNA fragment (clone A45F)	1.7
342	AL049337.1	Homo sapiens mRNA; cDNA DKFZp564P016 (from clone DKFZp564P016)	1.7
343	Z60848	H.sapiens CpG island DNA genomic MseI fragment, clone 36g10, forward read cpg36g10.ft1a	1.7
344	Z28054	S.cerevisiae chromosome XI reading frame ORF YKL054c	1.7
345	S79213	phosphatase inhibitor-2=cytosolic regulatory subunit of type 1 protein phosphatase [rats, brain, mRNA, 867 nt]	1.7
346	X82265	C.anuum mRNA for 1-aminocyclopropane-1-carboxylate	1.6
347	U46561	Tetrahymena thermophila polyubiquitin (TTU3) gene, complete cds, and RNA polymerase II subunit 2	1.5
348	M12132	Quail fast skeletal muscle troponin I gene, complete cds.	1.5
349	X98097	M.musculus CD22 promoter region	1.4
350	D29963	Homo sapiens mRNA for CD151, complete cds	1.4
351	D10471	Herpes simplex virus type 2 genomic DNA for 0.74-0.84 region, complete cds	1.4
352	U34673	Micoureus demerarae cytochrome b light strand gene, mitochondrial gene encoding mitochondrial protein,	1.3
353	M15274	Human Pro-tRNA and Leu-tRNA genes.	1.3
354	AJ000486	Trichomonas vaginalis mgl1 gene	1.3
355	Z47075	Caenorhabditis elegans cosmid E02H1, complete sequence [Caenorhabditis elegans]	1.3
356	NM_001854.1	Homo sapiens collagen, type XI, alpha 1 type XI collagen (COL11A1) mRNA, complete cds.	1.3
357	U37056	Clostridium cellulovorans endo-1,4-beta glucanase EngF (engF) gene, complete cds	1.3
358	U53328	Human cyclin G mRNA, complete cds.	1.3
359	Z48230	Caenorhabditis elegans cosmid F42G10, complete sequence [Caenorhabditis elegans]	1.3
360	L42102	Homo sapiens (subclone 2_c7 from P1 H25) DNA sequence.	1.3
361	X89417	S.cerevisiae DNA for protein phosphatase T gene	1.3
362	Z79884	H.sapiens chromosome 22 CpG island DNA genomic MseI fragment, clone 303c5, complete read	1.3
363	Z68129	H.sapiens IDH gamma gene and TRAP delta gene	1.3
364	U13800	Human insulin-like growth factor I (IGF1) gene, intron 4.	1.3
365	L28995	Oryza sativa 3-hydroxy-3-methylglutaryl coenzyme A reductase gene, complete cds.	1.3
366	L43493	Saccharomyces cerevisiae Jsn1 gene, complete cds	1.3
367	X08066	Caenorhabditis elegans myo-2 gene for myosin heavy chain 2 (MHC-C)	1.3
368	U37056	Clostridium cellulovorans endo-1,4-beta glucanase EngF (engF) gene, complete cds	1.3
369	U19905	Rickettsia tsutsugamushi TA716 56 kDa type-specific antigen gene, complete cds.	1.3
370	U74496	Human chromosome 4q35 subtelomeric sequence	1.3
371	U46781	Pasteurella haemolytica putative coproporphyrinogen III oxidase (hemN) gene, partial cds, leukotoxin transcriptional activator and restriction modification methylase subunit	1.3
372	X77300	S.scrofa genomic DNA microsatellite SO344	1.3

Table 2A Nearest Neighbor (BlastN vs. GenBank)

SEQ ID	ACCESSION	DESCRIPTION	P VALUE
373	U53745	Feline immunodeficiency virus isolate FIV-Pco336-7 pol polyprotein (pol) gene, partial cds	1.3
374	L08266	Mouse Facc mRNA, complete cds.	1.3
375	X52519	Human gene for tyrosine aminotransferase (TAT)	1.3
376	U87543	Aedes aegypti steroid hormone receptor homolog protein gene, complete cds	1.3
377	D16682	Mycoplasma hyopneumoniae gene for 46 kDa surface antigen, complete cds	1.3
378	AF022725	Hordeum vulgare limit dextrinase (HvLD99) gene, complete	1.3
379	L18987	Human alpha-2 type XI collagen mRNA, partial cds.	1.3
380	Y09400	S.scrofa mRNA for apical organic cation transporter protein	1.3
381	U10117	Human endothelial-monocyte activating polypeptide II mRNA, complete cds.	1.3
382	U02618	Saccharomyces cerevisiae molasses resistance	1.3
383	Z60848	H.sapiens CpG island DNA genomic MseI fragment, clone 36g10, forward read cpg36g10.ft1a	1.3
384	X63203	H.sapiens gene for pregnancy specific beta-1 glycoprotein > :: gb S49771 S49771 pregnancy-specific beta 1 glycoprotein {5' region, promoter} [human, placenta, Genomic, 3036 nt]	1.3
385	L31854	Mus musculus Ig epsilon-chain C gene, exon 4, M gene,	1.3
386	X16588	B. nigra repeat DNA (clone pBN 35)	1.3
387	U25342	Xenopus laevis epithelial sodium channel, gamma subunit (gammamaxENaC) mRNA, complete cds.	1.3
388	L40806	Neurospora crassa open reading frame gene, complete cds, met-10+ gene, complete cds	1.3
389	S49760	diacylglycerol kinase [rats, brain, mRNA, 3043 nt]	1.3
390	L15328	Saccharomyces cerevisiae RNA helicase gene, complete cds.	1.3
391	S50809	protein LG=immunoglobulin binding protein Recombinant,	1.3
392	U14662	Baboon herpesvirus HVP2 gB glycoprotein (UL27) gene, complete cds.	1.3
393	U13173	Human intestinal H+/peptide cotransporter (Hpept1) gene, complete cds	1.3
394	W71212	me33e04.r1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone 389310 5' similar to SW:S105_HUMAN P33763 S100 CALCIUM-BINDING PROTEIN A5 ; > :: emb X99921 MMS100A13 M.musculus	1.3
395	U25536	Petunia hybrida alcohol dehydrogenase-2 (Adh2) gene, promoter, 5'UTR, and partial cds.	1.3
396	X75014	M.musculus Phox2 mRNA for homeodomain protein	1.3
397	Z49436	S.cerevisiae chromosome X reading frame ORF YJL161w	1.3
398	X12780	Chicken MHC class I (B-F) mRNA F10	1.3
399	X04319	E. coli fhuB gene involved in transport of ferrichrome	1.3
400	U61297	Human progesterone receptor (PGR) gene, far 5' flanking	1.3
401	X99518	Herpesvirus saimiri virion, transformation-associated region, strain C139	1.3
402	M24001	Mink enteritis virus antigenic type 2 capsid protein genes VP1 and VP2, complete cds.	1.3
403	U44877	Arabidopsis thaliana geranylgeranyl pyrophosphate synthase (GGPS3) mRNA, partial cds	1.3
404	AB003431	Incilaria fruhstorferi mRNA for Incilarin B, complete cds	1.3
405	M12792	Human steroid 21-hydroxylase (P-450(C21)) B gene, complete cds, clone lambda-C21B-1.	1.3
406	M28548	Human mutant 21-hydroxylase B gene, complete cds.	1.3

Table 2A

Table 2A Nearest Neighbor (BlastN vs. GenBank)

SEQ ID	ACCESSION	DESCRIPTION	P VALUE
407	Y10260	H.sapiens EYA1A gene	1.3
408	U41740	Human trans-Golgi p230 mRNA, complete cds	1.3
409	X02295	Paramecium 5' region of gene for surface protein 51A	1.3
410	S45791	band 3-related protein=renal anion exchanger AE2 homolog [rabbits, New Zealand White, ileal epithelial cells, mRNA,	1.3
411	AE000625.1	Helicobacter pylori 26695 section 103 of 134 of the	1.3
412	X16028	R.norvegicus gene encoding alkaline phosphatase, exon 3 and joined CDS	1.3
413	M73461	Saccharomyces cerevisiae FL100 RNA14 gene, complete	1.3
414	L08845	Drosophila melanogaster disabled mRNA, complete cds	1.3
415	AE000635.1	Helicobacter pylori 26695 section 113 of 134 of the	1.2
416	L39962	Medicago sativa middle repetitive DNA	1.2
417	U55371	Caenorhabditis elegans cosmid T19F4.	1.2
418	X13679	Oryza sativa H3 histone pseudogene H3R-12	1.2
419	J00223	Homo sapiens epsilon-1 pseudogene (IGHEP1) gene, CH3 and CH4 regions, exons 3 and 4 and partial sequence	1.2
420	AE000649.1	Helicobacter pylori 26695 section 127 of 134 of the	1.2
421	X52256	A.thaliana tufA gene for elongation factor Tu	1.2
422	M81388	Chilo iridescent virus DNA-directed RNA polymerase and helicase genes, complete cds's. > :: gb S75674 S75674 DNA helicase homolog, DNA-depenent RNA polymerase largest subunit homolog {fragment M} [Chilo iridescent virus CIV,	1.2
423	S57565	histamine H2-receptor [rats, Genomic, 1928 nt]	1.2
424	X84347	H.sapiens mRNA for sperm adhesion molecule hPH-20	1.2
425	X53579	A.thaliana agamous (AG) gene	1.2
426	Y09539	L.japonicus gene encoding RING finger protein	1.2
427	L05500	Human fetal brain adenylyl cyclase mRNA, 3' end.	1.2
428	X68019	Feline Immunodeficiency Virus GAG gene	1.2
429	L76739	Human immunodeficiency virus type 2 (HIV-2 ARM) proviral surface glycoprotein (gp125) gene, partial cds. Type 2 partial envelope sequence, isolate arm from mother in	1.2
430	L38769	Pisolithus tinctorius (F00035) mRNA, EST0049.	1.2
431	L39786	Lupinus angustifolius conglutin gamma gene, complete cds	1.2
432	D10510	Homo sapiens MAT gene for mitochondrial acetoacetyl-CoA thiolase, exon 11	1.2
433	U47687	Streptococcus pneumoniae immunoglobulin A1 protease (iga) gene, complete cds	1.2
434	U63922	Xenopus laevis beta-transducin repeat containing protein-3 mRNA, partial cds	1.2
435	Z27234	S.tuberosum STACS2 gene for 1-Aminocyclopropane-1-carboxylate synthase	1.2
436	X65365.1	R.norvegicus GHF1 gene, exon 2B and alternative spliced	1.2
437	X04336	Podospira anserina race A mitochondrial DNA class II intron downstream of alpha-sen DNA near Col gene 5'end	1.2
438	X12864	Yeast (S.douglasi) NAM2 gene for mitochondrial leucyl-tRNA synthetase (EC 6.1.1.4)	1.2
439	U66032	Methanosarcina thermophila CO dehydrogenase/acetyl-CoA synthase alpha subunit (cdhA), epsilon subunit (cdhB), beta subunit (cdhC), and NifH class IV protein homolog genes, complete cds, CO dehydrogenase/acetyl-CoA synthas...	1.2
440	L08266	Mouse Facc mRNA, complete cds.	1.2
441	M64085	Mouse spi2 proteinase inhibitor (spi2/eb1) mRNA, 3' end.	1.2
442	X12773	Strongylocentrotus purpuratus Spec2d gene 5'-flank and	1.2

Table 2A Nearest Neighbor (BlastN vs. GenBank)

SEQ ID	ACCESSION	DESCRIPTION	P VALUE
443	U13988	Peanut chlorotic streak caulimovirus, complete genome.	1.2
444	U23180	Caenorhabditis elegans cosmid C28F5	1.2
445	M20537	Mouse thyrotropin beta-subunit gene, exon 5.	1.2
446	U25881	Agrius cingulata NADH dehydrogenase subunit 1 protein,	1.2
447	Y08581	F.rubripes hsp70-4 gene, complete	1.2
448	L31848	Homo sapiens serine/threonine kinase receptor 2	1.2
449	M15840	Human interleukin 1-beta (IL1B) gene, complete cds.	1.2
450	Z23977	H. sapiens (D6S443) DNA segment containing (CA) repeat; clone AFM277wb5; single read	1.2
451	X14592	P.hybrida chsB gene for chalcone synthase	1.2
452	Z49900	P.sativum mRNA for small GTP-binding protein	1.2
453	U28154	Haemophilus somnus cryptic prophage genes, capsid scaffolding protein gene, partial cds, major capsid protein precursor, endonuclease, capsid completion protein, tail synthesis proteins, holin, and lysozyme genes, complet...	1.2
454	D13987	Brassica napus PE3-PEPCase gene for phosphoenolpyruvate carboxylase, complete cds	1.2
455	D45243	Mouse mRNA for ctk, complete cds	1.2
456	U81144	Caenorhabditis elegans non-alpha nicotinic acetylcholine receptor subunit precursor (unc-29) gene, complete cds	1.2
457	Z92970	Caenorhabditis elegans cosmid H06O01, complete sequence [Caenorhabditis elegans]	1.2
458	L44118	Homo sapiens proximal CMT1A-REP repeat	1.2
459	M17120	D.melanogaster achaete gene encoding nerve differentiation, complete cds.	1.2
460	U55737	Human ataxia-telangiectasia (ATM) exon 40	1.2
461	X63525	P.vulgaris loxA gene for lipoxygenase	1.2
462	D16402	Fruitfly Dcdrk gene for Dcdrk kinase, complete cds	1.2
463	M65287	Mouse activin receptor (ActR) mRNA, complete cds.	1.2
464	X13679	Oryza sativa H3 histone pseudogene H3R-12	1.2
465	D28484	Aspergillus oryzae pgkA gene for phosphoglycerate kinase, complete cds > :: dbj E04898 E04898 gDNA encoding	1.2
466	AE000283	Escherichia coli K-12 MG1655 section 173 of 400 of the complete genome	1.2
467	X99832	H.sapiens CLN3 gene, complete CDS	1.2
468	U06864	Rattus norvegicus follistatin-related protein precursor mRNA, complete cds.	1.2
469	M87710	Human simple repeat polymorphism.	1.2
470	M64497	Human apolipoprotein AI regulatory protein (ARP-1) mRNA, complete cds.	1.2
471	M87710	Human simple repeat polymorphism.	1.2
472	X60196	D.melanogaster partial Mhc gene for myosin heavy chain	1.2
473	X99719	S.enterica hsdM, hsdS & hsdR genes	1.2
474	Z95706	Microtus rossiaemeridionalis repetitive DNA	1.2
475	L76372	Musca domestica (clone F0) arylphorin mRNA fragment.	1.2
476	D26359	Exogenous mouse mammary tumor virus gene for superantigen, complete cds	1.2
477	NM_000694.1	Homo sapiens aldehyde dehydrogenase 7 (ALDH7) mRNA > :: gb U10868 HSU10868 Human aldehyde dehydrogenase ALDH7 mRNA, complete cds.	1.2
478	AF015882	Caenorhabditis elegans protein tyrosine phosphatase (ptp-2) mRNA, complete cds	1.2
479	M58047	Mouse 2',3'-cyclic-nucleotide 3'-phosphodiesterase gene,	1.2

Table 2A

Table 2A Nearest Neighbor (BlastN vs. GenBank)

SEQ ID	ACCESSION	DESCRIPTION	P VALUE
480	U71121	Arabidopsis pyruvate decarboxylase-1 (Pdc1) gene,	1.2
481	U60804	Danio rerio tumor suppressor p53 (p53) mRNA, complete	1.2
482	X99254	P.falciparum gene encoding primase, small subunit	1.2
483	D10197	Bovine mRNA for histamine H1 receptor, complete cds	1.2
484	Y09764	Homo sapiens GABRE gene, exon 2-8	1.2
485	U72396	Lycopersicon esculentum class II small heat shock protein Le-HSP17.6 mRNA, complete cds	1.2
486	X72950	X.laevis H3l gene for histone H3	1.2
487	D29956	Human mRNA for KIAA0055 gene, complete cds	1.2
488	X56003	E.coli (plasmid pFM205) faeE and faeF genes	1.2
489	M64269	Human mast cell chymase gene, complete cds.	1.2
490	AB002963	Human immunodeficiency virus type 1 env gene for envelope glycoprotein, partial cds, clone 205E5B2t	1.2
491	X90846	H.sapiens mRNA for mixed lineage kinase 2	1.2
492	X03715	Spiroplasma melliferum tRNA gene cluster	1.2
493	U83494	Tropidurus hispidus ATPase subunit 6 (ATPase6) gene, mitochondrial gene encoding mitochondrial protein, partial	1.2
494	U60804	Danio rerio tumor suppressor p53 (p53) mRNA, complete	1.2
495	M24081	Tetrahymena pyriformis (clone pTU2) ubiquitin genes, 3' and	1.2
496	U54803	Mus musculus cysteine protease (Lice) gene, exons 3-7, and complete cds	1.2
497	L13748	Human dihydrolipoamide dehydrogenase gene, exon 1.	1.2
498	U29390	Chrysosporium parvum 18S ribosomal RNA gene, partial	1.2
499	L81694	Homo sapiens (subclone 1_d1 from P1 H56) DNA sequence	1.2
500	X65366.1	R.norvegicus GHF1 gene, intron 2	1.2
501	U74651	Human DNA polymerase gamma (polg) gene, promoter region and partial cds	1.2
502	X65591	S.mansoni mRNA for myosin II heavy chain	1.2
503	D17255	Human HepG2 3' region MboI cDNA, clone hmd5c12m3	1.2
504	L33792	Senecio odorus lipid transfer protein mRNA, 3' end.	1.2
505	L13612	Drosophila melanogaster dead-box protein (dbp45A) gene, complete cds. > :: emb Z23266 DMDEADBXA D.melanogaster DEAD-box gene, complete CDS	1.2
506	X81650	M.musculus mRNA for c-ros protooncogene	1.2
507	NM_000037.1	Homo sapiens ankyrin 1, erythrocytic (ANK1) mRNA > :: gb M28880 HUMANK Human erythroid ankyrin mRNA,	1.2
508	X98543	A.thaliana endo-1,4-beta-glucanase gene	1.2
509	D89501	Human PBI gene, complete cds	1.2
510	Z82174	Human DNA sequence from cosmid B20F6 on chromosome 22, complete sequence [Homo sapiens]	1.2
511	M36881	Human lymphocyte-specific protein tyrosine kinase	1.2
512	U92014	Human clone 121711 defective mariner transposon Hsmar2 mRNA sequence	1.2
513	U09948	Morone saxatilis Hox-B5-like homeodomain protein gene,	1.2
514	M58155	African swine fever virus multigene families 360 and 110.	1.2
515	U30500	Sicilian sandfly fever virus glycoprotein precursor polypeptide mRNA, complete cds.	1.2
516	L09190	Human trichohyalin (TRHY) gene, complete cds.	1.2
517	U67508	Methanococcus jannaschii section 50 of 150 of the complete	1.2
518	M81186	Clostridium botulinum neurotoxin type B (botB) gene,	1.2
519	U93037	Homo sapiens elastin gene, exons 5-27 and alternatively spliced products, partial cds	1.2
520	D87454	Human mRNA for KIAA0265 gene, partial cds	1.2

Table 2A Nearest Neighbor (BlastN vs. GenBank)

SEQ ID	ACCESSION	DESCRIPTION	P VALUE
521	D87558	Gallus gallus mRNA for C-Serrate-2, partial cds	1.2
522	Z32847	L.infantum (10541) kinetoplast DNA	1.2
523	U09584	Human PL6 protein (PL6) mRNA, complete cds.	1.2
524	AC001530	Homo sapiens (subclone 2_b8 from P1 H56) DNA sequence	1.2
525	X74322	H.sapiens gap-I gene	1.2
526	D29792	Mouse gene for T cell receptor gamma chain	1.2
527	M24001	Mink enteritis virus antigenic type 2 capsid protein genes VP1 and VP2, complete cds.	1.2
528	K02819	Rabbit MHC RLA region class I 19-1 gene, complete cds.	1.2
529	L33879	Insertion sequence IS1245 (from Mycobacterium avium) transposase gene, complete cds.	1.2
530	AE000607.1	Helicobacter pylori 26695 section 85 of 134 of the complete	1.2
531	W71212	me33e04.r1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA clone 389310 5' similar to SW:S105_HUMAN P33763 S100 CALCIUM-BINDING PROTEIN A5 ; > :: emb X99921 MMS100A13 M.musculus	1.2
532	X83078	M.musculus nid gene (exon 4)	1.2
533	U95041	Rattus norvegicus transcriptional corepressor KAP1/TIF1B mRNA, partial cds	1.2
534	X58907	H.sapiens CYP21 gene for steroid 21-monooxygenase	1.2
535	L11669	Human tetracycline transporter-like protein mRNA,	1.2
536	L37053	Gorilla gorilla (clone Gor-ID) Rhesus-like protein mRNA,	1.2
537	M33782	Human TFEB protein mRNA, partial cds.	1.2
538	D78172	Spinacia oleracea mRNA for 26S proteasome beta subunit, complete cds	1.2
539	M33782	Human TFEB protein mRNA, partial cds.	1.2
540	M33782	Human TFEB protein mRNA, partial cds.	1.2
541	Z54312	L.sake las[A,M,P,T] genes	1.1
542	S81773	inwardly rectifying K+ channel IRK3(HIT) [hamsters, insulinoma cell line HIT-T15, mRNA Partial, 1791 nt]	1.1
543	Z78910	H.sapiens flow-sorted chromosome 6 HindIII fragment,	1.1
544	U08408	Xenopus laevis arginase 3 mRNA, complete cds.	1.1
545	U26444	Bacillus subtilis 2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase (dhbA), isochorismate synthase (dhbC), 2,3-dihydroxybenzoate-AMP ligase (dhbE), and isochorismatase (dhbB) genes, complete cds, and (dhbF) gene, partial cds	1.1
546	X62170	N.crassa bli-7 gene	1.1
547	U94403	Rattus norvegicus proton gated cation channel ASIC1 mRNA, complete cds	1.1
548	AJ000498	Homo sapiens DNA for integration site of HBV in a hepatocellular carcinoma	1.1
549	X99485	L.luteus mRNA for alpha-subunit of G protein	1.1
550	U67520	Methanococcus jannaschii section 62 of 150 of the complete	1.1
551	L25415	Mycoplasma pulmonis glutamyl tRNA synthetase (gltX) gene, restriction-modification enzyme subunits S1A, R1, M1, S1B (hsds1A, hsdR1, hsdM1, hsds1B) genes, complete cds's, DNA polymerase III (polC) gene, 3' region.	1.1
552	X68107	M.sativa msCHSII mRNA for chalcone synthase	1.1
553	X89246	D.melanogaster mRNA for DHR38 protein	1.1
554	X64332	C.lewisii PgiC2-a gene for phosphoglucose isomerase	1.1
555	U47331	Rattus norvegicus metabotropic glutamate receptor 4b mRNA, complete cds.	1.1
556	X16055	Bacteriophage T4 gene 20 encoding gp20, structural protein	1.1

Table 2A

Table 2A Nearest Neighbor (BlastN vs. GenBank)

SEQ ID	ACCESSION	DESCRIPTION	P VALUE
557	D00596	Homo sapiens gene for thymidylate synthase, exons 1, 2, 3, 4, 5, 6, 7, complete cds	1.1
558	X14639	Tomato ribosomal DNA intergenic spacer	1.1
559	U67520	Methanococcus jannaschii section 62 of 150 of the complete	1.1
560	Y11786	R.prowazekii ksgA gene and 2 open reading frames	1.1
561	Z81065	Caenorhabditis elegans cosmid F16C3, complete sequence [Caenorhabditis elegans]	1.1
562	X60694	C.perfringens plasmid epsilon-toxin gene	1.1
563	X52648	Schizosaccharomyces pombe p68 gene for p68 protein	1.1
564	X04078	Potato patatin pseudogene (SA10C)	1.1
565	U38783	Schizosaccharomyces pombe brefeldin A resistance protein (hba1) and unknown orf genes, complete cds	1.1
566	U32769	Haemophilus influenzae Rd section 84 of 163 of the	1.1
567	D89066	Staphylococcus aureus DNA for DnaA, complete cds	1.1
568	U07797	Rattus norvegicus Sprague-Dawley (T1-alpha) mRNA,	1.1
569	L14710	C. elegans cosmid K02D10.	1.1
570	U42599	Borrelia burgdorferi plasmid cp18, OspE (ospE) gene,	1.1
571	U48726	Human epidermal growth factor receptor (EGFR) precursor-mRNA, exons 8 and 9, partial cds	1.1
572	U38844	Xenopus laevis cyclin-dependent kinase inhibitor p28 gene, complete cds	1.1
573	S82864	Elk-3=Ets transcription factor [mice, 16-day embryos,	1.1
574	X65720	M.musculus gene for protein kinase C-gamma (exon1 and	1.1
575	D14484	Hepatitis C virus strain J33 genomic RNA, complete genome	1.1
576	L11998	Staphylococcus aureus conjugative transfer gene complex	1.1
577	D14339	Rice mitochondrion DNA for ATPase subunit 6 and ORFs, complete cds	1.1
578	D38413	Yeast DNA for Ppf2p, complete cds	1.1
579	D90210	Bacteriophage c-st (from C. botulinum) C1-tox gene for botulinum C1 neurotoxin	1.1
580	X67838	B.napus DNA for myrosinase	1.1
581	X17053	Rat immediate-early serum-responsive JE gene	1.1
582	X12426	Xenopus laevis U1 70K gene exon 4, 5, 6 and 7	1.1
583	U55043	Bacillus subtilis plasmid pPOD2000 Rep, RapAB, RapA, ParA, ParB, and ParC genes, complete cds.	1.1
584	M34046	Human placental protein 14 (PP14) gene, complete cds.	1.1
585	U52367	Clostridium acetobutylicum ATCC 824 F-type ATP synthase subunit a (atpA) gene, F-type ATP synthase subunit c (atpC) gene, and F-type ATP synthase subunit b	1.1
586	Z35955	S.cerevisiae chromosome II reading frame ORF YBR086c	1.1
587	U53179	Caenorhabditis elegans cosmid T27B2.	1.1
588	X77253	C.herbarum Cla h III mRNA > :: gb I26207 I26207 Sequence 1 from patent US 5556953	1.1
589	X72713	A.franciscana mRNA for Sarco/endoplasmic reticulum Ca-	1.1
590	U29145	Caenorhabditis elegans (mab-18) mRNA, transcript	1.1
591	U06061	Cubanichthys pengelleyi mitochondrial control region, partial sequence	1.1
592	X62244	B.mycoides blaC1 gene for beta-lactamase I	1.1
593	M88355	Mouse oxytocin-neurophysin I gene, complete cds	1.1
594	U83489	Emericella nidulans septin B (aspB) mRNA, complete cds	1.1
595	M18193	Human inter-alpha-trypsin inhibitor heavy chain mRNA, partial cds, clones lambda-HuHIT1-[9,33].	1.1
596	U71273	Sus scrofa glucosidase II mRNA, complete cds	1.1

Table 2A Nearest Neighbor (BlastN vs. GenBank)

SEQ ID	ACCESSION	DESCRIPTION	P VALUE
597	S53497	immunoglobulin epsilon chain constant region=secreted form {3' region} [human, B cell myeloma U-266, Genomic,	1.1
598	U25119	Caenorhabditis elegans calcium channel alpha-1 subunit homolog Unc-2 (unc-2) gene, partial cds.	1.1
599	U56959	Caenorhabditis elegans cosmid T21F4.	1.1
600	X99485	L.luteus mRNA for alpha-subunit of G protein	1.1
601	L35848	Homo sapiens IgE receptor beta chain (HTm4) mRNA,	1.1
602	U93237	Human menin (MEN1) gene, complete cds	1.1
603	L07042	Medicago sativa MAP kinase MsERK1 mRNA, complete	1.1
604	Z36977	N.plumbaginifolia mRNA for catalase (cat3 gene)	1.1
605	J00738	Rattus norvegicus submaxillary gland alpha-2u globulin mRNA, complete cds.	1.1
606	X03018	Xenopus laevis histone gene cluster XIH3-A with genes H1A, H2B, H3 and H4	1.1
607	X68449	L.esculentum U6 snRNA pseudogene (LeU6.1ps)	1.1
608	U53921	Pneumocystis carinii major surface glycoprotein	1.1
609	M87106	Human immunodeficiency virus type 2 (FOPOLC2) polymerase fragment. > :: gb M87107 HIVPOLC3 Human immunodeficiency virus type 2 (FOPOLC3) polymerase	1.1
610	U84539	Human dystrobrevin (DTN) gene, exon 11A	1.1
611	J02896	S.purpuratus speract egg protein mRNA, complete cds.	1.1
612	J02896	S.purpuratus speract egg protein mRNA, complete cds.	1.1
613	AF016253	Klebsiella aerogenes D-amino acid dehydrogenase	1.1
614	L22173	Saccharomyces cerevisiae aminonitrophenyl propanediol (ANP1), UV excision repair protein (RAD23), cytochrome c isozyme (CYC7) genes, complete cds.	1.1
615	U41357	Tetrahymena thermophila P-type ATPase (TPA11) gene,	1.1
616	X14383	Bunyamwera virus L protein RNA, complete cds	1.1
617	U50378	Mus musculus DNA repair enzyme (Ku 70) gene, exon 13 and complete cds	1.1
618	Z18278	Mus musculus of 5HT5 receptor cDNA gene encoding 5HT5 serotonin receptor	1.1
619	U14172	Mus musculus p162 protein mRNA, complete cds.	1.1
620	X76762	H.sapiens serotonin transporter gene, exon 14	1.1
621	U62055	Bacillus subtilis CzcD (czcD) gene, partial cds, TrkA (trkA) gene, complete cds	1.1
622	X81847	E.carotovora pel1, pel2 and pel3 genes	1.1
623	M25477	Caenorhabditis elegans collagen (col6) gene, complete cds.	1.1
624	X97196	D.melanogaster X gene	1.1
625	L39059	Homo sapiens transcription factor SL1 mRNA, complete	1.1
626	M21790	X.laevis complement component 3 (C3) mRNA, 3' end.	1.1
627	X95161	H.sapiens brca2 gene exon 11 > :: emb A62786.1 A62786 Sequence 27 from Patent WO9719110	1.1
628	K02446	Chicken smooth-muscle alpha-tropomyosin gene, complete	1.1
629	U24171	Mus musculus p21 (WAF1) gene, partial promoter sequence	1.1
630	Z26306	H.sapiens isoform 1 gene for L-type calcium channel, exons	1.1
631	U23070	Human putative transmembrane protein (nma) mRNA,	1.1
632	AE000046	Mycoplasma pneumoniae section 46 of 63 of the complete	1.1
633	X17548	D. melanogaster singed gene, exon 1	1.1
634	U54497	Xenopus laevis integrin alpha 4 mRNA, complete cds.	1.1
635	J02793	Mouse R and L1 (3' end) repetitive elements.	1.1
636	D10832	Equine herpesvirus genomic DNA for 'TREC' OCT-	1.1
637	X51766	L.polyphyllus mRNA for ribosomal protein S16	1.1

Table 2A Nearest Neighbor (BlastN vs. GenBank)

SEQ ID	ACCESSION	DESCRIPTION	P VALUE
638	U60804	Danio rerio tumor suppressor p53 (p53) mRNA, complete	1.1
639	Z79068	H.sapiens flow-sorted chromosome 6 HindIII fragment,	1.1
640	Z73585	S.cerevisiae chromosome XVI reading frame ORF	1.1
641	U22818	Cricetulus griseus SRD-2 mutant sterol regulatory element binding protein-2 (SREBP-2) mRNA, complete cds.	1.1
642	M25710	Human thyroid peroxidase (TPO) gene, exon 11.	1.1
643	L12591	Human alkaline phosphatase gene, 5' flanking region.	1.1
644	L25616	Homo sapiens kinectin mRNA, complete cds	1.1
645	U32251	Bos taurus clone 9 immunoglobulin lambda light chain variable region (Vlambda1b) mRNA, partial cds	1.1
646	M97516	Mouse alpha-2 adrenergic receptor gene, complete cds.	1.1
647	AJ000060	Mus musculus gene encoding lysosomal hyaluronidase,	1.1
648	L07067	Simian varicella virus tegument protein gene, complete cds; serine/threonine protein kinase genes, complete cds; membrane glycoprotein genes, complete cds's.	1.1
649	L00619	Mouse T-cell-specific tyrosine kinase (Itk) mRNA, complete	1.1
650	M76981	Glycine max vspA gene, complete cds.	1.1
651	D87460	Human mRNA for KIAA0270 gene, partial cds	1.1
652	D17466	Streptomyces setonii crtS gene for sigma factor, complete	1.1
653	D89066	Staphylococcus aureus DNA for DnaA, complete cds	1.1
654	X96853	P.persica mRNA for endo-beta-1,4-glucanase, pcell	1.1
655	NM_002248.1	Homo sapiens potassium intermediate/small conductance calcium-activated channel, subfamily N, member 1 (KCNN1) mRNA > :: gb U69883 HSU69883 Human calcium-activated potassium channel hSK1 (SK) mRNA,	1.1
656	Z63493	H.sapiens CpG island DNA genomic MseI fragment, clone 85c1, reverse read cpg85c1.r11a	1.1
657	M21995	Human coagulation factor XIII a subunit gene, exon 9.	1.1
658	X60367	Mouse CRBPI mRNA for cellular retinol binding protein I	1.1
659	M63224	Wheat germin 9f-3.8 gene, complete cds.	1.1
660	M74515	Mouse GA binding protein (GABP-alpha subunit) mRNA, complete cds.	1.1
661	X52949.1	G.intestinalis DNA for rRNA tandem repeat unit	1.1
662	D11388	Rattus norvegicus gene for ribosomal protein S15, exon 1, 2, 3, 4, complete cds	1.1
663	U22302	Human histo blood group ABO glycosyltransferase	1.1
664	M38132	S.pombe rad1 gene, complete cds.	1
665	U07261	Perissodus microlepis T51a mitochondrion NADH dehydrogenase subunit 2 gene, complete cds	1
666	Z75244	S.cerevisiae chromosome XV reading frame ORF YOR336w	1
667	D63816	Mouse DNA for glutamate transporter Slc1a3, exon 1	1
668	U04699	Euproctus platycephalus mitochondrion 16S rRNA gene, partial sequence.	1
669	M19881	P.falciparum knop protein (KP) gene, complete cds.	1
670	X64310	H.sapiens DNA for pu-py sequence on 11p13	1
671	X56469	Mouse HSA-A gene coding for heat stable antigen	1
672	L76262	Meloidogyne hapla mitochondrion COII gene, 3' end of cds; transfer RNA-His gene; 16S ribosomal RNA gene; ND3 gene, complete cds; cytochrome b (cytb) gene, 5' end of cds.	1
673	X52574	Mouse mRNA from Mov10 locus	1
674	Z11711	H.sapiens gene for alpha-2 macroglobulin, exon 1	1
675	M37240	P.junceae N8 family repetitive sequence DNA.	1
676	Z72947	S.cerevisiae chromosome VII reading frame ORF YGR162w	1

Table 2A Nearest Neighbor (BlastN vs. GenBank)

SEQ ID	ACCESSION	DESCRIPTION	P VALUE
677	X58713	N.crassa phr gene for photolyase	1
678	M30502	Human immunodeficiency virus type 2 (HIV-2), complete proviral genome.	1
679	M23082	Chicken embryo fibroblast tropomyosin mRNA, complete	1
680	K03203	Human PRH1 locus salivary proline-rich protein mRNA	1
681	M86844	Microtus chrotorrhinus tandem satellite array DNA sequence	1
682	U55381	Leishmania tropica P-glycoprotein E gene, complete cds	1
683	D11388	Rattus norvegicus gene for ribosomal protein S15, exon 1, 2, 3, 4, complete cds	1
684	L43496	Xenopus laevis ligase I (ligI) mRNA, complete cds	1
685	X69103	C.glutamicum csp2 gene	0.99
686	M32883	Alfalfa leghemoglobin gene, complete cds.	0.98
687	M30502	Human immunodeficiency virus type 2 (HIV-2), complete proviral genome.	0.98
688	K02212	Human alpha-1-antitrypsin gene (S variant), complete cds.	0.96
689	Y09746	H.oligactis mRNA for heat shock protein 70	0.96
690	D12580	Group II phytoplasma gene for 16S ribosomal RNA	0.95
691	L10465	Haematobia irritans (clone Horn.fly.3.7) mariner transposase pseudogene, partial cds.	0.95
692	U22541	Enterococcus hirae insertion sequence.	0.95
693	U66261	Caenorhabditis elegans multidrug resistance related protein 2 (mrp-2) mRNA, complete cds	0.93
694	L05517	Plasmodium chabaudi DNA sequence, exon 1.	0.91
695	S40532	NSCL-2= basic domain helix-loop-helix gene [mice, embryo, mRNA, 2230 nt]	0.91
696	L48339	Pseudomonas aureofaciens phzFABCD genes, complete cds's. > :: gb AR008980 AR008980 Sequence 11 from patent	0.65
697	X77515	R.rubrum nifJ gene	0.65
698	X51394	Xenopus mRNA for APEG protein, containing a highly repetitive amino acid sequence	0.65
699	AF097906	Rana catesbeiana myosin heavy chain (MHC-3) mRNA,	0.64
700	X64724	M.musculus NKR-P1 2 gene for natural killer cell receptor,	0.62
701	NM_001462.1	Homo sapiens formyl peptide receptor-like 1 (FPRL1) mRNA > :: gb M84562 HUMFPRL1A Human formyl peptide receptor-like receptor (FPRL1) mRNA, complete	0.61
702	AF110966.1	HIV-1 isolate C-96BW04.10 country Botswana, complete	0.6
703	Y10743	S.scrofa mRNA for p120-PI3K protein	0.6
704	U39669	Xenopus laevis pyruvate dehydrogenase E1-beta subunit (PdhE1beta-2) mRNA, partial cds	0.59
705	AJ004952	Bos taurus mRNA for fibroblast growth factor receptor type	0.59
706	AF125454	Caenorhabditis elegans cosmid Y47G7C	0.59
707	X59002	Leukemogenic retrovirus T1223/B env gene	0.59
708	Z73039	S.cerevisiae chromosome VII reading frame ORF YGR254w	0.59
709	Z28236	S.cerevisiae chromosome XI reading frame ORF YKR011c	0.58
710	U39669	Xenopus laevis pyruvate dehydrogenase E1-beta subunit (PdhE1beta-2) mRNA, partial cds	0.58
711	Z16651	H. sapiens (D10S199) DNA segment containing	0.58
712	X60163	Human TSK39.1 telomere junction	0.58
713	D10465	Zymomonas mobilis invA gene for intracellular invertase E1, complete cds	0.58
714	Z33280	M.capricolum DNA for CONTIG MC376	0.57
715	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.57

Table 2A Nearest Neighbor (BlastN vs. GenBank)

SEQ ID	ACCESSION	DESCRIPTION	P VALUE
716	AB014572	Homo sapiens mRNA for KIAA0672 protein, complete cds	0.57
717	NM_002714.1	Homo sapiens protein phosphatase 1, regulatory subunit 10 (PPP1R10) mRNA > :: emb Y13247 HSFB19 Homo sapiens	0.57
718	M10630	Bacteriophage U3 cleavage site for phage phi-X174 gene A	0.56
719	Z55474	H.sapiens CpG island DNA genomic MseI fragment, clone 42d3, reverse read cpg42d3.r1a	0.56
720	U96697	Drosophila melanogaster DPP2C1 (dpp2c1) mRNA,	0.56
721	AC001048	Homo sapiens (subclone 1_f12 from P1 H55) DNA	0.56
722	M32245	Human aromatase gene, 5' flank.	0.55
723	AF051944	Gallus gallus Xin mRNA, complete cds	0.55
724	AF077539	Caenorhabditis elegans cosmid T25D3	0.54
725	U43841	Entamoeba histolytica U6 small nuclear RNA gene, complete sequence	0.54
726	NM_000551.1	Homo sapiens von Hippel-Lindau syndrome (VHL) mRNA, and translated products	0.54
727	U55215	Cavia porcellus interleukin-5 receptor alpha precursor (gpIL-5ra) mRNA, complete cds	0.53
728	D16471	Human mRNA, Xq terminal portion	0.53
729	X76245	S.cerevisiae NOP77 gene for essential nucleolar protein	0.52
730	Z11993	V.proteolyticus aminopeptidase	0.51
731	L34620	Eubacterium fossor 16S ribosomal RNA.	0.49
732	U28757	Sus scrofa lysozyme gene, complete cds	0.49
733	U75187	Arabidopsis thaliana germin-like protein (GLP1) mRNA,	0.49
734	Z96514	H.sapiens telomeric DNA sequence, clone 2PTEL005, read 2PTELOO005.seq	0.48
735	AE000579.1	Helicobacter pylori 26695 section 57 of 134 of the complete	0.48
736	Y13852	Drosophila diptera clone D3 inactive Bari-1 family	0.47
737	X14036	Tomato cab-7 gene for type II chlorophyll a/b-binding	0.47
738	X84308	H.vulgare mRNA for photosysteme I antenna protein	0.47
739	S78378	Oct-4 (t12 haplotype) [mice, Genomic, 1191 nt, segment 3	0.46
740	NM_000254.1	Homo sapiens 5-methyltetrahydrofolate-homocysteine methyltransferase synthase mRNA, complete cds	0.46
741	L04161	Plasmodium falciparum (clone Pfg377 [PfsXLX]) DNA sequence, complete cds	0.46
742	X95887	H.sapiens PLP gene, intron 1	0.45
743	U38179	Rattus norvegicus cyclic nucleotide phosphodiesterase (RNPDE3A) mRNA, complete cds.	0.45
744	U41833	Macaca mulatta MHC class I antigen Mamu B*02 mRNA, complete cds	0.45
745	L01794	Plasmid pAD1 (from Enterococcus faecalis) replication-associate protein (repA, repB, and repC) genes, complete	0.45
746	U64573	Human connexin43 gap junction protein (connexin43) gene, exon 1 and promoter region	0.44
747	X60832	P.sativum gene (GS 3A) for glutamine synthase	0.44
748	Z93997	Unidentified bacterium DNA for 16S ribosomal RNA	0.44
749	U32818	Haemophilus influenzae Rd section 133 of 163 of the	0.44
750	AF018161	Sphaerozoum punctatum 16S-like ribosomal RNA gene, complete sequence	0.44
751	D78156	Human mRNA for rasGTPase activating protein, partial cds	0.44
752	AB000173	Porcine mRNA for endopeptidase 24.16, complete cds	0.44
753	M36626	Rat simple sequence DNA, clone 5.	0.44
754	Y09922	M.musculus flanking region of exon 1 of SEZ-6 gene including promoter sequence	0.44

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SEQ ID	ACCESSION	DESCRIPTION	P VALUE
755	X13602	Caldocellum saccharolyticum celB gene for cellobiohydrolase/endocellulase	0.44
756	AF005664	Homo sapiens properdin (PFC) gene, complete cds	0.44
757	M63312	Chinese hamster cAMP-dependent protein kinase, catalytic subunit-beta mRNA, complete cds.	0.44
758	U43382	Human Down Syndrome region of chromosome 21 DNA.	0.44
759	U75187	Arabidopsis thaliana germin-like protein (GLP1) mRNA,	0.44
760	U21914	Human duplicate spinal muscular atrophy mRNA, clone 5G7, partial cds.	0.43
761	AF010537	Plasmodium falciparum microsatellite TA3 sequence	0.43
762	X05034	Rat C2A gene for prostatic binding protein (PBP)	0.43
763	D16579	Dictyostelium discoideum mitochondrial DNA for NADH dehydrogenase subunits and cytochrome oxidase subunit	0.43
764	M58155	African swine fever virus multigene families 360 and 110.	0.43
765	Z82587	R.prowazekii genomic DNA fragment (clone A315R)	0.43
766	X13011	Bacillus subtilis DNA for glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12)	0.43
767	X59952	T.thermophila SB2040 micronuclear limited DNA element	0.43
768	Z70730	L.lactis gene for beta-phosphoglucosylase	0.43
769	X94445	S.pombe cw11 gene	0.43
770	X63628	S.pombe MFm2 gene	0.43
771	X60049	O.berteriana mitochondrial nad5 gene for NADH dehydrogenase subunit 5, exons d and e	0.43
772	D45241	Rat MHC class II gene (RT1.DOa), exon 2, 3, 4 and 5	0.43
773	D83472.1	Bos taurus gene for adrenodoxin reductase, exon 1, 2	0.43
774	M34044	Pig Na ⁺ /glucose cotransporter protein (SGLT1) mRNA, 3'	0.43
775	U28488	Human putative G protein-coupled receptor (AZ3B) mRNA, complete cds	0.43
776	X89398	H.sapiens ung gene for uracil DNA-glycosylase	0.43
777	Z36879	F.pringlei gdcSPa gene for P-protein of the glycine cleavage	0.43
778	M73760	Mouse serine proteinase, complete cds.	0.43
779	Z36803	H.sapiens (xs151) mRNA, 355bp	0.43
780	M33940	Human Val-tRNA and Lys-tRNA genes.	0.43
781	M96159	Rattus norvegicus adenylyl cyclase type V mRNA, complete	0.43
782	X54134	Human HPTP epsilon mRNA for protein tyrosine	0.43
783	Z73039	S.cerevisiae chromosome VII reading frame ORF YGR254w	0.43
784	AB002312	Human mRNA for KIAA0314 gene, partial cds	0.43
785	AB002312	Human mRNA for KIAA0314 gene, partial cds	0.43
786	U88667	Human ATP binding cassette transporter (ABCR) mRNA, complete cds	0.43
787	U88667	Human ATP binding cassette transporter (ABCR) mRNA, complete cds	0.43
788	Z65552	H.sapiens CpG island DNA genomic MseI fragment, clone 46b12, reverse read cpg46b12.rtl1a	0.43
789	X15599	Phanerochaete chrysosporium LIP2 gene for lignin	0.43
790	U22106	Drosophila melanogaster dopamine D1-like receptor mRNA, partial cds.	0.43
791	M13177	Mouse transforming growth factor beta mRNA	0.43
792	NM_002135.1	Homo sapiens hormone receptor (growth factor-inducible nuclear protein N10) (HMR) mRNA > :: gb L13740 HUMTR3A Human TR3 orphan receptor mRNA,	0.42
793	U19617	Mus musculus Ets-family transcription factor Elf-1 mRNA, complete cds	0.42

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SEQ ID	ACCESSION	DESCRIPTION	P VALUE
794	M60858	Human nucleolin gene, complete cds.	0.42
795	Z71179	Caenorhabditis elegans cosmid F07D3, complete sequence [Caenorhabditis elegans]	0.42
796	Z11804	D.discoideum ras gene	0.42
797	L07572	Equus caballus (clone GEN2-9) germline Ig lambda chain gene, J4-C4 region, last 2 exons. > :: gb L07573 HRSIGLL	0.42
798	L25637	Equus caballus (clone HVL1) germline Ig lambda chain	0.42
799	AE000293	Xenopus laevis HNF-3beta gene, complete cds.	0.42
800	Z55829	Escherichia coli K-12 MG1655 section 183 of 400 of the complete genome	0.42
801	Y11280	H.sapiens CpG island DNA genomic MseI fragment, clone 68a3, forward read cpg68a3.ft1a	0.42
802	Y08925	A.vinelandii yoh-1, ibpB, cynR, leuC, leuD, leuB, asd, usg-1	0.42
803	X89961	P.falciparum aarp3 gene, exon	0.42
804	X82330	H.sapiens DNA for MCS gene	0.42
805	D89655	A.hypogaea chi2.2 gene for chitinase (class II)	0.42
806	U70730	Rattus norvegicus mRNA for scavenger receptor class B, complete cds	0.42
807	Y09922	Human SnoN2 mRNA, complete cds	0.42
808	X57638	M.musculus flanking region of exon 1 of SEZ-6 gene including promoter sequence	0.42
809	M33196	Mouse mRNA for peroxisome proliferator activated receptor	0.42
810	X13602	Human Fc-epsilon-receptor gamma-chain gene, complete	0.42
811	X13602	Caldocellum saccharolyticum celB gene for cellobiohydrolase/endocellulase	0.42
812	U23947	Caldocellum saccharolyticum celB gene for cellobiohydrolase/endocellulase	0.42
813	U37312	Mycoplasma pulmonis putative lipoprotein (lipA), VsaB lipoprotein (vsaB), VsaC2 lipoprotein (vsaC2), VsaE2 lipoprotein (vsaE2), VsaD lipoprotein (vsaD) genes, partial cds, VsaA lipoprotein (vsaA) gene, complete cds, VsaC1 l...	0.42
814	U70998	Sus scrofa clone ARO34B cytochrome P450 aromatase mRNA, complete cds	0.42
815	U70998	Phanerochaete chrysosporium manganese peroxidase isozyme 3 (mnp3) gene, complete cds	0.42
816	X59379	Phanerochaete chrysosporium manganese peroxidase isozyme 3 (mnp3) gene, complete cds	0.42
817	X54134	Mouse mRNA for amyloid beta precursor (protease nexin II)	0.42
818	Z32676	Human HPTP epsilon mRNA for protein tyrosine	0.42
819	U28938	H.sapiens x11 gene, promoter region	0.42
820	L41867	Rattus norvegicus protein tyrosine phosphatase D30 mRNA, complete cds	0.42
821	AF004659	Drosophila extra sex combs gene, exon 1-4, complete cds.	0.42
822	U75187	Andes virus G1 protein gene, partial cds	0.42
823	U27120	Arabidopsis thaliana germin-like protein (GLP1) mRNA, Chlamydomonas reinhardtii ADP-ribosylation factor (ARF) mRNA, complete cds.	0.42
824	U41759	Chlamydia psittaci RecJ recombination protein gene, partial cds and ORF2, ORF4, glutamyl-tRNA synthetase, outer membrane protein 3 (omp3), outer membrane protein 2 (omp2), and hypothetical sulfur-rich protein (srp) genes, ...	0.41
825	D12716	Candida maltosa ALK4 (CYP52D1) gene for n-alkane inducible cytochrome P-450, complete cds	0.41

Table 2A Nearest Neighbor (BlastN vs. GenBank)

SEQ ID	ACCESSION	DESCRIPTION	P VALUE
826	J01261	<i>P.vulgaris</i> lectin gene, complete cds.	0.41
827	K00131	mouse b2 repeat sequence from clone mm61.	0.41
828	AF000949	<i>Canis familiaris</i> keratin (KRT9) gene, complete cds	0.41
829	U67580	<i>Methanococcus jannaschii</i> section 122 of 150 of the	0.41
830	X98568	<i>H.sapiens</i> type X collagen gene	0.41
831	X13595	Bean DNA for glycine-rich cell wall protein GRP 1.0	0.41
832	Y13852	<i>Drosophila</i> diptera clone D3 inactive Bari-1 family	0.41
833	X53815	Human G6PD gene for glucose-6-phosphate dehydrogenase,	0.41
		Bovine (clone p59K2) 3',5'-cyclic nucleotide phosphodiesterase (BTPDE1A1) mRNA, complete cds. > :: gb I30433 I30433 Sequence 16 from patent US 5580771 > :: gb I35677 I35677 Sequence 16 from patent US 5602019 > ::	0.41
834	L34069		0.41
835	U26425	Human phospholipase C-beta-3 (PLCB3) gene, complete	0.41
		Homo sapiens transforming growth factor-beta 1 gb I14074 I14074 Sequence 1 from patent US 5445941	0.41
836	J04431		0.41
837	U32802	<i>Haemophilus influenzae</i> Rd section 117 of 163 of the	0.41
838	U24676	<i>Drosophila melanogaster</i> twinstar (tsr) gene, complete cds	0.41
		<i>Bacillus thuringiensis</i> kurstaki insecticidal delta-endotoxin CryIA(c) (cryIA(c)) gene, complete cds	0.41
839	U87793		0.41
		<i>Mus musculus</i> domestic insulin-like growth factor 2 receptor (Igf2r) gene, exon 2 and partial cds	0.41
840	L06446		0.41
		<i>Candida tropicalis</i> POX9 gene for peroxisomal catalase (PXP-9) > :: dbj E01922 E01922 DNA encoding catalase of	0.41
841	X06660		0.41
842	U05349	Equine rotavirus glycoprotein VP7 mRNA, complete cds.	0.41
		<i>Clostridium sordellii</i> 7-alpha-hydroxysteroid dehydrogenase gene, complete cds.	0.41
843	L12058		0.41
844	X71327	<i>M. musculus</i> mRNA for MRE-binding transcription factor	0.41
845	AE000534.1	<i>Helicobacter pylori</i> 26695 section 12 of 134 of the complete	0.41
		Mouse 43kDa acetylcholine receptor-associated protein (Rapsn) gene, exons 3-8	0.41
846	L33727		0.41
847	Y11270	<i>E.histolytica</i> INO1 gene	0.41
		<i>Camptotheca acuminata</i> 3-hydroxy-3-methylglutaryl coenzyme A reductase gene, complete cds.	0.41
848	L10390		0.41
849	M34044	Pig Na ⁺ /glucose cotransporter protein (SGLT1) mRNA, 3'	0.41
850	M20543	Human skeletal alpha-actin gene, complete cds.	0.41
851	U97192	<i>Caenorhabditis elegans</i> cosmid C01F4	0.41
		<i>Mus musculus</i> strain BALB/c IgH C alpha gene, 3' regulatory region enhancer E	0.41
852	U65625		0.41
853	X78344	<i>S.cerevisiae</i> CAT8 gene	0.41
854	Z26280	<i>H.sapiens</i> isoform 1 gene for L-type calcium channel, exon	0.41
		<i>H. sapiens</i> (D1S469) DNA segment containing (CA) repeat; clone AFM280za5; single read	0.41
855	Z23995		0.41
		<i>Xenopus</i> mRNA for APEG protein, containing a highly repetitive amino acid sequence	0.41
856	X51394		0.41
857	U72719	<i>Streptococcus agalactiae</i> heat shock protein 70 cds	0.41
858	M95673	<i>Saccharomyces cerevisiae</i> ptal1 gene, complete cds.	0.41
		<i>Rattus norvegicus</i> protein tyrosine phosphatase D30 mRNA, complete cds	0.41
859	U28938		0.41
		Homo sapiens UDP glycosyltransferase 1 phenol UDP-glucuronosyltransferase (UDPGT) mRNA, complete cds.	0.41
860	NM_001072.1		0.41
861	Z72884	<i>S.cerevisiae</i> chromosome VII reading frame ORF YGR099w	0.41
862	X96883	<i>H.sapiens</i> spcDNA, tetranucleoid and O-LTR like repeat,	0.4
863	M14602	Human myoglobin gene, exon 2.	0.4

Table 2A Nearest Neighbor (BlastN vs. GenBank)

SEQ ID	ACCESSION	DESCRIPTION	P VALUE
864	D00844	Gallus gallus mRNA for virus activating protease, complete	0.4
865	D49817	Homo sapiens mRNA for 6-phosphofructo-2-kinase/fructose-2, 6-bisphosphatase, complete cds	0.4
866	L78742	Homo sapiens (subclone 10_b11 from P1 H16) DNA	0.4
867	X51772	Rat DNA for calpain II large subunit (EC 3.4.22.17) (exon	0.4
868	U09473	Luxilus chrysocephalus chrysocephalus Meramec R., Jefferson Co., MO, USA, mitochondrion 12S rRNA and 16S rRNA genes, partial sequence, and tRNA-Val gene,	0.4
869	X52614	Maize chloroplast rps15 gene for ribosomal protein S15	0.4
870	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.4
871	M30467	D.discoideum uridine diphosphoglucose pyrophosphorylase (UDPGP1) gene, 5' end.	0.4
872	NM_002248.1	Homo sapiens potassium intermediate/small conductance calcium-activated channel, subfamily N, member 1 (KCNN1) mRNA > :: gb U69883 HSU69883 Human calcium-activated potassium channel hSK1 (SK) mRNA,	0.4
873	M81686	Petunia hybrida Sx-protein	0.4
874	S39508	myelin P2 [mice, Genomic, 3694 nt]	0.4
875	U82966	Oryza sativa Ca2+-ATPase gene, complete cds	0.4
876	X16323	Human mRNA for hepatocyte growth factor (HGF)	0.4
877	U31631	Dictyostelium discoideum class II apurinic/aprimidinic(AP)-endonuclease (DdapeA) gene, complete cds	0.4
878	X60753	P.sylvestris BBS gene for bibenzyl synthase	0.4
879	V00711	Mus musculus mitochondrial genome > :: gb J01420 MUSMTCG Mouse mitochondrion, complete	0.4
880	U66274	Rattus norvegicus neuropeptide Y5 receptor (NPYR5) mRNA, complete cds	0.4
881	X83673	X.laevis SSB1 gene	0.4
882	X14036	Tomato cab-7 gene for type II chlorophyll a/b-binding	0.4
883	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.4
884	X64467	H.sapiens ALAD gene for porphobilinogen synthase	0.4
885	L81673	Homo sapiens (subclone 1_f8 from P1 H49) DNA sequence	0.4
886	L36887	Saccharomyces cerevisiae mitochondrion transfer RNA-Leu, Gln, Lys, Arg, Gly, Asp, Ser2, Arg2, Ala, Ile, Tyr, Asn	0.4
887	L24905	Bombyx mori nuclear polyhedrosis virus hr5 gene.	0.4
888	K00841	human beta-tubulin pseudogene, clone 21-beta.	0.4
889	K02819	Rabbit MHC RLA region class I 19-1 gene, complete cds.	0.4
890	L24905	Bombyx mori nuclear polyhedrosis virus hr5 gene.	0.4
891	X69491	G.gallus gene for gonadotrophin releasing hormone I	0.4
892	X95887	H.sapiens PLP gene, intron 1	0.4
893	Z96576	H.sapiens telomeric DNA sequence, clone 3PTEL001, read 3PTELO001.seq	0.4
894	Z16503	H. sapiens (D1S196) DNA segment containing (CA) repeat; clone AFM063xg9; single read	0.4
895	M20572	Mouse interleukin 6 (IL-6) gene, complete cds.	0.4
896	AF022372	Candida albicans proteinase (Kex2) gene, complete cds	0.4
897	Z77964	H.sapiens flow-sorted chromosome 6 HindIII fragment,	0.4
898	Z58874	H.sapiens CpG island DNA genomic MseI fragment, clone 110g9, reverse read cpg110g9.rt1a	0.4
899	X53422	D. grimshawi s18, s15, s19 and s16 chorion protein genes	0.4

Table 2A Nearest Neighbor (BlastN vs. GenBank)

SEQ ID	ACCESSION	DESCRIPTION	P VALUE
900	NM_002435.1	Homo sapiens mannose phosphate isomerase (MPI) mRNA > :: emb X76057 HSRPMI H.sapiens PMI1 mRNA for phosphomannose isomerase	0.4
901	X05914	D. virilis mitochondrial DNA for origin of replication, small mitochondrial ribosomal RNA, transfer tRNAs tRNA-fMet, tRNA-Gln and tRNA-Ile	0.4
902	Z95179	G.gallus microsatellite DNA (LEI0290 (= EC11EO7))	0.4
903	X65627	M.musculus mRNA TNZ2 for p68 RNA helicase	0.4
904	U87940	Salmonella typhimurium hydroxyethyl thiazole kinase (thiM) and HMP-P kinase (thiD) genes, complete cds	0.4
905	U15450	Sus scrofa clone pvg13 Ig heavy chain variable VDJ region mRNA, partial cds.	0.4
906	M27902	Rat cardiac specific sodium channel alpha-subunit mRNA, complete cds.	0.4
907	U22893	Rattus norvegicus muscle Y-box protein YB2 mRNA,	0.4
908	NM_003632.1	Homo sapiens neurexin 4 (contactin associated protein) (NRXN4) mRNA > :: gb U87223 HSU87223 Homo sapiens contactin associated protein (Caspr) mRNA, complete cds	0.4
909	AF001504	Homo sapiens myasthenia gravis autoantigen gravin mRNA, partial cds	0.4
910	AB002384	Human mRNA for KIAA0386 gene, complete cds	0.4
911	U40145	Mus musculus Mdm2 (Mdm2) gene, complete cds.	0.4
912	NM_002714.1	Homo sapiens protein phosphatase 1, regulatory subunit 10 (PPP1R10) mRNA > :: emb Y13247 HSFB19 Homo sapiens	0.4
913	Y09762	Mokola virus genes encoding nucleoprotein, phosphoprotein, matrice protein, glycoprotein and	0.4
914	U75187	Arabidopsis thaliana germin-like protein (GLP1) mRNA,	0.4
915	Z82448	R.prowazekii genomic DNA fragment (clone A503F)	0.39
916	Z50864	L.delbrueckii sp. lactis plasmid pWS58 DNA, complete	0.39
917	K03196	Human interferon-beta-3 gene.	0.39
918	U66614	Marinococcus halophilus L-2,4-diaminobutyric acid acetyl transferase (ectA) gene, L-2,4-diaminobutyric acid transaminase (ectB) gene, ectoine synthase (ectC) gene, putative transposase orfA gene, complete cds, and putative...	0.39
919	L48522	Homo sapiens tuberin (TSC2) gene, exons 6, 7, and 8	0.39
920	Z68133	Caenorhabditis elegans cosmid F23C11, complete sequence [Caenorhabditis elegans]	0.39
921	U60973	Candida albicans oligopeptide transporter (OPT1) gene,	0.39
922	L31398	Mus musculus dynamin (UDnm) mRNA, complete cds.	0.39
923	X15966	Rabbit DNA for L1Oc4 repeat	0.39
924	Z95122	Caenorhabditis elegans cosmid VZC374L, complete sequence [Caenorhabditis elegans]	0.39
925	X55036	M.musculus long mosaic repeated sequence (LMRS)	0.39
926	U35640	Arabidopsis thaliana thioredoxin h (TRX3) gene, complete	0.39
927	V00094	Fibroin gene intervening sequence from Bombyx mori (silk moth), with 5' flank and partial coding sequence	0.39
928	U47687	Streptococcus pneumoniae immunoglobulin A1 protease (iga) gene, complete cds	0.39
929	Z93381	Caenorhabditis elegans cosmid F28G4, complete sequence [Caenorhabditis elegans]	0.39
930	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.39
931	X71600	H.sapiens DNA sequence of polymorphic pentanucleotide	0.39

Table 2A Nearest Neighbor (BlastN vs. GenBank)

SEQ ID	ACCESSION	DESCRIPTION	P VALUE
932	NM_000958.1	Homo sapiens prostaglandin E receptor 4 sapiens prostaglandin E2 receptor EP2 subtype mRNA, complete cds. > :: gb I36298 I36298 Sequence 1 from patent US	0.39
933	Y07648	A.thaliana nit2 gene, nit1 gene and nit3 gene	0.39
934	Y13852	Drosophila diptera clone D3 inactive Bari-1 family	0.39
935	M57851	Human S protein-alpha (PS-alpha) gene, exon 13.	0.39
936	X52270	Maize chloroplast 3'part of rpoC2 gene, rps2 gene, atpI gene and 5'part of atpH gene	0.39
937	U50948	Rattus norvegicus taste bud receptor protein TB 567 (TB 567) gene, complete cds	0.39
938	X60435	H.sapiens gene PACAP for pituitary adenylate cyclase activating polypeptide	0.39
939	U12972	Tetrahymena thermophila CU428.1VII micronuclear R	0.39
940	X54709	Kluyveromyces lactis BiP gene for BiP/GRP78	0.39
941	Z73360	Human DNA sequence from cosmid 92M18, BRCA2 gene region chromosome 13q12-13	0.39
942	L13841	Plasmid pX01 (from Bacillus anthracis UM23-1) trans-acting positive regulator (Atx A) gene, complete cds.	0.39
943	Z72554	S.cerevisiae chromosome VII reading frame ORF YGL032c	0.39
944	L24905	Bombyx mori nuclear polyhedrosis virus hr5 gene.	0.39
945	Z11486	Pinus strobus L. mRNA for pine globulin-1	0.39
946	X70675	M.musculus gene for MERANTES protein	0.39
947	AF010537	Plasmodium falciparum microsatellite TA3 sequence	0.39
948	X78219	D.melanogaster (Barton) SED5 mRNA	0.39
949	D42055	Human mRNA for KIAA0093 gene, partial cds	0.39
950	Z30698	Rinderpest virus (RBOK) RNA for RNA polymerase (L)	0.39
951	M64715	Plasmodium falciparum DNA polymerase-delta gene,	0.39
952	Z32774	H.sapiens gene for N-methyl-D-aspartate receptor R1 exons	0.39
953	U70998	Phanerochaete chrysosporium manganese peroxidase isozyme 3 (mnp3) gene, complete cds	0.39
954	Z72884	S.cerevisiae chromosome VII reading frame ORF YGR099w	0.39
955	S78378	Oct-4 (t12 haplotype) [mice, Genomic, 1191 nt, segment 3	0.39
956	U78098	Pyrococcus furiosus ribonucleotide reductase (rnr) gene, complete cds	0.38
957	U78857	Rattus norvegicus protein serine/threonine kinase CPG16 (cpg16) mRNA, complete cds	0.38
958	Z54096	S.pombe chromosome I cosmid c13A11	0.38
959	Z72778	S.cerevisiae chromosome VII reading frame ORF YGL256w	0.38
960	D14718	Human chromosomal protein HMG1 related gene	0.38
961	U09138	Mus musculus peroxisome proliferator activated protein-gamma-2 mRNA, complete cds.	0.38
962	U32818	Haemophilus influenzae Rd section 133 of 163 of the	0.38
963	X89398	H.sapiens ung gene for uracil DNA-glycosylase	0.38
964	X69440	N.tabacum NTP303 gene	0.38
965	U62660	Toxoplasma gondii micronemal protein MIC2, complete cds	0.38
966	AE000042	Mycoplasma pneumoniae section 42 of 63 of the complete	0.38
967	V00190	Gene for small nuclear RNA D2 of slime mold (D.	0.38
968	X98568	H.sapiens type X collagen gene	0.38
969	U54776	Human NTT gene, L1, Alu, and MER 38 repeat regions	0.38
970	Z72888	S.cerevisiae chromosome VII reading frame ORF YGR103w	0.38
971	U97128	Plasmodium falciparum HMG-like protein Pf16 (Pf16) mRNA, partial cds	0.38
972	J02846	Human tissue factor gene, complete cds.	0.38

Table 2A

Table 2A Nearest Neighbor (BlastN vs. GenBank)

SEQ ID	ACCESSION	DESCRIPTION	P VALUE
973	J00803	Sheep corticotropin-releasing factor (CRF) mRNA, complete	0.38
974	X04310	Rat thymocyte mRNA for 37K chain of CD8 antigen	0.38
975	Y13129	Rickettsia akari fnt gene, partial	0.38
976	X95099	C.albicans mRNA for neutral trehalase	0.38
977	D83948	Rat adult liver mRNA for S1-1 protein, complete cds	0.38
978	Z84722	Human DNA sequence from cosmid GG4 from a contig from the tip of the short arm of chromosome 16, spanning	0.38
979	U40604	Listeria monocytogenes ClpC ATPase (mec) gene, complete	0.38
980	Z92808	Caenorhabditis elegans cosmid M04C3, complete sequence [Caenorhabditis elegans]	0.38
981	X91882	Z.mays ZEMa gene	0.38
982	M26394	M.sexata larval cuticle protein (LCP-14) gene, exon 1.	0.38
983	U32021	Gossypium tomentosum 5S ribosomal RNA gene and non-transcribed spacer, clone 11	0.38
984	X54061	D. melanogaster mRNA coding for a 205K microtubule-associated protein (MAP)	0.38
985	X14612	Chicken c-myb proto-oncogene 5' region exons 1-5	0.38
986	U12594	Sus scrofa immunoglobulin alpha heavy chain constant region (IgA C alpha) mRNA, partial cds.	0.38
987	U64841	Caenorhabditis elegans cosmid ZC142.	0.38
988	M93148	Mouse homeobox protein (Hox-1.11) gene, complete cds.	0.38
989	X14049	Canis familiaris RDC4 mRNA for G protein-coupled	0.38
990	X94616	M.musculus mRNA for glycogen synthase	0.38
991	S78378	Oct-4 (t12 haplotype) [mice, Genomic, 1191 nt, segment 3	0.38
992	D50091	Drosophila ezoana G-3-P dehydrogenase	0.37
993	Y11874	M.musculus uPA gene, promoter sequence	0.37
994	X63628	S.pombe MFm2 gene	0.37
995	Z69652	Human DNA sequence from cosmid L75B9, Huntington's Disease Region, chromosome 4p16.3	0.37
996	Y08305	L.esculentum lap17.1a gene, promoter region and CDS	0.37
997	U64453	Human ELK1 pseudogene (ELK2) and immunoglobulin heavy chain gamma pseudogene (IGHGP)	0.37
998	X82286	H.sapiens Fas, Apo-1 gene (exon IX)	0.37
999	Z48231	E.coli IncQ plasmid pIE639 sat3 gene and aphA gene	0.37
1000	L36679	Amycolatopsis methanolica plasmid pMEA300 stf gene,	0.37
1001	X95275	P.falciparum complete gene map of plastid-like DNA	0.37
1002	Z58565	H.sapiens CpG island DNA genomic MseI fragment, clone 44a5, forward read cpg44a5.ft1a	0.37
1003	L14625	Arcobacter skirrowi 16S ribosomal RNA.	0.37
1004	U72236	Dictyostelium discoideum ModA (modA) gene, complete	0.37
1005	X73940	B.taurus microsatellite DNA INRA190	0.37
1006	L06092	Mesocricetus auratus acidic fibroblast growth factor gene, 5' flank and non-coding exon 1.	0.37
1007	X98918	Human rotavirus gene encoding outer capsid glycoprotein	0.37
1008	X14448	Human GLA gene for alpha-D-galactosidase A (EC	0.37
1009	AF003533	Homo sapiens cytosolic phagocyte oxidase protein	0.37
1010	X67711	O.sativa hsp70 gene for heat shock protein 70	0.37
1011	Z33465	B.occidentalis gene for 18S rRNA	0.37
1012	Z12652	R.norvegicus upstream of gene for catechol	0.37
1013	U45934	Human papillomavirus type 68, isolate IS362, major capsid protein L1 (L1) gene, partial cds	0.37
1014	U17084	Human neurofibromin (NF1) gene, promoter region and	0.37
1015	X95668	B.burgdorferi gidA, gidB and moxR genes	0.37

Table 2A Nearest Neighbor (BlastN vs. GenBank)

SEQ ID	ACCESSION	DESCRIPTION	P VALUE
1016	X58541	Mink mRNA for plasminogen activator inhibitor type 1	0.37
1017	U48706	Dictyostelium discoideum small aggregate formation	0.37
1018	M77176	H.sapiens carbonic anhydrase II (CAII) gene, exons 1 and 2.	0.37
1019	Z72888	S.cerevisiae chromosome VII reading frame ORF YGR103w	0.37
1020	Y13234	Chironomus tentans mRNA for chitinase, 1695 bp	0.37
1021	AF004166	Lycopersicon pennellii 2-isopropylmalate synthase (Ip- ipmsb) mRNA, complete cds	0.37
1022	D85240	Aspergillus niger DNA for isopullulanase precursor,	0.37
1023	Y00684	Rabbit mRNA for gamma-subunit of phosphorylase kinase (EC 2.7.1.38)	0.37
1024	X54016	D.discoideum mRNA for 24 kDa protein, homologous to C- terminal repeat sequence of rhodopsin and synaptophysin	0.37
1025	M22015	Influenza virus type C (C/JJ/50) nonstructural	0.37
1026	M62798	F.ferrugineum 16S ribosomal RNA.	0.37
1027	X76652	M.musculus mRNA for 3f8	0.37
1028	X56047	P. chrysosporium trpC gene for trifunctional polypeptide	0.37
1029	Z74896	S.cerevisiae chromosome XV reading frame ORF YOL154w	0.37
1030	U20238	Mus musculus GTPase-activating protein GAPIII mRNA, complete cds.	0.37
1031	Z54240	L.plantarum pyrimidine biosynthetic operon genes	0.36
1032	X54742	Nicotiana plumbaginifolia beta-(1,3)-glucanase gene for a vacuolar isoform	0.36
1033	AF001415	Arabidopsis thaliana 14-3-3-like protein GF14 upsilon (GRF5) gene, complete cds	0.36
1034	X77801	S.beecheyi genomic DNA with direct repeats and integrated Hepatitis B virus	0.36
1035	Z84431	D.ligulata internal transcribed spacer 2 DNA	0.36
1036	X60753	P.sylvestris BBS gene for bibenzyl synthase	0.36
1037	D28503	Clostridium josui hemA, hemC, hemD and hemB genes of porphyrin biosynthesis	0.36
1038	X66131	R.americana mRNA for elongation factor 1-alpha	0.36
1039	X69601	B.burgdorferi p93 gene (partial)	0.36
1040	M83758	Mytilus edulis mitochondrial cytochrome oxidase subunit II (COII) gene, 3' end and NADH dehydrogenase subunit 1	0.36
1041	Z27392	G.raimondii (D61) copia-like reverse transcriptase	0.36
1042	U28832	Infectious laryngotracheitis virus US10, US2, protein kinase, UL47, glycoprotein G, ORF5, glycoprotein D, glycoprotein I, glycoprotein E, ORF9 genes, complete cds	0.36
1043	AB002384	Human mRNA for KIAA0386 gene, complete cds	0.36
1044	M22345	Mouse endogenous provirus gag, pol, and env region DNA.	0.36
1045	U16850	Human calmodulin-I (CALM1) mRNA, 3'UTR, partial	0.36
1046	M19197	Dengue virus type 2 (S1 vaccine strain), complete genome.	0.36
1047	Z49535	S.cerevisiae chromosome X reading frame ORF YJR035w	0.36
1048	Z74369	S.cerevisiae chromosome IV reading frame ORF YDR073w	0.36
1049	S78378	Oct-4 (t12 haplotype) [mice, Genomic, 1191 nt, segment 3	0.36
1050	X60686	B.taurus mRNA for transglutaminase	0.36
1051	NM_001670.1	Homo sapiens armadillo repeat gene deleted in velo-cardio- facial syndrome (ARVCF) mRNA > :: gb U51269 HSU51269 Human armadillo repeat protein	0.35
1052	X63149	Y.enterocolitica ampC and ampR genes for beta-lactamase and AmpR regulatory protein	0.35
1053	L25779	Kluyveromyces lactis (HAP3) gene, complete cds,	0.35

Table 2A Nearest Neighbor (BlastN vs. GenBank)

SEQ ID	ACCESSION	DESCRIPTION	P VALUE
1054	U77368	<i>Listeria monocytogenes</i> internalin (inlC2), inlD, and inlE genes, complete cds	0.35
1055	M62750	<i>Homo sapiens</i> intergenic locus pYNZ32 variable number tandem repeat (VNTR) sequence associated with Huntington	0.35
1056	K03073	Slime mold (<i>D.discoideum</i>) mRNA complementary to the right inverted terminal repeat of DIRS-1, clone pLZ12.	0.35
1057	U78025	<i>Sus scrofa</i> microsatellite S0399 sequence	0.35
1058	M17478	<i>Drosophila melanogaster</i> transformer (tra) gene, complete cds, and non-sex-specific transformer processed pseudogene	0.35
1059	L09708	<i>Homo sapiens</i> complement component 2 (C2) gene allele b, exons 10 through 18 and complete cds	0.35
1060	Z16708	<i>H. sapiens</i> (D6S275) DNA segment containing	0.35
1061	M74201	Rabbit cytochrome P450IIC4 (CYP2C4) gene, exons 2 and	0.35
1062	U63634	<i>Mesembryanthemum crystallinum</i> inositol methyltransferase (Imt1) gene, complete cds	0.35
1063	U73126	<i>Oryctolagus cuniculus</i> calcitonin receptor isoform mRNA, complete cds	0.35
1064	X52614	Maize chloroplast rps15 gene for ribosomal protein S15	0.35
1065	X52614	Maize chloroplast rps15 gene for ribosomal protein S15	0.35
1066	X57520	<i>L.micdadei</i> DNA for gro ELS operon	0.35
1067	D38574	<i>Pyrodictium occultum</i> polB gene for DNA polymerase II (family B) (alpha-like DNA polymerase), complete cds	0.35
1068	Z47075	<i>Caenorhabditis elegans</i> cosmid E02H1, complete sequence [Caenorhabditis elegans]	0.35
1069	Y10686	<i>C.capreolus</i> DNA, tandem repeat region	0.35
1070	U17771	<i>Blaberus giganteus</i> mitochondrion 16S ribosomal RNA, partial sequence	0.35
1071	U12186	<i>Oryctolagus cuniculus</i> sodium/dicarboxylate cotransporter mRNA, partial cds.	0.35
1072	L25677	<i>Schizosaccharomyces pombe</i> cdc42+ (Cdc42p) gene,	0.35
1073	X63628	<i>S.pombe</i> MFm2 gene	0.35
1074	D67071	Rat gene for regucalcin, exon1 (non-coding exon)	0.35
1075	X93218	<i>Impatiens necrotic spot virus</i> L gene	0.35
1076	U16301	Human lysyl hydroxylase (PLOD) gene, intron 15, complete	0.35
1077	M37277	Human Ig germline H-chain D-region genes, partial cds.	0.35
1078	X14448	Human GLA gene for alpha-D-galactosidase A (EC	0.34
1079	X79930	<i>O.gibsoni</i> Tbb gene	0.34
1080	Z37352	<i>H.sapiens</i> rearranged immunoglobulin lambda light chain V-region (V1-3)	0.34
1081	X59013	Rat mRNA for trypsin V b-form	0.34
1082	X90761	<i>Homo sapiens</i> hHa2 gene	0.33
1083	L23498	Bovine microsatellite repeats	0.33
1084	Z18361	<i>O.aries</i> trichohyalin	0.33
1085	L18785	<i>Plasmodium falciparum</i> DNA polymerase alpha (Pol alpha)	0.33
1086	X96685	<i>B.burgdorferi</i> cell division genes	0.33
1087	M58509	Human adrenodoxin reductase gene, exons 3 to 12.	0.33
1088	X70809	<i>C.reptans</i> gene for 18S ribosomal RNA	0.32
1089	D38116	Pygmy chimpanzee mitochondrial DNA, complete sequence	0.32
1090	U00310	Human immunodeficiency virus type 1 isolate 583-78 envelope glycoprotein, V3 region (env) gene, partial cds.	0.31
1091	L35670	<i>Homo sapiens</i> (subclone H8 10_g5 from P1 35 H5 C8) DNA	0.3
1092	M63960	Human protein phosphatase-1 catalytic subunit mRNA,	0.3
1093	Z50747	<i>C.psittaci</i> DNA for kdsA, dsk1 and dsk2 genes	0.22

Table 2A

Table 2A Nearest Neighbor (BlastN vs. GenBank)

SEQ ID	ACCESSION	DESCRIPTION	P VALUE
1094	M80215	<i>Streptococcus pneumoniae</i> uvs402 protein gene, complete	0.22
1095	M98776	Human keratin 1 gene, complete cds	0.22
1096	X66313	<i>H.sapiens</i> GLUDP2 gene (exon 2)	0.21
1097	AB001025	<i>Homo sapiens</i> mRNA for brain ryanodine receptor, complete	0.21
1098	AE000956	<i>Archaeoglobus fulgidus</i> section 151 of 172 of the complete	0.21
1099	Z46268	Simian herpesvirus B DNA for glycoprotein G	0.21
1100	X99403.1	<i>N.tabacum</i> mRNA for defensin	0.21
1101	U20335	<i>Drosophila pseudoobscura</i> EP arrangement, BC p430#4 pAP5 clone alpha-amylase (amy1) gene, complete cds. > :: gb U20337 DP020337 <i>Drosophila pseudoobscura</i> HI arrangement, Mex a-176x pAP9 clone alpha-amylase (amy1)	0.21
1102	X04077	Potato patatin pseudogene (SB6B)	0.2
1103	L11236	<i>Rattus rattus</i> mRNA sequence.	0.2
1104	X63547	<i>H.sapiens</i> mRNA for tre oncogene (clone 213) > :: gb I76205 I76205 Sequence 9 from patent US 5691147	0.2
1105	M69051	Human liver glucokinase (ATP:D-hexose 6-phosphotransferase) mRNA, complete cds.	0.2
1106	U14950	<i>Rattus norvegicus</i> synapse-associated protein 97 mRNA, complete cds.	0.2
1107	NM_002583.1	<i>Homo sapiens</i> PRKC, apoptosis, WT1, regulator apoptosis response protein par-4 mRNA, complete cds	0.2
1108	X66313	<i>H.sapiens</i> GLUDP2 gene (exon 2)	0.2
1109	U48485	Human skeletal muscle ryanodine receptor gene	0.2
1110	AF018116	<i>Dendroica pityophila</i> cytochrome oxidase I protein, partial	0.2
1111	X87108	<i>S.cerevisiae</i> CKI3 gene	0.19
1112	M55249	<i>E.coli</i> retron Ec67 DNA encoding reverse transcriptase and Dam methylase functions.	0.19
1113	L06898	<i>Actinomyces viscosus</i> sialidase (nanH) gene, complete cds.	0.19
1114	Y13631	<i>Clostridium botulinum</i> P-21, P-47 ntnh, bonT genes	0.18
1115	L24904	<i>Bombyx mori</i> nuclear polyhedrosis virus hr4R gene.	0.18
1116	M85049	<i>Drosophila melanogaster</i> brahma protein mRNA, complete	0.18
1117	X60777	<i>Shigella dysenteriae</i> ipaBCD genes	0.17
1118	L42936	<i>Pseudoxyscheila bipustulata</i> mitochondrial large subunit 16S ribosomal RNA (16S rRNA) gene	0.17
1119	AE001359	<i>Chlamydia trachomatis</i> section 86 of 87 of the complete	0.17
1120	K00899	yeast(<i>s.cerevisiae</i>) histone 3 gene (h3) fused with <i>e.coli</i> lacZ gene and promoter, clone prm115.	0.17
1121	M83994	<i>Staphylococcus aureus</i> prolipoprotein signal peptidase (lsp) gene, complete cds.	0.17
1122	Z28050	<i>S.cerevisiae</i> chromosome XI reading frame ORF YKL050c	0.16
1123	L23971	<i>Mus musculus</i> fragile X mental retardation syndrome protein (Fmr1) (homologue) mRNA, complete cds.	0.16
1124	Z98560	<i>S.pombe</i> chromosome I cosmid c4C5	0.15
1125	U89258	<i>Oxytricha fallax</i> 'D,D35E' type transposase gene, partial cds	0.15
1126	X62522	<i>R.norvegicus</i> gene for CNS-myelin proteolipid protein (exon	0.15
1127	X74504	<i>M.musculus</i> T10 mRNA	0.15
1128	D50931	Human mRNA for KIAA0141 gene, complete cds	0.15
1129	Z48951	<i>S.cerevisiae</i> chromosome XVI cosmid 9723	0.15
1130	L12395	<i>Brassica napus</i> small GTP-binding protein (bra) mRNA,	0.15
1131	U39367	<i>Blepharoneura manchesteri</i> 16S ribosomal RNA gene, mitochondrial gene encoding mitochondrial RNA, partial	0.15
1132	D50357	<i>Leptocarabus procerulus</i> mitochondrial DNA for NADH dehydrogenase subunit 5, partial cds	0.15

Table 2A Nearest Neighbor (BlastN vs. GenBank)

SEQ ID	ACCESSION	DESCRIPTION	P VALUE
1133	L35272	Glycine max heat shock protein (SB100) mRNA, complete	0.15
1134	U63641	Legionella pneumophila rpoD operon LporfX, LpdnaG, and LprpoD genes, complete cds	0.15
1135	X72186	H.sapiens C6 gene, exons 10, 11 and 12	0.15
1136	D45893	Neurospora crassa acr-2 DNA, complete cds	0.15
1137	L47106	Neurospora crassa kinesin (NKIN) mRNA, complete cds	0.15
1138	L04457	Phytophthora megasperma mitochondrial ORF152, complete cds, cytochrome c oxidase subunit I (cox1) gene, complete cds, cytochrome c oxidase subunit II	0.15
1139	L04457	Phytophthora megasperma mitochondrial ORF152, complete cds, cytochrome c oxidase subunit I (cox1) gene, complete cds, cytochrome c oxidase subunit II	0.15
1140	U12539	Schizosaccharomyces pombe scd2 (scd2) gene, complete	0.15
1141	U12539	Schizosaccharomyces pombe scd2 (scd2) gene, complete	0.15
1142	AB001901	Homo sapiens PACE4 gene, exon 4-7	0.15
1143	M97550	Maize sucrose phosphate synthase mRNA, complete cds. > :: emb A17878.1 A17878 Synthetic SPS sequence >	0.15
1144	AB001901	Homo sapiens PACE4 gene, exon 4-7	0.15
1145	X07438	Human DNA for cellular retinol binding protein	0.14
1146	Z57339	H.sapiens CpG island DNA genomic MseI fragment, clone 171g3, reverse read cpg171g3.rtl a	0.14
1147	X05034	Rat C2A gene for prostatic binding protein (PBP)	0.14
1148	U55712	Human ataxia-telangiectasia (ATM) gene, exon 12	0.14
1149	M20273	Human hepatitis virus type A RNA, complete genome.	0.14
1150	J01764	Plasmid pT181, complete genome.	0.14
1151	X61109	G.gorilla beta-globin gene	0.14
1152	Z30587	S.hominis (972) genes for potential ABC transporter and potential membrane spanning protein	0.14
1153	U60400	Babanki virus polymerase nsP4 gene, partial cds virus polymerase nsP4 gene, partial cds	0.14
1154	U67478	Methanococcus jannaschii section 20 of 150 of the complete	0.14
1155	Z71641	S.cerevisiae chromosome XIV reading frame ORF	0.14
1156	X53522	M.musculus VL1 gene (1G-5)	0.14
1157	Z21753	O.tanganicae mitochondrion genes for tRNA-Thr	0.14
1158	L33841	Carthamus tinctorius glycerol-3-phosphate acyltransferase mRNA, complete cds.	0.14
1159	AF003277	Glossiphonia complanata cytochrome c oxidase subunit I (COI) gene, partial cds	0.14
1160	U89035	Oxytricha fallax transposon TBE1, insertion fal6, 42 kDa transposase gene, partial cds	0.14
1161	L36923	Streptococcus pneumoniae beta-N-acetylhexosaminidase (strH) gene, complete cds	0.14
1162	U64830	Dictyostelium discoideum AX2 protein tyrosine kinase gene, complete cds.	0.14
1163	U43082	Zea mays T cytoplasm male sterility restorer factor 2 (rf2) mRNA, complete cds	0.14
1164	Z26492	T.repens TrMT1A mRNA for metallothionein-like protein	0.14
1165	X83683	V.sativa mRNA for early nodulin 40	0.14
1166	D63861	Homo sapiens DNA for cyclophilin 40, complete cds	0.14
1167	D86594	Japanese jack bean clone CgHMGY1 DNA for high mobility group protein, complete cds	0.14
1168	Z18859	H.sapiens gene for cone transducin alpha subunit	0.14

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SEQ ID	ACCESSION	DESCRIPTION	P VALUE
1169	L28038	Trypanosoma rangeli kinetoplast DNA sequence with conserved sequence blocks	0.14
1170	U72057	Mus musculus chloride channel regulator (IcIn) gene, exon 1	0.14
1171	AF003836	Mesocricetus auratus isopentenyl diphosphate:dimethylallyl diphosphate isomerase mRNA, complete cds	0.14
1172	X78422	A.thaliana HYP1 mRNA	0.14
1173	U28042	Human DEAD box RNA helicase-like protein mRNA,	0.14
1174	U01070	Mycoplasma flocculare Ms42 5S rRNA gene.	0.14
1175	U54776	Human NTT gene, L1, Alu, and MER 38 repeat regions	0.14
1176	U40375	Mus musculus Supt6h mRNA, complete cds	0.14
1177	X71083	G.max gene for coproporphyrinogen oxidase	0.14
1178	D86253	Human MHC (HLA) DRB intron 1 DNA, partial sequence	0.14
1179	M55002	Synechococcus sp. 6-phosphogluconate dehydrogenase gene, complete cds.	0.14
1180	X14036	Tomato cab-7 gene for type II chlorophyll a/b-binding	0.14
1181	L35272	Glycine max heat shock protein (SB100) mRNA, complete	0.14
1182	D50931	Human mRNA for KIAA0141 gene, complete cds	0.14
1183	L35272	Glycine max heat shock protein (SB100) mRNA, complete	0.14
1184	X05034	Rat C2A gene for prostatic binding protein (PBP)	0.14
1185	X89553	Echovirus 26 DNA for VP2 capsid protein gene	0.14
1186	Z77656	Caenorhabditis elegans cosmid F07B10, complete sequence [Caenorhabditis elegans]	0.14
1187	Z84739	H.sapiens flow-sorted chromosome 6 HindIII fragment,	0.14
1188	L34219	Homo sapiens retinaldehyde-binding protein (CRALBP) gene, complete cds.	0.14
1189	M30168	D.melanogaster nested repetitive sequences F and G,	0.14
1190	U07260	Perissodus microlepis T32a mitochondrion NADH dehydrogenase subunit 2 gene, complete cds	0.14
1191	X15308	H.sapiens NF-H gene, exon 3	0.14
1192	J02763	Human calcyclin gene, complete cds.	0.14
1193	M76175	Mouse elongation factor 2 pseudogene, complete cds.	0.14
1194	X67735	M.musculus mas gene for Mas proto-oncogene	0.14
1195	NM_002816.1	Homo sapiens proteasome (prosome, macropain) 26S subunit, non-ATPase, 12 (PSMD12) mRNA > :: dbj AB003103 AB003103 Homo sapiens mRNA for 26S	0.14
1196	U20754	Felis catus chromosome D2 mtDNA tandem repeat Numt	0.14
1197	L00727	Human myotonin protein kinase (Mt-PK) gene, complete cds. > :: gb I25678 I25678 Sequence 10 from patent US	0.14
1198	M57750	S.pombe cut2+ gene, complete cds.	0.14
1199	X03000	Adenovirus type 7 genome left end (0.0 to 31 %)	0.14
1200	NM_002911.1	Homo sapiens regulator of nonsense transcripts 1 (RENT1) mRNA > :: gb U65533 HSU65533 Human regulator of nonsense transcript stability (RENT1) mRNA, complete cds	0.14
1201	Z71367	S.cerevisiae chromosome XIV reading frame ORF	0.14
1202	J04809	Human cytosolic adenylate kinase (AK1) gene, complete	0.14
1203	X75014	M.musculus Phox2 mRNA for homeodomain protein	0.14
1204	Y12259	R.norvegicus mRNA for Kir3.1 protein	0.14
1205	X81981	L.helveticus plasmid pLH2 DNA (4 ORFs)	0.14
1206	AB001901	Homo sapiens PACE4 gene, exon 4-7	0.14
1207	D38548	Human mRNA for KIAA0076 gene, complete cds	0.14
1208	X64273	Herpesvirus saimiri gene 15 > :: gb I41338 I41338 Sequence 9 from patent US 5624837 > :: gb I49086 I49086 Sequence 9 from patent US 5627264	0.13

Table 2A Nearest Neighbor (BlastN vs. GenBank)

SEQ ID	ACCESSION	DESCRIPTION	P VALUE
1209	Z92779	Caenorhabditis elegans cosmid C44E1, complete sequence [Caenorhabditis elegans]	0.13
1210	X14384	Astasia longa chloroplast rpl5 gene for ribosomal protein L5	0.13
1211	M97880	Bacillus thuringiensis cryIC-related gene sequence. > :: gb I82521 I82521 Sequence 1 from patent US 5712248 > :: gb I93759 I93759 Sequence 1 from patent US 5731194	0.13
1212	X58049	H.sapiens DNA for ferredoxin repeat region	0.13
1213	U47542	Vibrio cholerae ADP-L-glycero-D-mannoheptose-6-epimerase (rfaD) gene, complete cds.	0.13
1214	M90758	Sheep (clone C5-2) MHC class II cell surface glycoprotein OLA-DRB (OLA-DRB) pseudogene, exon 4. > :: gb S83918 S83914S3 DRB=MHC class II B {pseudogene}	0.13
1215	U67478	Methanococcus jannaschii section 20 of 150 of the complete	0.13
1216	U90889	Mus musculus transketolase (TKT) gene, partial cds	0.13
1217	K03273	C.elegans heat shock protein genes (hsp16-48 and hsp16-1), complete cds.	0.13
1218	D90736	Escherichia coli genomic DNA. (22.6 - 23.0 min)	0.13
1219	X63546	H.sapiens mRNA for tre oncogene (clone 210)	0.13
1220	L16770	Anas platyrhynchos mitochondrial complete transfer RNA-Glu, transfer RNA-Phe, transfer RNA-Val, transfer RNA-Leu, 12S ribosomal RNA, and 16S ribosomal RNA genes	0.13
1221	U94410	Dictyostelium discoideum plasmid Ddp6 Rep protein	0.13
1222	AC001083	Homo sapiens (subclone 2_a6 from BAC H75) DNA	0.13
1223	Z96048	Caenorhabditis elegans cosmid F57A10, complete sequence [Caenorhabditis elegans]	0.13
1224	M92914	Drosophila virilis mastermind gene, complete cds	0.13
1225	Z82961	Bacterial sp. partial 16S rRNA gene (clone group T4A)	0.13
1226	U66535	Human beta4-integrin (ITGB4) gene, exons	0.13
1227	NM_001432.1	Homo sapiens epiregulin (EREG) mRNA > :: dbj D30783 D30783 Homo sapiens mRNA for epiregulin,	0.13
1228	X96468	P.tetraulera gamma1-51D immobilisation antigen gene, 3' coding and non-coding region	0.13
1229	X05918	Kluyveromyces fragilis beta-glucosidase gene	0.13
1230	Z48243	A.thaliana PARP mRNA for PARP protein	0.13
1231	X56276	Human Hut 2 End gene	0.13
1232	X55318	Mus musculus Hox-3.2 gene	0.13
1233	U90009	Phalacrocorax pelagicus cytochrome b gene, mitochondrial gene encoding mitochondrial protein, partial cds	0.13
1234	L76571	Homo sapiens nuclear hormone receptor (shp) gene, 3' end	0.13
1235	U60581	Human c-jun gene, promoter region with flanking evolutionary conserved sequences	0.13
1236	Z26886	B.mori gene for Nd-sD mutant fibroin light chain	0.13
1237	L19740	Canis familiaris Kv1.2 delayed rectifier K+ channel mRNA, complete cds	0.13
1238	U26948	Glycine max ribosomal protein S16 (rps16) gene, partial cds, beta-carboxyltransferase (accD), photosystem I component (psaI), ORF 202 protein (ORF 203), ORF 151 protein (ORF 151), ORF 103 protein (ORF 103), ORF 229 precursor...	0.13
1239	U48288	Rattus norvegicus A-kinase anchoring protein AKAP 220 mRNA, complete cds	0.13
1240	X70064	P.deltoides gene for poplar bark storage protein	0.13
1241	L22857	Colletotrichum gloeosporioides pectin lyase (pnlA) gene,	0.13
1242	X75607	P.halophilus RepA and RepB genes	0.13

Table 2A Nearest Neighbor (BlastN vs. GenBank)

SEQ ID	ACCESSION	DESCRIPTION	P VALUE
1243	X82584	M.musculus mRNA for immunoglobulin heavy chain, V	0.13
1244	M76713	Spodoptera frugiperda 16S rRNA gene, Val-tRNA, and Leu-tRNA genes, and ND-1 protein gene, 5' end.	0.13
1245	X57075	H.sapiens FGF6 gene	0.13
1246	Z17201	H. sapiens (DXS1003) DNA segment containing	0.13
1247	D50931	Human mRNA for KIAA0141 gene, complete cds	0.13
1248	D80002	Human mRNA for KIAA0180 gene, partial cds	0.13
1249	M58600	Human heparin cofactor II (HCF2) gene, exons 1 through 5.	0.13
1250	Z79998	Human DNA sequence from cosmid B5E3 on chromosome 22 Contains CpG island, EST	0.13
1251	X82868	G.gallus microsatellite DNA (63G2)	0.13
1252	AF009074	Hepatitis C virus genomic RNA, 3' nontranslated region, partial sequence. clone #19	0.13
1253	M26716	Rat cAMP phosphodiesterase mRNA, complete cds., clone	0.13
1254	Z57339	H.sapiens CpG island DNA genomic MseI fragment, clone 171g3, reverse read cpg171g3.rt1a	0.13
1255	U76524	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.13
1256	AF000582	Mus musculus nuclear receptor coactivator protein 2 mRNA, complete cds	0.13
1257	D12917	Yeast gene for a component of the pheromone signal transduction pathway, complete cds	0.13
1258	X70326	H.sapiens MacMarcks mRNA	0.13
1259	X82237	S.chinensis RAPD DNA (523 bp)	0.13
1260	U10116	Human superoxide dismutase (SOD3) gene, complete cds.	0.13
1261	X73293	M.vannielii genes rpoH, rpoB and rpoA	0.13
1262	U01766	Mycoplasma genitalium major adhesion protein MgPa gene, partial cds	0.13
1263	X79706	C.aetinum capr1 mRNA for pathogenesis-related protein	0.13
1264	U45957	Nicotiana glauca SA2-RNase precursor gene, complete cds.	0.13
1265	X66313	H.sapiens GLUDP2 gene (exon 2)	0.13
1266	X07946	Yeast plasmid DNA coding for RNA polymerase subunit	0.13
1267	X07870	Drosophila melanogaster bicoid gene bcd	0.13
1268	X15308	H.sapiens NF-H gene, exon 3	0.13
1269	Z22551	H.sapiens kinectin gene	0.13
1270	X89398	H.sapiens ung gene for uracil DNA-glycosylase	0.13
1271	D10654	S.coelicolor afsQ1 and afsQ2 genes	0.13
1272	U10516	Human DNA polymerase beta gene, exons 1 and 2	0.13
1273	X57075	H.sapiens FGF6 gene	0.13
1274	U71193	Mus musculus Rpl23 matrix-attachment region	0.13
1275	X69908	H.sapiens gene for mitochondrial ATP synthase c subunit	0.13
1276	M81322	Macaca fascicularis proline-rich protein (MnP4) gene,	0.13
1277	X78401	Bacteriophage P22 right operon, orf 48, replication genes 18 and 12, nin region genes, ninG phosphatase, late control gene 23, orf 60, complete cds, late control region, start of	0.13
1278	X78401	Bacteriophage P22 right operon, orf 48, replication genes 18 and 12, nin region genes, ninG phosphatase, late control gene 23, orf 60, complete cds, late control region, start of	0.13
1279	Y09852	H.sapiens FGFR3 gene, partial	0.13
1280	Z71367	S.cerevisiae chromosome XIV reading frame ORF	0.13
1281	U38292	Human microtubule-associated protein 1a (MAP1A) mRNA, complete cds	0.13
1282	Z71367	S.cerevisiae chromosome XIV reading frame ORF	0.13

Table 2A Nearest Neighbor (BlastN vs. GenBank)

SEQ ID	ACCESSION	DESCRIPTION	P VALUE
1283	Z71367	<i>S.cerevisiae</i> chromosome XIV reading frame ORF	0.13
1284	M87623	<i>Babesia bovis</i> variable antigen 1 mRNA, 5' end.	0.13
1285	M91452	<i>Sus scrofa</i> ryanodine receptor (RYR1) gene, complete cds.	0.13
1286	M91452	<i>Sus scrofa</i> ryanodine receptor (RYR1) gene, complete cds.	0.13
1287	M87623	<i>Babesia bovis</i> variable antigen 1 mRNA, 5' end.	0.13
1288	X96616	<i>P.primaurelia</i> gene encoding 156D surface antigen	0.13
1289	Z33222	<i>M.capricolum</i> DNA for CONTIG MC303	0.12
1290	X52626	<i>Phaseolus vulgaris</i> gene for alpha-phaseolin	0.12
1291	L32699	<i>Paracentrotus lividus</i> glutamine synthetase (GS) mRNA,	0.12
1292	M63669	Dog arginine esterase gene, complete cds.	0.12
1293	X75653	<i>A.longa</i> plastid genes for ribosomal proteins and tRNAs	0.12
1294	Z11839	<i>T.maritima</i> nusG gene and genes for ribosomal proteins	0.12
1295	AB005744	<i>Perilla frutescens</i> DNA for 1-limonene synthase, complete	0.12
1296	X84904	<i>Plasmodium falciparum</i> encoding Pfg27/25	0.12
1297	L02074	<i>Drosophila melanogaster</i> ribosomal protein S6 gene and two potential alternatively spliced proteins, complete cds	0.12
1298	Z84812	Human DNA sequence from phage pTEL from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3 Contains ESTs	0.12
1299	X95276	<i>P.falciparum</i> complete gene map of plastid-like DNA	0.12
1300	NM_001432.1	Homo sapiens epiregulin (EREG) mRNA > :: dbj D30783 D30783 Homo sapiens mRNA for epiregulin,	0.12
1301	X84726	<i>M.musculus</i> neurocan gene	0.12
1302	Z35810	<i>S.cerevisiae</i> chromosome II reading frame ORF YBL049w	0.12
1303	L01655	<i>Plasmodium falciparum</i> T9/106 triosephosphate isomerase	0.12
1304	U36796	<i>Mus musculus</i> presynaptic protein SNAP-25 (Snap-25) gene,	0.12
1305	U22361	<i>Saccharomyces cerevisiae</i> Rlr1p (RLR1) gene, complete cds.	0.12
1306	L04161	<i>Plasmodium falciparum</i> (clone Pfg377 [PfsXLX]) DNA sequence, complete cds	0.12
1307	U32768	<i>Haemophilus influenzae</i> Rd section 83 of 163 of the	0.12
1308	D28808	<i>Mycoplasma capricolum</i> mtla and gyrB genes for DNA gyrase subunit B and mannitol-specific phosphotransferase	0.12
1309	L05920	Human constitutively expressed serum amyloid A protein (SAA4) gene, exons 1 through 4.	0.12
1310	M96642	<i>Paramecium tetraurelia</i> P126 repetitive element.	0.12
1311	L81724	Homo sapiens (subclone 2_a3 from P1 H69) DNA sequence	0.12
1312	AF010331	<i>Tenebrio molitor</i> thermal hysteresis protein isoform YL-3 precursor, mRNA, complete cds	0.12
1313	U74496	Human chromosome 4q35 subtelomeric sequence	0.12
1314	U17295	<i>Haemophilus influenzae</i> dppB, dppC, dppD, dppF, isn, artP, artI/J, artQ, and artM genes, complete cds, and opa gene,	0.12
1315	X53921	<i>A. thaliana</i> T-DNA insertion genomic target sequence 621-	0.12
1316	X75653	<i>A.longa</i> plastid genes for ribosomal proteins and tRNAs	0.12
1317	U09347	Human variant urokinase plasminogen activator receptor (uPAR2) mRNA, partial cds.	0.12
1318	S83182	hyaluronan-binding protein=hepatocyte growth factor activator homolog [human, plasma, mRNA, 2408 nt]	0.12
1319	U21164	Human dopamine D5 receptor gene, 5' flanking and	0.12
1320	AF022391	Feline herpesvirus 1 immediate early protein, glycoprotein gL, and uracil DNA glycosylase genes, complete cds	0.12
1321	M74569	<i>Clostridium acetobutylicum</i> heat shock protein	0.12
1322	X15359	<i>Drosophila virilis</i> hunchback (hb) gene for zinc-finger protein transcription factor	0.12

Table 2A

Table 2A Nearest Neighbor (BlastN vs. GenBank)

SEQ ID	ACCESSION	DESCRIPTION	P VALUE
1323	U67478	Methanococcus jannaschii section 20 of 150 of the complete	0.12
1324	X77052	Entomopoxvirus gene for spherulin	0.12
1325	M97514	Saccharomyces douglasii mitochondrial cytochrome c oxidase subunit I (COXI) gene, complete cds	0.12
1326	X56495	H.sapiens DNA for the upstream regulatory region of the c-erbB2 gene	0.12
1327	D61398	Human MSH3 gene, exon3	0.12
1328	Z81595	Caenorhabditis elegans cosmid T22H2, complete sequence [Caenorhabditis elegans]	0.12
1329	D61398	Human MSH3 gene, exon3	0.12
1330	Z79998	Human DNA sequence from cosmid B5E3 on chromosome 22 Contains CpG island, EST	0.12
1331	NM_001280.1	Homo sapiens cold inducible RNA-binding protein (CIRBP) mRNA > :: dbj D78134 HUMCIRPA Homo sapiens mRNA	0.12
1332	Z49867	Caenorhabditis elegans cosmid C33D3, complete sequence [Caenorhabditis elegans]	0.12
1333	X14036	Tomato cab-7 gene for type II chlorophyll a/b-binding	0.12
1334	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.12
1335	U19159	Human P protein (P) gene, exon 8	0.12
1336	X74987	H.sapiens mRNA for 2'-5' oligoadenylate binding protein > :: gb L24115 HUMAAZ Human DNA fragment. > :: emb A49723.1 A49723 Sequence 2 from Patent	0.12
1337	U32112	Dictyostelium discoideum 34 kDa actin binding protein gene, complete cds > :: emb Z50156 DD30KDABP D.discoideum gene for 34 kD actin binding protein	0.12
1338	M55002	Synechococcus sp. 6-phosphogluconate dehydrogenase gene, complete cds.	0.12
1339	AF019225	Homo sapiens apolipoprotein L mRNA, complete cds	0.12
1340	U14190	Mycobacterium smegmatis diphtheria toxin repressor homolog (dtxR) gene, complete cds.	0.12
1341	J05276	Rat 5-hydroxytryptamine-1a receptor (5-HT-1a) gene,	0.12
1342	AE000603.1	Helicobacter pylori 26695 section 81 of 134 of the complete	0.12
1343	X15308	H.sapiens NF-H gene, exon 3	0.12
1344	L35600	Homo sapiens DNA sequence.	0.12
1345	Z73360	Human DNA sequence from cosmid 92M18, BRCA2 gene region chromosome 13q12-13	0.12
1346	U93721	Homo sapiens green cone photoreceptor pigment gene, 5' flanking region	0.12
1347	X78401	Bacteriophage P22 right operon, orf 48, replication genes 18 and 12, nin region genes, ninG phosphatase, late control gene 23, orf 60, complete cds, late control region, start of	0.12
1348	Z71367	S.cerevisiae chromosome XIV reading frame ORF	0.12
1349	U43673	Mus musculus putative transmembrane receptor IL-1Rrp mRNA, complete cds > :: gb AR016448 AR016448 Sequence 3 from patent US 5776731	0.12
1350	X72863	A.thaliana TMKL1 mRNA	0.12
1351	U13769	Vibrio sp. ppGpp synthetase I (relA) gene, complete cds.	0.12
1352	M32732	Chicken progesterone receptor gene, encoding forms A and	0.11
1353	X04668	Xenopus laevis XK81A1 keratin gene > :: emb X04804 XLXK81A1 Xenopus laevis DNA for stage-specific epidermal type I keratin A1 (embryo- and larval-	0.11

Table 2A Nearest Neighbor (BlastN vs. GenBank)

SEQ ID	ACCESSION	DESCRIPTION	P VALUE
1354	Z82197	Human DNA sequence from PAC 293L6 on chromosome 22, complete sequence [Homo sapiens]	0.11
1355	M84214	Cucumis sativus ORF 1, chitinase, and ORF 3 genes, complete cds > :: gb I38466 I38466 Sequence 36 from patent US 5614395 > :: gb I56941 I56941 Sequence 36 from patent US 5650505 > :: gb I59807 I59807 Sequence 36 from patent US 5654414 > :: gb I75134 I7513	0.11
1356	Y08503	F.domesticus mitochondrial 12S rRNA gene	0.11
1357	L03286	Hamster P-glycoprotein class I (pgp1) gene exons 1-2.	0.11
1358	X57171	D.caryophyllus CARSR12 gene	0.11
1359	L07307	Mus musculus ATPase mRNA-ampifying genomic DNA MOR6.5 sequence. > :: gb S55685 S55685 MOR6.5=ouabain resistance gene {repeat sequence} [mice, Caenorhabditis elegans cosmid K01F9, complete sequence [Caenorhabditis elegans]	0.11
1360	Z22175	T.maritima nusG gene and genes for ribosomal proteins	0.1
1361	Z11839	Pisum sativum GTP-binding protein (IAP86) mRNA,	0.096
1362	L36857	Homo sapiens ubiquitous TPR motif, Y isoform	0.07
1363	AF000994	Caenorhabditis elegans cosmid C45E5	0.069
1364	U61950	Mus musculus putative breast/ovarian cancer susceptibility protein homolog (Brca1) mRNA, complete cds.	0.068
1365	U32446	Homo sapiens PACE4 gene, exon 23-25, complete cds	0.068
1366	AB001914	Anopheles gambiae complete mitochondrial genome	0.066
1367	L20934	Mus musculus mRNA for neuroserpin	0.065
1368	AJ001700	Mus musculus mRNA for neuroserpin	0.065
1369	AJ001700	Drosophila melanogaster plexin A (plexA) mRNA, complete	0.065
1370	AF106932	Populus kitakamiensis cyp73b gene for cinnamic acid 4-hydroxylase, partial cds	0.065
1371	D82813	Hemagglutinin gene of influenza virus strain	0.065
1372	V01087	Borrelia burgdorferi (section 64 of 70) of the complete	0.064
1373	AE001178	H.sapiens MLN51 mRNA	0.064
1374	X80199	Homo sapiens BC-2 protein mRNA, complete cds	0.064
1375	AF042384	Enoplateuthis higginsii mitochondrial 16S rRNA	0.063
1376	AJ223485	Homo sapiens full length insert cDNA clone YZ87H06	0.061
1377	AF086094	African swine fever virus lectin homolog (8CR) gene,	0.061
1378	AF017027	Bordetella bronchiseptica electron transfer flavoprotein alpha subunit (etfA) gene, partial cds, and exogenous ferric siderophore receptor (bfrA) gene, complete cds	0.06
1379	U56084	Human debrisouine 4-hydroxylase (CYP2D8P) and	0.057
1380	M33387	Homo sapiens (clone pAT 464) potential lymphokine/cytokine mRNA, complete cds.	0.057
1381	M25315	Homo sapiens mRNA for KIAA0549 protein, partial cds	0.055
1382	AB011121	Homo sapiens phosphatidylinositol 3-kinase, class 3 (PIK3C3) mRNA > :: emb Z46973 HSPITR1 H.sapiens mRNA for phosphatidylinositol 3-kinase	0.051
1383	NM_002647.1	Homo sapiens satellite DNA	0.05
1384	Z18274	Homo sapiens integral nuclear envelope inner membrane protein (LBR) gene, complete cds.	0.049
1385	L25941	Trypanosoma cruzi kinetoplast putative maxicircle divergent	0.049
1386	U28171	R.norvegicus mRNA for connexin 30.3	0.049
1387	X76168	Morganella morganii xylitol repressor, complete cds; xylitol dehydrogenase, complete cds; xylulokinase, 5' end.	0.049
1388	L34345		

Table 2A Nearest Neighbor (BlastN vs. GenBank)

SEQ ID	ACCESSION	DESCRIPTION	P VALUE
1389	K01322	Human Ig germline kappa L-chain V-region gene germline kappa L-chain V-region gene (HK189), V-kappa-1.	0.049
1390	S72468	capsid protein {RNA 3} [tomato aspermy virus TAV-B, Blencowe, Genomic RNA, 2213 nt]	0.049
1391	L08426	Zea mays auxin-binding protein (abp4) gene, exons 1-5 and complete cds.	0.048
1392	X96972	D.buzzatii copia element DNA	0.048
1393	X17147	Canine mRNA for thyrotropin (TSH) receptor variant	0.048
1394	L13164	Saccharomyces cerevisiae k9 killer toxin resistant	0.047
1395	X66451	E.octocarinatus RPA2 gene for RNA polymerase I second largest subunit	0.047
1396	X75426	G.biloba (developing endosperm) ginnacin mRNA	0.047
1397	M95171	Aedes aegypti LINE retrotransposon Juan-A including DNA binding protein and reverse transcriptase-like protein mRNA, complete coding regions.	0.047
1398	Z49076	R.prowazekii gene (unknown)	0.047
1399	K01323	Human Ig germline kappa L-chain V-region gene germline immunoglobulin heavy chain, kappa chain,	0.047
1400	L48713	Homo sapiens galactose-1-phosphate uridyl transferase (GALT) mutant V44L gene, exon 7 (M96246 bases 303-	0.047
1401	U77310	Drosophila melanogaster porcupine mRNA, complete cds	0.047
1402	J01323	Yeast (S. cerevisiae) enolase gene (clone peno8) and flanks.	0.047
1403	L14321	Bovine herpesvirus type 1 immediate-early transcriptional control protein (BICP4) gene, 5' end.	0.047
1404	L19266	Homo sapiens myotonic dystrophy-associated protein kinase and 59 genes.	0.047
1405	M58600	Human heparin cofactor II (HCF2) gene, exons 1 through 5.	0.046
1406	D86964	Human mRNA for KIAA0209 gene, partial cds	0.046
1407	Z83329	S.salar mRNA for transport associated protein Tap2B	0.046
1408	L27331	Glyphinaphis bambusae mitochondrial cytochrome oxidase subunit I gene, 3' end, and cytochrome oxidase subunit II	0.046
1409	U57613	Human interleukin-2 receptor alpha chain (IL2RA) gene, promoter region	0.046
1410	U24088	Solanum tuberosum sucrose synthase gene, clone gPOSS65, complete cds.	0.046
1411	V01087	Hemagglutinin gene of influenza virus strain	0.046
1412	S76792	OX40=cell surface antigen [human, mRNA Partial, 1034 nt]	0.046
1413	U72396	Lycopersicon esculentum class II small heat shock protein Le-HSP17.6 mRNA, complete cds	0.046
1414	U51677	Human non-histone chromatin protein HMG1 (HMG1) gene, complete cds	0.046
1415	X98743	H.sapiens mRNA for RNA helicase (Myc-regulated dead	0.046
1416	M63868	C.hircus alpha-lactalbumin gene, exons 1-4.	0.046
1417	Z92970	Caenorhabditis elegans cosmid H06O01, complete sequence [Caenorhabditis elegans]	0.045
1418	M29482	Human leukocyte adhesion protein p150,95 alpha subunit gene, exons 2 - 6.	0.045
1419	Z78942	H.sapiens flow-sorted chromosome 6 HindIII fragment,	0.045
1420	L06863	Cricetulus griseus type VII collagen mRNA, 3' end.	0.045
1421	X86449	E.caballus DNA segment containing microsatellite	0.045
1422	U32446	Mus musculus putative breast/ovarian cancer susceptibility protein homolog (Brca1) mRNA, complete cds.	0.045

Table 2A Nearest Neighbor (BlastN vs. GenBank)

SEQ ID	ACCESSION	DESCRIPTION	P VALUE
1423	K01323	Human Ig germline kappa L-chain V-region gene germline immunoglobulin heavy chain, kappa chain,	0.045
1424	M13555	Human Ia-associated invariant gamma-chain gene, exon 1, clones lambda-y(1,2,3).	0.045
1425	U68562	Rattus norvegicus chaperonin 60 (Hsp60) and chaperonin 10 (CPN10) genes, nuclear genes encoding mitochondrial	0.045
1426	AB003286	Homo sapiens DNA for choline kinase like protein and muscle type carnitine palmitoyltransferase I, partial and	0.045
1427	U34372	Human tyrosine kinase TXK (txk) gene, exon 6.	0.045
1428	U51677	Human non-histone chromatin protein HMG1 (HMG1) gene, complete cds	0.045
1429	U23476	Dictyostelium discoideum phosphatidylinositol-4,5-diphosphate 3-kinase (PIK1) mRNA, complete cds.	0.045
1430	Z98975	S.pombe chromosome I cosmid c19E9	0.044
1431	X16465	Trypanosoma brucei mRNA for cysteine proteinase	0.044
1432	D85274	Macaca fascicularis mitochondrial DNA for NADH dehydrogenase subunit 4, subunit 5, partial cds	0.044
1433	X16876	Soybean ENOD2B gene for Ngm-75	0.044
1434	U19755	Mus domesticus thyroid transcription factor 1 gene,	0.044
1435	L77700	Gallus gallus 18C15 mRNA, complete cds.	0.044
1436	AF019981	Dictyostelium discoideum HeE (heE) gene, partial cds	0.044
1437	L13469	Saccharomyces cerevisiae antiviral protein Ski2p	0.044
1438	M26238	D.discoideum spore coat protein SP70 gene, complete cds.	0.044
1439	U65391	Lycopersicon esculentum PRF (Prf) gene, complete cds	0.044
1440	AF000582	Mus musculus nuclear receptor coactivator protein 2 mRNA, complete cds	0.044
1441	X98880	C.albicans ARG5,6 gene	0.044
1442	D89609	Oryzias latipes mRNA for choriogenin H, complete cds	0.044
1443	Y13544	Homo sapiens cosmid C1	0.044
1444	Y14952	Mus musculus gene encoding immunoglobulin J chain	0.043
1445	Z69660	Caenorhabditis elegans cosmid F39B1, complete sequence [Caenorhabditis elegans]	0.043
1446	X53404	Glycine max glycinin A(1a)B(1b) and A(2)B(1a) boundary	0.043
1447	U48271	Dictyostelium discoideum UbpA deubiquitinase mRNA,	0.043
1448	U24187	Saccharomyces cerevisiae origin recognition complex, subunit 5 (ORC5) gene, complete cds > :: gb I32734 I32734 Sequence 9 from patent US 5589341 > :: gb I38710 I38710 Sequence 9 from patent US 5614618	0.043
1449	Z28177	S.cerevisiae chromosome XI reading frame ORF YKL178c	0.043
1450	X05951	Drosophila melanogaster calmodulin gene exon 4 and intron III (partial)	0.043
1451	L12999	Daltonia sp. mitochondrial 16S ribosomal RNA	0.043
1452	U68098	Human poly(A)-binding protein (PABP) gene, exons 6 and 7	0.043
1453	U55774	Caenorhabditis elegans cosmid F35G8.	0.043
1454	Z46941	H.sapiens DNA for alu repeats	0.043
1455	U41747	Caenorhabditis elegans cosmid ZK1131.	0.043
1456	M30168	D.melanogaster nested repetitive sequences F and G,	0.043
1457	U05350	Human immunodeficiency virus type 2 isolate HIV2CBL21 gp160 envelope (env) gene, complete cds.	0.042
1458	U44129	Rattus norvegicus p58 mRNA, complete cds	0.042
1459	L13377	Staphylococcus aureus enterotoxin gene, 3' end.	0.042
1460	X83758	P.falciparum topoisomerase I gene	0.042

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SEQ ID	ACCESSION	DESCRIPTION	P VALUE
1461	U64896	Anagrapha falcifera nuclear polyhedrosis virus protein-tyrosine phosphatase, lef-2, polyhedrin, vp78 and protein kinase genes, complete cds	0.042
1462	J02175	Influenza A/wsn/33 (h1n1), defective interfering l3, cdna.	0.042
1463	D86608	Arabidopsis thaliana DNA for inorganic phosphate transporter, complete cds	0.042
1464	M93716	Pan paniscus DNA fragment.	0.042
1465	X14385	Astasia longa chloroplast rps7 and tufA genes for ribosomal protein S7 and elongation factor Tu respectively	0.042
1466	M74069	Saccharomyces cerevisiae endochitinase (CTS1-1) gene, complete cds.	0.042
1467	M73257	C.parasitica laccase (lac-1) gene, complete cds.	0.042
1468	M31126	Human pregnancy-specific beta-1-glycoprotein (SP1) mRNA, complete cds, clone hPS2.	0.042
1469	U70826	Fundulus heteroclitus vitellogenin II precursor mRNA,	0.041
1470	AF000299	Caenorhabditis elegans cosmid E03H12	0.041
1471	X83390	Albinaria coerulea complete mitochondria DNA	0.041
1472	L12582	Human ornithine decarboxylase (ODC) gene, 5' flanking	0.041
1473	D89655	Rattus norvegicus mRNA for scavenger receptor class B, complete cds	0.041
1474	Z23267	P.anserina AS1 gene, complete CDS	0.041
1475	M63868	C.hircus alpha-lactalbumin gene, exons 1-4.	0.041
1476	U56440	Human His-1 gene sequence	0.04
1477	L06863	Cricetulus griseus type VII collagen mRNA, 3' end.	0.04
1478	U02928	Dictyostelium discoideum Ax3 Rab7 mRNA, complete cds.	0.04
1479	M19828	Human apolipoprotein B-100 (apoB) gene, exons 22 through	0.04
1480	M34434	Human angiotensin-converting enzyme (ACE) gene, 5' end.	0.04
1481	Z68884	Human DNA sequence from cosmid L21F12, Huntington's Disease Region, chromosome 4p16.3	0.04
1482	M99367	Pig alveolar macrophage-derived chemotactic factor-I (AMCF-I) mRNA, complete cds.	0.04
1483	U70370	Human hindlimb expressed homeobox protein backfoot (Bft) mRNA, complete cds	0.04
1484	U10698	Rattus norvegicus liver microsomal carboxylesterase mRNA, complete cds.	0.04
1485	U28171	Trypanosoma cruzi kinetoplast putative maxicircle divergent	0.04
1486	U79297	Human clone 23589 mRNA sequence	0.04
1487	X13764	Yeast centromere CEN1 repetitive DNA PSS113, part of	0.04
1488	Z24568	H. sapiens (D9S286) DNA segment containing	0.04
1489	M63868	C.hircus alpha-lactalbumin gene, exons 1-4.	0.04
1490	X64143	F.trinervia ppcA1 gene for phosphoenolpyruvate	0.039
1491	M16339	Entamoeba histolytica actin mRNA, complete cds.	0.039
1492	U36475	Mus musculus breast and ovarian cancer susceptibility protein (Brca1) mRNA, complete cds	0.039
1493	X02570	Flesh fly gene for 25-kDa protein	0.039
1494	M32475	Rattus norvegicus carcinoembryonic antigen-related protein (CGM4) gene, exons 2 and 3.	0.039
1495	D89609	Oryzias latipes mRNA for choriogenin H, complete cds	0.039
1496	AF011573	Homo sapiens zinc finger protein (ZnF20) mRNA, complete	0.039
1497	X15050	Mouse mRNA for 3'-end of NCAM-120 isoform	0.039
1498	Z11533	D.discoideum rasG gene	0.038
1499	AB000450	Homo sapiens mRNA for VRK2, complete cds	0.038
1500	X78983	D.melanogaster Fab-7 regulatory region	0.038

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SEQ ID	ACCESSION	DESCRIPTION	P VALUE
1501	D89609	Oryzias latipes mRNA for choriogenin H, complete cds	0.038
1502	Z49535	S.cerevisiae chromosome X reading frame ORF YJR035w	0.038
1503	L13377	Staphylococcus aureus enterotoxin gene, 3' end.	0.035
1504	L12582	Human ornithine decarboxylase (ODC) gene, 5' flanking	0.035
1505	Z48584	Caenorhabditis elegans cosmid ZK1321, complete sequence [Caenorhabditis elegans]	0.023
1506	Y00204	Xenopus laevis mRNA fragment for nucleoplasmin	0.021
1507	S77817	light-chain fibroin [Galleria mellonella=waxmoths, larvae, cocoons, posterior silk glands, mRNA, 1191 nt]	0.021
1508	L13926	Trypanosoma cruzi (strain La Cruz, Jalisco) ribosomal RNA transcribed spacer and 18S ribosomal RNA gene, 5' end.	0.02
1509	Z78910	H.sapiens flow-sorted chromosome 6 HindIII fragment,	0.02
1510	AB007976	Homo sapiens mRNA, chromosome 1 specific transcript	0.02
1511	U01307	Human scRNA (BC200 beta) pseudogene.	0.017
1512	J03998	P.falciparum glutamic acid-rich protein gnen, complete cds.	0.017
1513	X93497	H.sapiens TRAP gene, intron 4 (partial)	0.017
1514	M15656	Human aldolase B (ALDOB) gene, exons 7 through 9.	0.016
1515	X74965	H.sapiens ACPP gene for prostatic acid phosphatase (non-coding region)	0.016
1516	X75653	A.longa plastid genes for ribosomal proteins and tRNAs	0.016
1517	X75653	A.longa plastid genes for ribosomal proteins and tRNAs	0.016
1518	X58852	Human MLC1emb gene for embryonic myosin alkaline light chain, exon 2	0.016
1519	U69695	Mus musculus hyaluronan synthase homolog mRNA,	0.016
1520	S45332	erythropoietin receptor [human, placental, Genomic, 8647	0.016
1521	U09865	Alcaligenes eutrophus pyruvate dehydrogenase dihydrolipoamide dehydrogenase (pdhL), and ORF3 genes,	0.016
1522	U67815	Human primary Alu transcript	0.016
1523	AE000466	Escherichia coli K-12 MG1655 section 356 of 400 of the complete genome	0.016
1524	M80785	M.musculus tissue factor promoter (Cf-3) gene, exon 1.	0.016
1525	L37035	Drosophila virilis brown protein (bw) gene, complete cds.	0.016
1526	M15009	Mouse steroid 21-hydroxylase A (21-OHase A) gene,	0.016
1527	U67500	Methanococcus jannaschii section 42 of 150 of the complete	0.016
1528	AB000044	Rhizoctonia solani 5.8S rRNA gene, complete sequence	0.016
1529	X52956	Human CAMII-psi3 calmodulin retropseudogene	0.016
1530	U80581	Pleurodeles waltl Wnt-7a mRNA, complete cds	0.016
1531	Z69918	Human DNA sequence from cosmid 91K3, Huntington's Disease Region, chromosome 4p16.3 contains CpG island	0.016
1532	Z98031	Human immunodeficiency virus type 1 nef gene	0.016
1533	D45858	immunodeficiency virus type 1 nef gene (strain KU15-1)	0.016
1534	L24549	Mus musculus mRNA for synaptotagmin III, complete cds	0.016
1535	U66291	Gallus gallus Gi2 protein alpha-subunit mRNA, complete	0.016
1536	X63436	Catagonus wagneri cytochrome b gene, mitochondrial gene encoding mitochondrial protein, partial cds	0.016
1537	L23498	B.taurus mRNA for poly(A) polymerase	0.016
1538	AF003086	Bovine microsatellite repeats	0.015
1539	U17377	Plasmodium falciparum transcription factor homolog PfSNF2L mRNA, complete cds	0.015
1540	L23498	Strongylocentrotus purpuratus cortical granule protein with LDL-receptor-like repeats mRNA, partial cds.	0.015
1541	X85117	Bovine microsatellite repeats	0.015
		H.sapiens epb72 gene exons 2,3,4,5,6,7	0.015

Table 2A Nearest Neighbor (BlastN vs. GenBank)

SEQ ID	ACCESSION	DESCRIPTION	P VALUE
1542	Z16906	H. sapiens (D14S73) DNA segment containing	0.015
1543	X99400	S.pneumoniae dacA gene and ORF	0.015
1544	M32061	Rat alpha-2B-adrenergic receptor (RNG-alpha-2) mRNA,	0.015
1545	X80930	S.cerevisiae RHC18 genes	0.015
1546	U09865	Alcaligenes eutrophus pyruvate dehydrogenase dihydrolipoamide dehydrogenase (pdhL), and ORF3 genes,	0.015
1547	Z22952	Mus musculus BALB/c of p65 gene encoding p65 subunit of transcription factor NF-kappaB	0.015
1548	L34610	Mus musculus parathyroid hormone/parathyroid hormone related-peptide receptor (PTHr) gene, exons 5 - 9.	0.015
1549	Z54850	H.sapiens CpG island DNA genomic MseI fragment, clone 169b5, reverse read cpg169b5.rt1a	0.015
1550	U01307	Human scRNA (BC200 beta) pseudogene.	0.015
1551	M54994	Human bile salt-activated lipase (BAL) mRNA, complete	0.015
1552	Z98031	Human immunodeficiency virus type 1 nef gene	0.015
1553	Z21858	immunodeficiency virus type 1 nef gene (strain KU15-1)	0.015
1554	M33518	M.Musculus mRNA for P domain protein	0.015
1555	AB001383	Human HLA-B-associated transcript 2 (BAT2) gene, 3' end.	0.015
1556	U72787	Rattus norvegicus mRNA for sialoprotein, complete cds	0.015
1557	AF012899	Homo sapiens cosmid clone U163C11 from Xp22.1-22.2, complete sequence [Homo sapiens]	0.014
1558	J03764	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.014
1559	AF012899	Human, plasminogen activator inhibitor-1 gene, exons 2 to	0.014
1560	AB003097	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.014
1561	AC001017	Fruitfly strain g20 mitochondrial DNA, A+T-rich region, partial sequence	0.014
1562	Z48484	Homo sapiens (subclone 2_g8 from P1 H43) DNA sequence	0.014
1563	AC001460	H.sapiens gene for tissue-type plasminogen activator	0.014
1564	U09865	Homo sapiens (subclone 2_f4 from BAC H107) DNA	0.014
1565	U00691	Alcaligenes eutrophus pyruvate dehydrogenase dihydrolipoamide dehydrogenase (pdhL), and ORF3 genes,	0.014
1566	D16482	Dictyostelium discoideum plasmid Ddp1 D2 orf, D1/D3 orf, G4/D5 orf, G5/D6 orf, G1 orf, G2/G3/D4 orf, complete cds	0.014
1567	AF012899	Sarcophaga peregrina mRNA for poly(ADP-ribose)	0.014
1568	M63599	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.014
1569	U03891	Human myelin basic protein (MBP) gene, exon 1.	0.014
1570	X53422	Human phorbolin I mRNA, partial cds.	0.014
1571	X01870	D. grimshawi s18, s15, s19 and s16 chorion protein genes	0.013
1572	Z92804	Yeast mitochondrial ori(o) repeat unit of petite mutant 4 (petite strain a-10/3/2/B11)	0.013
1573	M76377	Caenorhabditis elegans cosmid K05D4, complete sequence [Caenorhabditis elegans]	0.013
1574	D29801	Human cysteine-rich protein (CRP) gene, exons 3 and 4.	0.013
1575	U77984	Mouse mRNA for unknown product, complete cds	0.013
1576	Z55882	Sus scrofa microsatellite S0058 sequence	0.013
1577	V00531	H.sapiens CpG island DNA genomic MseI fragment, clone 70g8, reverse read cpg70g8.rt1a	0.013
1578	Z74361	Human interferon genes LeIF-L and LeIF-J and pseudogene LeIF-M with intergenic regions. These genes are located on	0.013
		S.cerevisiae chromosome IV reading frame ORF YDR065w	0.013

Table 2A Nearest Neighbor (BlastN vs. GenBank)

SEQ ID	ACCESSION	DESCRIPTION	P VALUE
1579	D00374	Herpes simplex virus type 1 (HSV-1) genome, rightmost part of the long unique region (UL) and all of the internal long	0.013
1580	U53502	Arabidopsis thaliana chromosome I cosmid g17311 DNA.	0.013
1581	K03196	Human interferon-beta-3 gene.	0.013
1582	M23456	Zea mays (clone pCIB808) encoding maize nitrite reductase (NiR) cDNA to mRNA, partial cds.	0.013
1583	X66120	H.sapiens F8VWFL DNA of the von Willebrand factor pseudogene (5'portion)	0.013
1584	M63962	Human gastric H,K-ATPase catalytic subunit gene, complete	0.011
1585	AF039592	Homo sapiens succinate dehydrogenase subunit C	0.007
1586	Y10908	B.cereus cysA and wapA genes	0.007
1587	AF048988	Homo sapiens MutS homolog 5 (MSH5) gene, exons 1	0.007
1588	AF048988	Homo sapiens MutS homolog 5 (MSH5) gene, exons 1	0.007
1589	D90822	E.coli genomic DNA, Kohara clone #331(40.1-40.4 min.)	0.007
1590	D87903	Mouse mRNA for ARF6, complete cds	0.006
1591	L38851	Mycobacterium tuberculosis cell surface protein	0.006
1592	U66362	Human neuronal nitric oxide synthase (nNOS) gene, alternatively spliced 5' exon Tex 2 and flanking sequences	0.005
1593	L11670	Human transmembrane glycoprotein (CD53) gene, exons 2	0.005
1594	U20587	Sus scrofa domestica sister of P-glycoprotein	0.005
1595	U53016	Human DXYS154 microsatellite sequence	0.005
1596	Z29641	Zea mays of USE gene encoding U3snRNA	0.005
1597	D16473	Human mRNA, Xq terminal portion	0.005
1598	X02175	Schizosaccharomyces pombe cdc10 start gene	0.005
1599	U25029	Human glucocorticoid receptor alpha mRNA, variant 3'	0.005
1600	Z68685	Human DNA sequence from cosmid N2E9 on chromosome 22, complete sequence [Homo sapiens]	0.005
1601	U40369	Human spermidine/spermine N1-acetyltransferase	0.005
1602	U06965	Aphytis melinus mitochondrion 16S rRNA gene, partial	0.005
1603	Z81014	Human DNA sequence from cosmid U65A4, between markers DXS366 and DXS87 on chromosome X *	0.005
1604	X91923	H.sapiens ECE-1 gene (exon 3)	0.005
1605	Z29641	Zea mays of USE gene encoding U3snRNA	0.005
1606	L11670	Human transmembrane glycoprotein (CD53) gene, exons 2	0.005
1607	U15605	Nicotiana glutinosa virus resistance (N) gene, complete cds.	0.005
1608	X57698	A.thaliana DNA for acyl carrier protein (ACP) gene A1	0.005
1609	L81391	Homo sapiens (subclone 2_a6 from P1 H39) DNA sequence	0.005
1610	X81789	H.sapiens mRNA for splicing factor SF3a60	0.005
1611	X82818	H.sapiens PTP1C/HCP gene	0.005
1612	U33465	Drosophila melanogaster S element and flanking sequence,	0.005
1613	Z75042	S.cerevisiae chromosome XV reading frame ORF YOR134w	0.005
1614	M98574	Mouse T cell receptor rearranged alpha-chain variable region, N region, joining region, and constant region	0.005
1615	X51907	Human vimentin gene 5' regulatory region	0.005
1616	U50383	Human retinoic acid-responsive protein (NN8-4AG) mRNA, complete cds	0.005
1617	M25140	Human cardiac alpha-myosin heavy chain (MYH6) gene, exons 2, 3 and 4.	0.005
1618	X66062	G.max tufA gene for chloroplast translation elongation	0.005
1619	U16345	Gallus gallus protein kinase gene (cPITSLRE) gene, exons 4	0.005
1620	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	0.005

Table 2A Nearest Neighbor (BlastN vs. GenBank)

SEQ ID	ACCESSION	DESCRIPTION	P VALUE
1621	U43834	Saccharomyces cerevisiae chromosome IV lambda 3073 and flanking region extending into right telomere	0.005
1622	X13602	Caldocellum saccharolyticum celB gene for cellobiohydrolase/endocellulase	0.005
1623	J04809	Human cytosolic adenylate kinase (AK1) gene, complete	0.005
1624	L49144	Homo sapiens neuroendocrine-specific protein (NSP) gene, exons 1B and 3	0.005
1625	L34028	Plasmodium falciparum (clone HB3) heat shock protein 86 gene, complete cds.	0.005
1626	U50383	Human retinoic acid-responsive protein (NN8-4AG) mRNA, complete cds	0.005
1627	U23829	Lucilia cuprina peritrophin-95 precursor gene, partial cds.	0.005
1628	AE000629.1	Helicobacter pylori 26695 section 107 of 134 of the	0.005
1629	M16446	Human adenine phosphoribosyltransferase (APRT) gene, complete cds.	0.005
1630	U34605	Human retinoic acid- and interferon-inducible 58K protein RI58 mRNA, complete cds.	0.005
1631	M25140	Human cardiac alpha-myosin heavy chain (MYH6) gene, exons 2, 3 and 4.	0.005
1632	X16426	Mouse MHC (Qa) Q10-k gene for class I antigen	0.005
1633	M83985	Mouse phosphoprotein (F1-20) mRNA, complete cds.	0.005
1634	U31850	Human dystonin isoform 1 mRNA, partial cds	0.005
1635	U31850	Human dystonin isoform 1 mRNA, partial cds	0.005
1636	X64615	O.berteriana chloroplast ORF80 (exon 1 and 2) and ORF2280 sequences	0.005
1637	X52647	E.coli dbpA gene for DEAD box protein A	0.005
1638	D90773	E.coli genomic DNA, Kohara clone #262(30.3-30.5 min.)	0.005
1639	M62946	S.glaucescens novel deletion/rearrangement sequence, partial sequence.	0.005
1640	M88597	Saccharomyces cerevisiae STP1 gene, complete cds.	0.005
1641	L31521	Homo sapiens (clone HG52) Z-crystallin/quinone reductase (CRYZ) gene sequence.	0.005
1642	D79986	Human mRNA for KIAA0164 gene, complete cds	0.004
1643	AC002183	Homo sapiens (subclone 2_h8 from BAC H111) DNA	0.004
1644	Z29641	Zea mays of USE gene encoding U3snRNA	0.004
1645	L22415	Homo sapiens DNA sequence, repeat region.	0.004
1646	U17357	Chlamydomonas reinhardtii chloroplast 30S ribosomal protein S4 (rps4) gene, complete cds.	0.004
1647	M67465	Rat 3-beta-hydroxysteroid dehydrogenase/delta-5-delta-4-ene-isomerase mRNA, complete cds.	0.004
1648	U08421	Murine rotavirus EC outer capsid protein VP4 gene,	0.004
1649	Z17089	H. sapiens (D3S1309) DNA segment containing	0.002
1650	L35531	Human Alu repeat region.	0.002
1651	M55120	Human cystic fibrosis transmembrane conductance regulator (CFTR) gene, exon 14b	0.002
1652	J00922	Gallus gallus ovalbumin (Y) gene, complete cds.	0.002
1653	U69695	Mus musculus hyaluronan synthase homolog mRNA,	0.002
1654	L15248	Human (clone: pHyTM1/60(R)) DNA sequence.	0.002
1655	L35676	Homo sapiens (subclone H8_2_e7 from P1 35 H5 C8) DNA	0.002
1656	L48612	Theileria parva (clone pTprUgB) ORF genes, partial cds.	0.002
1657	Y08925	P. falciparum aarp3 gene, exon	0.002
1658	M60441	Sheep lambda immunoglobulin V gene.	0.002
1659	X91857	Piromyces sp. mRNA for mannanase A	0.002

Table 2A

Table 2A Nearest Neighbor (BlastN vs. GenBank)

SEQ ID	ACCESSION	DESCRIPTION	P VALUE
1660	Z35948	S.cerevisiae chromosome II reading frame ORF YBR079c	0.002
1661	X16277	Human gene for ornithine decarboxylase ODC (EC 4.1.1.17)	0.002
1662	X78608	G.gallus genomic DNA repeat region, clone 9C2	0.002
1663	U48449	Human skeletal muscle ryanodine receptor gene	0.002
1664	X51875	Human breakpoint in translocation V-kappa gene region (WB) (partial) (537 bp)	0.002
1665	Z24205	H. sapiens (D12S348) DNA segment containing	0.002
1666	U85612	Mus musculus cartilage-derived retinoic acid-sensitive protein/melanoma inhibitory activity protein gene, complete	0.002
1667	M61829	Human alpha-1,3-mannosyl-glycoprotein beta-1, 2-N-acetylglucosaminyltransferase (MGAT) gene, complete cds.	0.002
1668	M61829	Human alpha-1,3-mannosyl-glycoprotein beta-1, 2-N-acetylglucosaminyltransferase (MGAT) gene, complete cds.	0.002
1669	V00571	Human gene encoding prepro form of corticotropin releasing	0.002
1670	D29760	Candida maltosa gene for chitin synthase 1, partial sequence	0.002
1671	AJ001817	Dama sp. mRNA for bone morphogenetic protein 2	0.002
1672	Z23575	H. sapiens (D17S926) DNA segment containing	0.002
1673	X59359	T.marmorata mRNA for acetylcholinesterase	0.002
1674	D12519	Rat SAP gene for synaptotagmin associated 35kDa protein	0.002
1675	U88534	Mus musculus glucose-6-phosphate dehydrogenase protein, exons 10, 11 and partial cds	0.002
1676	Z24391	H. sapiens (D11S1350) DNA segment containing	0.002
1677	M31773	Murine B cell 1 (mb-1) gene, complete cds.	0.002
1678	U28014	Human cysteine protease (ICERel-II) mRNA, complete cds.	0.002
1679	M33518	Human HLA-B-associated transcript 2 (BAT2) gene, 3' end.	0.002
1680	U70983	Pseudomonas aeruginosa heptosyl transferase II	0.002
1681	Z74854	S.cerevisiae chromosome XV reading frame ORF YOL112w	0.002
1682	M13498	Mouse renal kallikrein gene mGK-6, exon 1	0.002
1683	U17382	Streptococcus pyogenes putative multiple membrane domain protein gene, complete cds.	0.002
1684	U14189	Plasmodium falciparum MCP1 mRNA, complete cds	0.001
1685	M27314	Saccharomyces cerevisiae mitochondrial petite mutant BB5 origin of replication DNA.	0.001
1686	M64089	Dictyostelium discoideum calmodulin (calA) gene, complete	0.001
1687	J05138	Rabbit calcium binding protein (calreticulin) mRNA,	0.0009
1688	U92017	Human clone 199288 defective mariner transposon Hsmar2 mRNA sequence	0.0008
1689	AJ011915	Homo sapiens mRNA for synaptosome associated protein of 23 kilodaltons, isoform A	0.0008
1690	AJ223734	Sus scrofa SCAMP1 gene, exon 1 and joined CDS	0.0008
1691	Y08924	P.falciparum mRNA for AARP2 protein	0.0006
1692	X58139	Human coxVIb gene, last exon and flanking sequence	0.0006
1693	U47853	Araneus diadematus fibroin-1 (ADF-1) mRNA, partial cds	0.0006
1694	L34027	Plasmodium falciparum (clone Dd2) heat shock protein 86 gene, complete cds.	0.0006
1695	D88271	Human (lambda) DNA for immunoglobulin light chain	0.0006
1696	AC001546	Homo sapiens (subclone 2_b1 from P1 H69) DNA sequence	0.0006
1697	Z96325	H.sapiens telomeric DNA sequence, clone 16QTEL024, read 16QTELOO024.seq	0.0006
1698	U14974	Saccharomyces cerevisiae Nmd2p (NMD2) gene, complete cds. > :: gb I70400 I70400 Sequence 1 from patent US	0.0006
1699	AB002331	Human mRNA for KIAA0333 gene, partial cds	0.0006

Table 2A

Table 2A Nearest Neighbor (BlastN vs. GenBank)

SEQ ID	ACCESSION	DESCRIPTION	P VALUE
1700	AE000464	Escherichia coli K-12 MG1655 section 354 of 400 of the complete genome	0.0006
1701	Z79060	H.sapiens flow-sorted chromosome 6 HindIII fragment,	0.0005
1702	Z60233	H.sapiens CpG island DNA genomic MseI fragment, clone 197c9, reverse read cpg197c9.rt1a	0.0005
1703	U15018	Dugbe virus L protein gene, complete cds	0.0005
1704	X77607	H. sapiens genomic DNA (leukocyte), corresponding to the integration site of HPV 6a DNA in a tonsillar carcinoma	0.0005
1705	M59428	T.thermophila ribosomal protein L37 (L37) mRNA,	0.0005
1706	M59428	T.thermophila ribosomal protein L37 (L37) mRNA,	0.0005
1707	AC002219	Homo sapiens (subclone 2_d11 from P1 H43) DNA	0.0005
1708	X95276	P.falciparum complete gene map of plastid-like DNA (IR-B)	0.0005
1709	L18972	Homo sapiens anonymous gene, complete cds	0.0005
1710	U96974	Homo sapiens MET proto-oncogene, intron 5, 3' end	0.0005
1711	Z60916	H.sapiens CpG island DNA genomic MseI fragment, clone 39a5, forward read cpg39a5.ft1c	0.0005
1712	X99587	A.brasilense ipdC, gltX & cysS genes	0.0005
1713	J03998	P.falciparum glutamic acid-rich protein gnen, complete cds.	0.0005
1714	AE000464	Escherichia coli K-12 MG1655 section 354 of 400 of the complete genome	0.0005
1715	U21730	Human 5'-nucleotidase (CD73) gene, partial cds.	0.0004
1716	M22970	Human pancreatic phospholipase A-2 (PLA-2) gene, exons 1	0.0003
1717	U37022	Human cyclin-dependent kinase 4 (CDK4) gene, complete	0.0002
1718	AC001517	Homo sapiens (subclone 1_g5 from P1 H49) DNA sequence	0.0002
1719	X90383	A.thaliana DNA for Y13 gene	0.0002
1720	NM_003407.1	Homo sapiens zinc finger protein homologous to Zfp-36 in mouse (ZFP36) mRNA > :: gb M92843 HUMG0S24A	0.0002
1721	M86528	H.sapiens zinc finger transcriptional regulator mRNA,	0.0002
1722	M86528	Human neurotrophin-4 (NT-4) gene, complete cds.	0.0002
1723	U19241	Human neurotrophin-4 (NT-4) gene, complete cds.	0.0002
1724	M15205	Homo sapiens interferon-gamma receptor alpha chain gene, Human thymidine kinase gene, complete cds, with clustered Alu repeats in the introns.	0.0002
1725	M87510	Mouse Y specific region of AC11 DNA sequence, LINE repeat and Bkm satellite.	0.0002
1726	Z84723	Human DNA sequence from phage LAW2 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3 Contains Interleukin 9 receptor pseudogene	0.0002
1727	X01392	Human apolipoprotein CIII gene and apo A1-apo CIII	0.0002
1728	Z92910	H.sapiens HFE (HLA-H) gene	0.0002
1729	D87001	Human (lambda) DNA for immunoglobulin light chain	0.0002
1730	M35612	Yeast (S.cerevisiae) mitochondrial autonomously replicating sequence DNA.	0.0002
1731	Z16956	H. sapiens (D2S154) DNA segment containing	0.0002
1732	L42456	Mus musculus TGF-1 gene, promoter region and exon 1.	0.0002
1733	X90383	A.thaliana DNA for Y13 gene	0.0002
1734	L35657	Homo sapiens (subclone H8_5_a10 from P1 35 H5 C8) DNA	0.0002
1735	M57902	Mouse transforming growth factor-beta-1	0.0002
1736	U67167	Homo sapiens intestinal mucin (MUC2) gene, promoter region and partial cds	0.0002
1737	NM_002824.1	Homo sapiens parathymosin (PTMS) mRNA > :: gb M24398 HUMTHYP Human parathymosin mRNA,	0.0002
1738	J05138	Rabbit calcium binding protein (calreticulin) mRNA,	0.0002

Table 2A

Table 2A Nearest Neighbor (BlastN vs. GenBank)

SEQ ID	ACCESSION	DESCRIPTION	P VALUE
1739	U96566	HIV-1 patient JO population variant JOS17 from USA, envelope glycoprotein, C2-V5 region (env) gene, partial cds	0.0002
1740	AF043461	Homo sapiens I-REL gene, exon 9	9e-005
1741	M96943	Human profilaggrin gene exons 1-3, 5' end.	8e-005
1742	S45332	erythropoietin receptor [human, placental, Genomic, 8647	7e-005
1743	S45332	erythropoietin receptor [human, placental, Genomic, 8647	7e-005
1744	L28125	Podospira anserina beta transducin-like protein	7e-005
1745	U53017	Human microsatellite marker sJCW13	6e-005
1746	M86528	Human neurotrophin-4 (NT-4) gene, complete cds.	6e-005
1747	D17554	Human mRNA for DNA-binding protein, TAXREB107,	6e-005
1748	U26556	Human ferritin H (FTHL13) pseudogene.	6e-005
1749	Z79060	H.sapiens flow-sorted chromosome 6 HindIII fragment,	6e-005
1750	AC001460	Homo sapiens (subclone 2_f4 from BAC H107) DNA	6e-005
1751	AC001033	Homo sapiens (subclone 2_c2 from P1 H48) DNA sequence	6e-005
1752	AF007883	Homo sapiens MHC class II HLA-DRB1 (HLA-DRB1*10) intron 1 sequence	6e-005
1753	U12971	Tetrahymena thermophila CU428.1VII micronuclear M	6e-005
1754	X83872	H.vulgaris mRNA for cAMP response element binding	6e-005
1755	Z73360	Human DNA sequence from cosmid 92M18, BRCA2 gene region chromosome 13q12-13	5e-005
1756	X85116	H.sapiens epb72 gene exon 1	5e-005
1757	L81639	Homo sapiens (subclone 2_b2 from P1 H39) DNA sequence	3e-005
1758	D16184	Chicken mRNA for nuclear b-Zip protein MafF, complete	3e-005
1759	AF100694	Mus musculus Pontin52 mRNA, complete cds	3e-005
1760	Z30978	G.gorilla DNA for Mhc Alu elements	3e-005
1761	L23429	Canis beta-galactosides-binding lectin (LGALS3) mRNA,	2e-005
1762	X06559	Human interferon-inducible gene IFI-56K 5' region (56 kDa coding capacity of unknown function)	2e-005
1763	AC001546	Homo sapiens (subclone 2_b1 from P1 H69) DNA sequence	2e-005
1764	L35658	Homo sapiens (subclone H8_9_d12 from P1 35 H5 C8)	2e-005
1765	D16472	Human mRNA, Xq terminal portion	2e-005
1766	M83665	Human high mobility group 2 protein (HMG-2) gene,	2e-005
1767	U07977	Human T cell receptor beta (TCRBV9S1, TCRBV7S1) genes, TCRBV inserted and TCRBV deleted haplotype,	2e-005
1768	D83227	Populus nigra gene for extensin like protein, complete cds	2e-005
1769	U42053	Mustela vison microsatellite repeat (Mvi 24).	2e-005
1770	L29339	Homo sapiens Na ⁺ /glucose cotransporter (SGLT1) gene, exon 15 and complete cds.	2e-005
1771	Z33620	M.musculus (Balb/c) GATA-3 gene (partial)	2e-005
1772	D88271	Human (lambda) DNA for immunoglobulin light chain	2e-005
1773	AD000833	Homo sapiens DNA from chromosome 19-cosmid f19399 (~17 kb EcoRI restriction fragment)	2e-005
1774	U36755	Human thrombin receptor (F2R) gene, 5' region and partial	2e-005
1775	AC002252	Homo sapiens (subclone 1_g7 from BAC H76) DNA	2e-005
1776	AE000464	Escherichia coli K-12 MG1655 section 354 of 400 of the complete genome	2e-005
1777	X94768	H.sapiens RP3 gene (XLRP gene 3)	1e-005
1778	U57058	Human WD protein IR10 pre-mRNA, partial cds	9e-006
1779	AC001603	Homo sapiens (subclone 2_a9 from PAC H92) DNA	8e-006
1780	Z47046	Human cosmid QLL2C9 from Xq28	7e-006
1781	U93275	Mus musculus glucokinase gene, 5' flanking region	7e-006
1782	X60653	human Histone H3.3 pseudogene (CIR-456)	7e-006
1783	L81583	Homo sapiens (subclone 3_g2 from P1 H11) DNA sequence	6e-006

Table 2A Nearest Neighbor (BlastN vs. GenBank)

SEQ ID	ACCESSION	DESCRIPTION	P VALUE
1784	L13381	Plasmodium falciparum HB3\W2 transport protein	6e-006
1785	U97576	Homo sapiens TRE17 oncogene-associated G0S19-2/MIP1alpha gene, downstream sequence	6e-006
1786	Y11204	V.carteri gene encoding volvoxopsin	6e-006
1787	Z16794	H. sapiens (D4S409) DNA segment containing (CA) repeat; clone AFM183xd6; single read	6e-006
1788	D83737	Human coagulation factor XII gene, intron 2	6e-006
1789	X04871	Paramecium primaurelia macronuclear DNA telomeric	6e-006
1790	M14292	Human L1Heg repetitive element from the intergenic region of the epsilon and G-gamma globin genes.	6e-006
1791	NM_003734.1	Homo sapiens amine oxidase, copper containing 3 gb U39447 HSU39447 Human placenta copper monamine oxidase mRNA, complete cds	6e-006
1792	M27147	Human alpha-2-plasmin inhibitor, allele A, 5' end.	6e-006
1793	X86012	Human DNA sequence from intron 22 of the factor VIII gene, Xq28. Contains the end of a 9.5kb repeated region, int22h-1, involved in many cases of haemophilia	6e-006
1794	M33216	Human aortic-type smooth muscle alpha-actin	3e-006
1795	Z83334	H.sapiens RPS3a gene	2e-006
1796	M57682	Rat brain calcium channel alpha-1 subunit mRNA, complete	2e-006
1797	M19817	Human apolipoprotein B-100 (apoB) gene, intron J.	2e-006
1798	Z24068	H. sapiens (D22S427) DNA segment containing	2e-006
1799	Z50155	X.laevis mRNA for insulin-like growth factor I receptor	2e-006
1800	Y12839	H.sapiens BH30 mRNA	2e-006
1801	Z70041	Human DNA sequence from cosmid U39H5, between markers DXS6791 and DXS8038 on chromosome X	2e-006
1802	Z80128	H.sapiens CACNL1A4 gene, exons 16 and 17	2e-006
1803	U80893	Mus musculus CAG trinucleotide repeat mRNA, partial	2e-006
1804	Z63192	H.sapiens CpG island DNA genomic MseI fragment, clone 7a7, forward read cpg7a7.ft1d	2e-006
1805	U72964	Human hepatocyte nuclear factor 4-alpha gene, exon 5	2e-006
1806	AC002183	Homo sapiens (subclone 2_h8 from BAC H111) DNA	2e-006
1807	S73557	annexin II=36 kDa calcium-dependent phospholipid-binding protein [rats, RBL-2H3 basophilic leukemia cells, mRNA,	2e-006
1808	U79258	Human clone 23732 mRNA, partial cds	8e-007
1809	Z62146	H.sapiens CpG island DNA genomic MseI fragment, clone 64b2, forward read cpg64b2.ft1a	8e-007
1810	U44381	Human tissue inhibitor of metalloproteinases-2	8e-007
1811	Z65575	H.sapiens CpG island DNA genomic MseI fragment, clone 47c5, reverse read cpg47c5.rt1a	7e-007
1812	J03764	Human, plasminogen activator inhibitor-1 gene, exons 2 to	7e-007
1813	X75349	H.sapiens 5'flanking DNA for clotting factor IX	7e-007
1814	Z73360	Human DNA sequence from cosmid 92M18, BRCA2 gene region chromosome 13q12-13	7e-007
1815	Z73360	Human DNA sequence from cosmid 92M18, BRCA2 gene region chromosome 13q12-13	7e-007
1816	X77624	H.sapiens simple sequence clone pg2m3, 5' flank and repeats	7e-007
1817	S46857	SCL/TCL5/tal-1=stem-cell leukemia {germline chromosome 3 translocation/deletion breakpoint} [human, bone marrow cells, Genomic Mutant, 239 nt]	7e-007
1818	J03998	P.falciparum glutamic acid-rich protein gnen, complete cds.	7e-007
1819	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	3e-007

Table 2A Nearest Neighbor (BlastN vs. GenBank)

SEQ ID	ACCESSION	DESCRIPTION	P VALUE
1820	U47654	Human pyruvate kinase PK-R gene, partial cds, and pyruvate kinase PK-L gene, complete cds.	3e-007
1821	U78096	Human macrophage colony stimulating factor receptor (c-fms) gene, exon 1A, 2 and partial cds	3e-007
1822	L76927	Human galactokinase (GALK1) gene, complete cds	3e-007
1823	U22086	Ursus americanus clone G10H GT and ATTT microsatellite	3e-007
1824	J03069	Human MYCL2 gene, complete cds.	3e-007
1825	X82640	D.melanogaster mRNA for alpha 1,2 mannosidase	3e-007
1826	U18671	Human Stat2 gene, complete cds.	2e-007
1827	L02935	Human major breakpoint cluster region (BCR) gene, exons 1-3 and repeat regions.	2e-007
1828	L04193	Human lens membrane protein (mp19) gene, exon 11.	2e-007
1829	AC001050	Homo sapiens (subclone 3_e9 from P1 H55) DNA sequence	2e-007
1830	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	2e-007
1831	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	9e-008
1832	L78776	Homo sapiens (subclone 2_a7 from P1 H49) DNA sequence	9e-008
1833	U41315	Human ring zinc-finger protein (ZNF127-Xp) gene and 5' flanking sequence.	9e-008
1834	X95586	H.sapiens MB1 gene	9e-008
1835	M33387	Human debrisoquine 4-hydroxylase (CYP2D8P) and	9e-008
1836	U09954	Human ribosomal protein L9 gene, 5' region and complete	8e-008
1837	Z15030	H.sapiens gene for ventricular myosin light chain 2 > :: gb L01652 HUMVMLC Human ventricular myosin light chain 2 gene, seven exons.	8e-008
1838	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	8e-008
1839	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	8e-008
1840	Z77974	H.sapiens flow-sorted chromosome 6 HindIII fragment,	8e-008
1841	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	8e-008
1842	L81802	Homo sapiens (subclone 1_c12 from P1 H31) DNA	8e-008
1843	D87001	Human (lambda) DNA for immunoglobulin light chain	8e-008
1844	Z23971	H. sapiens (D2S338) DNA segment containing (CA) repeat; clone AFM276zf5; single read	8e-008
1845	X89398	H.sapiens ung gene for uracil DNA-glycosylase	3e-008
1846	Z68212	Phocine Herpesvirus 1 DNA (clone 4; 280 bp)	3e-008
1847	M85145	Human tumor necrosis factor receptor, 3' flank.	3e-008
1848	M17919	Human DNA with homology to EBV IR3 repeat, clone Hu3.	3e-008
1849	M21339	Human non-histone chromosomal protein HMG-14 gene, complete cds.	3e-008
1850	Z69655	Human DNA sequence from cosmid L98A6, Huntington's Disease Region, chromosome 4p16.3	3e-008
1851	S83526	red photopigment gene {Alu repeat region, long intron 1} [human, peripheral blood leucocytes, Genomic, 1987 nt]	3e-008
1852	M11809	Human (2'-5') oligo A synthetase E gene, exon 7 and flanks.	3e-008
1853	X94768	H.sapiens RP3 gene (XLRP gene 3)	3e-008
1854	X62025	H.sapiens rod cG-PDE G gene for 3', 5'-cyclic nucleotide phosphodiesterase	3e-008

Table 2A Nearest Neighbor (BlastN vs. GenBank)

SEQ ID	ACCESSION	DESCRIPTION	P VALUE
1855	NM_000694.1	Homo sapiens aldehyde dehydrogenase 7 (ALDH7) mRNA > :: gb U10868 HSU10868 Human aldehyde dehydrogenase ALDH7 mRNA, complete cds.	3e-008
1856	U22086	Ursus americanus clone G10H GT and ATTT microsatellite	3e-008
1857	AC001174	Homo sapiens (subclone 1_e2 from BAC H94) DNA	3e-008
1858	X69908	H.sapiens gene for mitochondrial ATP synthase c subunit	2e-008
1859	X91233	H.sapiens IL15 gene	2e-008
1860	M61835	Human lactase phlorizin hydrolase (LCT) gene, exon 2.	1e-008
1861	M29324	Mouse L1Md-A13 repetitive sequence.	1e-008
1862	AF021806	Rattus norvegicus connexin 40 (GJA5) mRNA, complete cds	1e-008
1863	AB002584	Rattus norvegicus mRNA for beta-alanine-pyruvate aminotransferase, complete cds	1e-008
1864	Z54147	Human DNA sequence from cosmid L129H7, Huntington's Disease Region, chromosome 4p16.3 contains CpG island	9e-009
1865	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	9e-009
1866	Z54349	H.sapiens MN/CA9 GENE	8e-009
1867	M21487	Human muscle creatine kinase gene (CKMM), 5' flank.	3e-009
1868	U02993	Human cytochrome P450 (Cyp1A2) gene, 5' region.	3e-009
1869	Z78893	H.sapiens flow-sorted chromosome 6 HindIII fragment,	3e-009
1870	U89387	Human RNA polymerase II subunit hsRPB4 gene, complete	3e-009
1871	X57413	Mouse mRNA for transforming growth factor-beta2	3e-009
1872	Z94828	G.gallus microsatellite DNA (LEI0260	3e-009
1873	D26067	Human mRNA for KIAA0033 gene, partial cds	3e-009
1874	AB001914	Homo sapiens PACE4 gene, exon 23-25, complete cds	3e-009
1875	Z75894	Human DNA sequence from cosmid U61F10, between markers DXS366 and DXS87 on chromosome X contains	3e-009
1876	AC001443	Homo sapiens (subclone 2_f10 from BAC 2913	3e-009
1877	M96851	Human CpG island containing upstream sequence	3e-009
1878	D64108	Human mRNA for DMC1 homologue, complete cds	3e-009
1879	S80861	{junction region} [human, KOPT-K1 cells, T-cell acute lymphoblastic leukemia patient, Genomic, 895 nt]	3e-009
1880	U79776	Mus musculus ajuba (Ajuba) mRNA, complete cds	2e-009
1881	S75283	thyrotropin-releasing hormone receptor [human, Genomic, 2312 nt, segment 2 of 2]	1e-009
1882	X14445	Human int-2 proto-oncogene	1e-009
1883	J03764	Human, plasminogen activator inhibitor-1 gene, exons 2 to	1e-009
1884	L36911	Pig microsatellite DNA (CA repeat)	1e-009
1885	U79746	Homo sapiens serotonin transporter (hSERT) gene, promoter region, exons 1B and 2, and partial cds	9e-010
1886	X56668	Human DNA for calretinin exon 1	9e-010
1887	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	9e-010
1888	X77738	H.sapiens red cell anion exchanger (EPB3, AE1, Band 3) gene, 3' region	4e-010
1889	L02897	Dog nonerythroid beta-spectrin mRNA, 3' end.	3e-010
1890	D45198	Human mRNA for template acyivating factor-I alpha,	3e-010
1891	X04981	H.sapiens gene for lecithin-cholesterol acyltransferase	3e-010
1892	M14292	Human L1Heg repetitive element from the intergenic region of the epsilon and G-gamma globin genes.	3e-010
1893	X14448	Human GLA gene for alpha-D-galactosidase A (EC	3e-010
1894	Z96616	H.sapiens telomeric DNA sequence, clone 4QTELO25, read 4QTELOO025.seq	3e-010

Table 2A

Table 2A Nearest Neighbor (BlastN vs. GenBank)

SEQ ID	ACCESSION	DESCRIPTION	P VALUE
1895	M12901	Human c-mos pseudogene with Alu repeat insertions, partial	2e-010
1896	Z68885	Human DNA sequence from cosmid L21F12B, Huntington's Disease Region, chromosome 4p16.3, contains EST	1e-010
1897	L77036	Homo sapiens (subclone 5_d9 from P1 H19) DNA	1e-010
1898	Z58927	H.sapiens CpG island DNA genomic MseI fragment, clone 116g2, reverse read cpg116g2.rt1a	1e-010
1899	L77036	Homo sapiens (subclone 5_d9 from P1 H19) DNA	1e-010
1900	Z79007	H.sapiens flow-sorted chromosome 6 HindIII fragment,	1e-010
1901	Z75891	Human DNA sequence from cosmid F45C1 on chromosome	1e-010
1902	Z72930	S.cerevisiae chromosome VII reading frame ORF YGR145w	1e-010
1903	Z36111	S.cerevisiae chromosome II reading frame ORF YBR242w	5e-011
1904	Z54147	Human DNA sequence from cosmid L129H7, Huntington's Disease Region, chromosome 4p16.3 contains CpG island	4e-011
1905	X87579	H.sapiens CD4 gene	4e-011
1906	U43604	Human unidentified mRNA, partial sequence.	4e-011
1907	U08024	Human clone A dehydroepiandrosterone sulfotransferase (STD) mRNA, complete cds.	4e-011
1908	M27825	B.lactucaea heat shock protein 70 (hsp70) gene, complete	4e-011
1909	Z15026	H.sapiens genes for tumor necrosis factor (Tnfa) and lymphotoxine (Tnfb)	3e-011
1910	Z67997	Human DNA sequence from cosmid L206D7, Huntington's Disease Region, chromosome 4p16.3	3e-011
1911	AC001046	Homo sapiens (subclone 3_f2 from P1 H54) DNA sequence	2e-011
1912	Z84518	H.sapiens flow-sorted chromosome 6 HindIII fragment,	1e-011
1913	M59709	Human carcinoembryonic antigen (CEA) gene, exon 10.	1e-011
1914	L35670	Homo sapiens (subclone H8_10_g5 from P1 35 H5 C8) DNA	1e-011
1915	AF012899	Sambucus nigra ribosome inactivating protein precursor mRNA, complete cds	1e-011
1916	Z96209	H.sapiens telomeric DNA sequence, clone 12PTEL055, read 12PTELOO055.seq	1e-011
1917	U34052	Human Down Syndrome region of chromosome 21, genomic sequence, clone A35A7-1A2.	1e-011
1918	Z96489	H.sapiens telomeric DNA sequence, clone 21QTEL007, read 21QTELOO007.seq	1e-011
1919	AC001036	Homo sapiens (subclone 2_f7 from P1 H48) DNA sequence	1e-011
1920	L42098	Homo sapiens (subclone 5_c7 from P1 H22) DNA sequence.	6e-012
1921	X93341	H.sapiens mitochondrial control region DNA	5e-012
1922	D26141	Human NF1 gene homologue	4e-012
1923	U80228	Human clotting factor VIII gene, intron 20 and exon 21, partial sequence	4e-012
1924	U16812	Human Bak-2 gene, complete cds.	4e-012
1925	Z68758	Human DNA sequence from cosmid cN85E10 on chromosome 22q11.2-qter	4e-012
1926	AC001449	Homo sapiens (subclone 2_f10 from P1 H103) DNA	4e-012
1927	D50561	Human DNA, replication enhancing element (REE1)	4e-012
1928	Z96387	H.sapiens telomeric DNA sequence, clone 18PTEL033, read 18PTELOO033.seq	1e-012
1929	AF004338	Homo sapiens 16S ribosomal RNA, mitochondrial gene, partial sequence	1e-012
1930	M15360	Human transposon-like element (THE) p2 solo LTR with inserted Alu element.	1e-012
1931	L81577	Homo sapiens (subclone 3_h8 from P1 H11) DNA sequence	1e-012
1932	U56979	Human complement factor H precursor (Cfh) gene, partial	1e-012

Table 2A Nearest Neighbor (BlastN vs. GenBank)

SEQ ID	ACCESSION	DESCRIPTION	P VALUE
1933	U14550	Human sialyltransferase SThM (sthm) mRNA, complete cds.	1e-012
1934	M31061	Human ornithine decarboxylase gene, complete cds.	1e-012
1935	U06752	Rattus norvegicus Fisher 344 pre-sialomucin complex (pSMC) mRNA, repeat sequences 10-14, partial cds.	1e-012
1936	U06752	Rattus norvegicus Fisher 344 pre-sialomucin complex (pSMC) mRNA, repeat sequences 10-14, partial cds.	1e-012
1937	L29096	Homo sapiens oriP binding protein (OBP-2) mRNA,	1e-012
1938	U50156	Human DNA segment containing CA repeat at locus	5e-013
1939	X65708	H.sapiens RRM1 gene for ribonucleoside diphosphate reductase M1 subunit	5e-013
1940	M61107	Human p22-phox (CYBA) gene, exons 3 and 4.	5e-013
1941	AC001502	Homo sapiens (subclone 2_c7 from P1 H43) DNA sequence	4e-013
1942	X69951	H.sapiens gene for casein kinase II alpha subunit > subunit alpha [human, Genomic, 18862 nt]	4e-013
1943	AC002252	Homo sapiens (subclone 1_g7 from BAC H76) DNA	4e-013
1944	Z74029	Caenorhabditis elegans cosmid C45B11, complete sequence [Caenorhabditis elegans]	4e-013
1945	U90544	Human sodium phosphate transporter (NPT3) mRNA,	4e-013
1946	L77032	Homo sapiens (subclone 3_e5 from P1 H16) DNA sequence.	2e-013
1947	X55367	Human alpha-satellite DNA from clone pTRA-2	2e-013
1948	U40369	Human spermidine/spermine N1-acetyltransferase	2e-013
1949	Z25749	H.sapiens gene for ribosomal protein S7	2e-013
1950	M96838	Human proteinase 3 gene, exons 2 and 3.	2e-013
1951	Z73116	S.cerevisiae chromosome XII reading frame ORF YLL011w	2e-013
1952	U90544	Human sodium phosphate transporter (NPT3) mRNA,	2e-013
1953	U90544	Human sodium phosphate transporter (NPT3) mRNA,	2e-013
1954	AC001016	Homo sapiens (subclone 2_f8 from P1 H43) DNA sequence	1e-013
1955	D00596	Homo sapiens gene for thymidylate synthase, exons 1, 2, 3, 4, 5, 6, 7, complete cds	1e-013
1956	X80240	H.sapiens endogenous retrovirus HERV-KC4 DNA	1e-013
1957	M86181	Human prosaposin (PSAP) gene.	5e-014
1958	V00710	Human mitochondrial genes for several tRNAs (Phe, Val, Leu) and 12S and 16S ribosomal RNAs	5e-014
1959	Z62151	H.sapiens CpG island DNA genomic MseI fragment, clone 64c7, forward read cpg64c7.f1a	5e-014
1960	NM_002187.1	Homo sapiens interleukin 12B (natural killer cell stimulatory factor 2, cytotoxic lymphocyte maturation factor 2, p40) (IL12B) mRNA > :: gb M65290 HUMNKSFP40 Human natural killer cell stimulatory factor (NKSF) mRNA,	5e-014
1961	M18680	Homo sapiens 5S rRNA pseudogene.	5e-014
1962	X06274	Human endogenous retrovirus-like sequence (LTR ERS-P1-1) 3'-LTR region	5e-014
1963	D00835	Human immunodeficiency virus type 2 proviral DNA, complete genome	5e-014
1964	V00581	Human Alu repetitive sequence located near the insulin gene > :: gb J00268 HUMINS02 Human insulin gene: repetitive sequence in 3' flank.	5e-014
1965	Z95437	Human DNA sequence from cosmid A1 on chromosome 6 contains ESTs. HERV like retroviral sequence	5e-014
1966	AB001051	Dugesia japonica mRNA for ADP-ribosylation factor,	5e-014
1967	AB001051	Dugesia japonica mRNA for ADP-ribosylation factor,	5e-014
1968	M59709	Human carcinoembryonic antigen (CEA) gene, exon 10.	2e-014
1969	X91233	H.sapiens IL15 gene	2e-014

Table 2A Nearest Neighbor (BlastN vs. GenBank)

SEQ ID	ACCESSION	DESCRIPTION	P VALUE
1970	X12718	Human Retrovirus mRNA for LTR (clone cPB-3)	2e-014
1971	V00531	Human interferon genes LeIF-L and LeIF-J and pseudogene LeIF-M with intergenic regions. These genes are located on	1e-014
1972	M14292	Human L1Heg repetitive element from the intergenic region of the epsilon and G-gamma globin genes.	1e-014
1973	X56998	Human UbA52 adrenal mRNA for ubiquitin-52 amino acid fusion protein	1e-014
1974	S74906	E1 beta=pyruvate dehydrogenase beta {promoter}	8e-015
1975	M18680	Homo sapiens 5S rRNA pseudogene.	6e-015
1976	L49046	Homo sapiens (subclone 2_h3 from P1 H25) DNA sequence.	6e-015
1977	M18680	Homo sapiens 5S rRNA pseudogene.	6e-015
1978	U93037	Homo sapiens elastin gene, exons 5-27 and alternatively spliced products, partial cds	6e-015
1979	M76741	Homo sapiens biliary glycoprotein (BGP) gene, partial cds.	6e-015
1980	U72787	Homo sapiens cosmid clone U163C11 from Xp22.1-22.2, complete sequence [Homo sapiens]	6e-015
1981	AB000931	Homo sapiens FUT2 gene, intron 1, complete sequence	6e-015
1982	M83137	Human scaffold-attached region (SAR) DNA.	6e-015
1983	M18680	Homo sapiens 5S rRNA pseudogene.	5e-015
1984	Z63454	H.sapiens CpG island DNA genomic MseI fragment, clone 84d2, reverse read cpg84d2.rt1a	5e-015
1985	Z63454	H.sapiens CpG island DNA genomic MseI fragment, clone 84d2, reverse read cpg84d2.rt1a	5e-015
1986	X97489	H.sapiens PIT1/GHF1 gene silencer region	5e-015
1987	X55367	Human alpha-satellite DNA from clone pTRA-2	2e-015
1988	Z22795	H.sapiens microsatellite repeat	2e-015
1989	D38112	Human mitochondrial DNA, complete sequence	2e-015
1990	X69951	H.sapiens gene for casein kinase II alpha subunit subunit alpha [human, Genomic, 18862 nt]	2e-015
1991	M59250	Homo sapiens cytochrome c oxidase subunit Vb	2e-015
1992	X15965	Rabbit DNA for L1Oc5 repeat	2e-015
1993	X70052	S.cerevisiae sof1 gene	2e-015
1994	M86667	H.sapiens NAP (nucleosome assembly protein) mRNA,	1e-015
1995	X78212	H.sapiens diamine oxidase gene	7e-016
1996	U21928	Human fructose-1,6-biphosphatase (FBP1) gene, exon 4	7e-016
1997	AB001051	Dugesia japonica mRNA for ADP-ribosylation factor,	7e-016
1998	AC002181	Homo sapiens (subclone 2_a12 from BAC H111) DNA	6e-016
1999	X91413	H.sapiens DNA for X-linked dinucleotide repeat polymorphism (clone YCA3CL149)	6e-016
2000	U65487	Human ribosomal RNA upstream binding transcription factor (UBTF) gene, partial cds	6e-016
2001	Z69920	Human DNA sequence from cosmid 91K3, Huntington's Disease Region, chromosome 4p16.3	6e-016
2002	U92818	Homo sapiens c33.28 unnamed HERV-H protein mRNA,	6e-016
2003	J03799	Human colin carcinoma laminin-binding protein mRNA,	3e-016
2004	Z68885	Human DNA sequence from cosmid L21F12B, Huntington's Disease Region, chromosome 4p16.3, contains EST	2e-016
2005	U75285	Homo sapiens apoptosis inhibitor survivin gene, complete	2e-016
2006	M23442	Human interleukin 4 (IL-4) gene, complete cds.	2e-016
2007	U18270	Human thymopoietin (TMPO) gene, exons 4 and 5, and complete cds for thymopoietin alpha	2e-016
2008	AD000833	Homo sapiens DNA from chromosome 19-cosmid f19399 (~17 kb EcoRI restriction fragment)	2e-016

Table 2A Nearest Neighbor (BlastN vs. GenBank)

SEQ ID	ACCESSION	DESCRIPTION	P VALUE
2009	AD000833	Homo sapiens DNA from chromosome 19-cosmid f19399 (~17 kb EcoRI restriction fragment)	2e-016
2010	Y14823	Drosophila melanogaster SURF-4 gene and gene encoding seryl-tRNA synthetase	2e-016
2011	U67167	Homo sapiens intestinal mucin (MUC2) gene, promoter region and partial cds	8e-017
2012	Z96177	H.sapiens telomeric DNA sequence, clone 10QTELO40, read 10QTELOO040.seq	7e-017
2013	AF003533	Homo sapiens cytosolic phagocyte oxidase protein (p47phox) gene, promoter region and partial cds	7e-017
2014	NM_000151.1	Homo sapiens glucose-6-phosphatase, catalytic glucose-6-phosphatase mRNA, complete cds. > :: gb I15157 I15157 Sequence 1 from patent US 5460942	7e-017
2015	X94912	H.sapiens Pr22 gene	7e-017
2016	U10580	Human junction sequence from chimeric/rearranged YAC yRM2252, chromosome 11p14.	7e-017
2017	M22970	Human pancreatic phospholipase A-2 (PLA-2) gene, exons 1	7e-017
2018	X02152	Human mRNA for lactate dehydrogenase-A (LDH-A, EC	6e-017
2019	Z68755	Human DNA sequence from cosmid L118D5, Huntington's Disease Region, chromosome 4p16.3	6e-017
2020	M64804	Human microsatellite DNA repeat region DNA. > :: gb I31115 I31115 Sequence 27 from patent US 5582979	3e-017
2021	Z92910	H.sapiens HFE (HLA-H) gene	3e-017
2022	X74984	H.sapiens 5' flanking region of CD14 gene	2e-017
2023	U05333	Mus musculus co-chaperonin 'cofactor A' mRNA, complete	2e-017
2024	U48485	Human skeletal muscle ryanodine receptor gene	2e-017
2025	X97869	H.sapiens gene encoding La autoantigen	2e-017
2026	X17579	Human specific HS5 DNA	2e-017
2027	U36445	Bos taurus calcium-activated chloride channel mRNA,	2e-017
2028	L06845	Human cysteinyl-tRNA synthetase mRNA, partial cds.	2e-017
2029	X93334	H.sapiens mitochondrial DNA, complete genome	8e-018
2030	X62996	H.sapiens mitochondrial genome (consensus sequence)	8e-018
2031	M98479	Human transglutaminase mRNA, 3' untranslated region.	8e-018
2032	L42568	Homo sapiens (clone ISW11-1) non-gastric H,K-ATPase (ATP1A1) gene, exons 15-17	8e-018
2033	S52659	lactoferrin {5' region, promoter} [human, placenta,	8e-018
2034	U66707	Rattus norvegicus densin-180 mRNA, complete cds	8e-018
2035	X76683	Plasmid vector pHM2 betalactamase gene	3e-018
2036	U66707	Rattus norvegicus densin-180 mRNA, complete cds	3e-018
2037	D17201	Human HepG2 3' region MboI cDNA, clone hmd3d04m3	3e-018
2038	Z24281	H. sapiens (D12S355) DNA segment containing	2e-018
2039	AC001443	Homo sapiens (subclone 2 f10 from BAC 2913	2e-018
2040	U73522	Homo sapiens AMSH mRNA, complete cds	1e-018
2041	L77040	Homo sapiens (subclone 8 c11 from P1 H22) DNA	9e-019
2042	X93496	H.sapiens TRAP gene, 5' flanking region	9e-019
2043	X54816	Human gene for alpha-1-microglobulin-bikunin, exons 1-5 (encoding alpha-1-microglobulin, N-terminus.)	9e-019
2044	L35240	Human enigma gene, complete cds	8e-019
2045	Z46940	H.sapiens PRM1 gene, PRM2 gene and TNP2 gene	8e-019
2046	U60801.1	Human poly(A)-binding protein (PABP) processed pseudogene2, complete cds	8e-019
2047	NM_002484.1	Homo sapiens nucleotide binding protein 1 Human nucleotide-binding protein mRNA, complete cds.	4e-019

Table 2A Nearest Neighbor (BlastN vs. GenBank)

SEQ ID	ACCESSION	DESCRIPTION	P VALUE
2048	X76683	Plasmid vector pHM2 betalactamase gene	3e-019
2049	U40369	Human spermidine/spermine N1-acetyltransferase	3e-019
2050	D13624	Human Wilms tumor gene encoding WT1 protein, exon 6	3e-019
2051	D13624	Human Wilms tumor gene encoding WT1 protein, exon 6	3e-019
2052	D86566	Human DNA for NOTCH4, partial cds	3e-019
2053	U72787	Homo sapiens cosmid clone U163C11 from Xp22.1-22.2, complete sequence [Homo sapiens]	3e-019
2054	U86759	Human netrin-2 like protein (NTN21) mRNA, complete cds	3e-019
2055	X78454	X.laevis AB21 mRNA for RPD3 homologue	3e-019
2056	NM_000969.1	Homo sapiens ribosomal protein L5 (RPL5) mRNA	1e-019
2057	U49869	Human ubiquitin gene, complete cds	1e-019
2058	X78901	H.sapiens (lambda63) DNA of apolipoprotein cluster	9e-020
2059	U32515	Human putative tumor suppressor (MX11) gene, exons 4, 5, and 6, and complete cds	9e-020
2060	D87717	Human mRNA for KIAA0013 gene, complete cds	5e-020
2061	Z68758	Human DNA sequence from cosmid cN85E10 on chromosome 22q11.2-qter	3e-020
2062	Z30584	R.norvegicus (wistar) mRNA for ZG-16p	3e-020
2063	Z68758	Human DNA sequence from cosmid cN85E10 on chromosome 22q11.2-qter	3e-020
2064	M58600	Human heparin cofactor II (HCF2) gene, exons 1 through 5.	3e-020
2065	U93037	Homo sapiens elastin gene, exons 5-27 and alternatively spliced products, partial cds	3e-020
2066	L38951	Homo sapiens importin beta subunit mRNA, complete cds	2e-020
2067	D26141	Human NF1 gene homologue	1e-020
2068	M18796	Orangutan beta- and delta-globin gene intergenic region with 2 Alu repeats.	1e-020
2069	Z47046	Human cosmid QLL2C9 from Xq28	1e-020
2070	AC001443	Homo sapiens (subclone 2_f10 from BAC 2913	1e-020
2071	X15965	Rabbit DNA for L1Oc5 repeat	1e-020
2072	U86453	Human phosphatidylinositol 3-kinase catalytic subunit p110delta mRNA, complete cds	6e-021
2073	M90058	Human serglycin gene, exons 1,2, and 3.	4e-021
2074	L81932	Homo sapiens (subclone 9_h2 from P1 H21) DNA sequence	4e-021
2075	X68258	Bicistronic transcription units (pSBC-2)	3e-021
2076	L78777	Homo sapiens (subclone 2_b8 from P1 H49) DNA sequence	3e-021
2077	J01415	Human mitochondrion, complete genome	1e-021
2078	L43411	Homo sapiens (subclone 5_g5 from P1 H25) DNA sequence.	1e-021
2079	NM_000967.1	Homo sapiens ribosomal protein L3 (RPL3) mRNA protein	1e-021
2080	Z81014	Human DNA sequence from cosmid U65A4, between markers DXS366 and DXS87 on chromosome X *	1e-021
2081	U93037	Homo sapiens elastin gene, exons 5-27 and alternatively spliced products, partial cds	1e-021
2082	X78454	X.laevis AB21 mRNA for RPD3 homologue	1e-021
2083	X82825	A.thaliana PRL1 mRNA	1e-021
2084	J01415	Human mitochondrion, complete genome	4e-022
2085	Z68885	Human DNA sequence from cosmid L21F12B, Huntington's Disease Region, chromosome 4p16.3, contains EST	4e-022
2086	L81690	Homo sapiens (subclone 1_c2 from P1 H56) DNA sequence	4e-022
2087	Z47046	Human cosmid QLL2C9 from Xq28	4e-022
2088	Z73360	Human DNA sequence from cosmid 92M18, BRCA2 gene region chromosome 13q12-13	1e-022
2089	L78776	Homo sapiens (subclone 2_a7 from P1 H49) DNA sequence	1e-022

Table 2A Nearest Neighbor (BlastN vs. GenBank)

SEQ ID	ACCESSION	DESCRIPTION	P VALUE
2090	Z96210	H.sapiens telomeric DNA sequence, clone 12PTEL057, read 12PTELOO057.seq	5e-023
2091	Z50751	H.sapiens mRNA for B4B	4e-023
2092	U14567	***ALU WARNING: Human Alu-J subfamily consensus	4e-023
2093	L35657	Homo sapiens (subclone H8 5_a10 from P1 35 H5 C8) DNA	4e-023
2094	Z81315	Human DNA sequence from fosmid F62D4 on chromosome 22q12-qter > :: emb Z81316 HSF62D4A Human DNA sequence from fosmid F62D4 on chromosome 22, complete	4e-023
2095	U93237	Human menin (MEN1) gene, complete cds	1e-023
2096	M16660	Human 90-kDa heat-shock protein gene, cDNA, complete	1e-023
2097	Z93943	Human DNA sequence from cosmid U235H3 on	6e-024
2098	M84334	Macacca mulatta hnRNP A1-gamma isoform mRNA,	5e-024
2099	Z73360	Human DNA sequence from cosmid 92M18, BRCA2 gene region chromosome 13q12-13	5e-024
2100	L32754	Homo sapiens Ig-associated signalling molecule	5e-024
2101	AC002252	Homo sapiens (subclone 1_g7 from BAC H76) DNA	5e-024
2102	NM_000982.1	Homo sapiens ribosomal protein L21 (RPL21) mRNA > :: gb U25789 HSU25789 Human ribosomal protein L21 mRNA, complete cds.	5e-024
2103	NM_000397.1	Homo sapiens cytochrome b-245, beta polypeptide encoding mitochondrial protein, mRNA > :: emb X04011 HSXCGD Human mRNA of X-CGD gene involved in chronic granulomatous disease located on chromosome X	5e-024
2104	L19086	Human LINE1 (L1.3) repetitive element DNA sequence.	4e-024
2105	U88531	Bos taurus phosphatidylinositol 4-kinase mRNA, complete	2e-024
2106	D38112	Human mitochondrial DNA, complete sequence	2e-024
2107	NM_003011.1	Homo sapiens SET translocation (myeloid leukemia-associated) (SET) mRNA > :: gb M93651 HUMSET Human	2e-024
2108	M98512	Human NFG genomic fragment.	2e-024
2109	NM_001019.1	Homo sapiens ribosomal protein S15a for ribosomal protein	2e-024
2110	X70991	H.sapiens MADER mRNA	2e-024
2111	X14445	Human int-2 proto-oncogene	2e-024
2112	AC001174	Homo sapiens (subclone 1_e2 from BAC H94) DNA	2e-024
2113	D86566	Human DNA for NOTCH4, partial cds	2e-024
2114	Z78885	H.sapiens flow-sorted chromosome 6 HindIII fragment,	1e-024
2115	X82272	Human endogenous retrovirus env mRNA	1e-024
2116	Z96167	H.sapiens telomeric DNA sequence, clone 10QTEL017, read 10QTELOO017.seq	6e-025
2117	L38951	Homo sapiens importin beta subunit mRNA, complete cds	6e-025
2118	X53575	Yeast RPL7 gene for ribosomal protein L7	6e-025
2119	L77040	Homo sapiens (subclone 8_c11 from P1 H22) DNA	5e-025
2120	Z23957	H. sapiens (D2S336) DNA segment containing (CA) repeat; clone AFM275yf5; single read	5e-025
2121	X14445	Human int-2 proto-oncogene	5e-025
2122	L39062	Homo sapiens interleukin 9 receptor IL9R pseudogene,	2e-025
2123	Z84723	Human DNA sequence from phage LAW2 from a contig from the tip of the short arm of chromosome 16, spanning 2Mb of 16p13.3 Contains Interleukin 9 receptor pseudogene	2e-025
2124	AC001174	Homo sapiens (subclone 1_e2 from BAC H94) DNA	2e-025
2125	NM_001423.1	Homo sapiens epithelial membrane protein 1 Progression Associated Protein	2e-025
2126	X14445	Human int-2 proto-oncogene	2e-025

Table 2A Nearest Neighbor (BlastN vs. GenBank)

SEQ ID	ACCESSION	DESCRIPTION	P VALUE
2127	M68841	Human L1 repetitive sequence with a region homologous to a mouse ORF.	2e-025
2128	X97489	H.sapiens PIT1/GHF1 gene silencer region	2e-025
2129	X73501	H.sapiens gene for cytokeratin 20	1e-025
2130	U48363	Mus musculus transcriptional activator alpha-NAC	1e-025
2131	X01037	Human 7SL RNA sequence	7e-026
2132	M22485	Human ring chromosome 21 [r(21)] breakpoint DNA.	2e-026
2133	K03429	Ape (chimpanzee) 28S ribosomal RNA gene.	2e-026
2134	AF053644	Homo sapiens cellular apoptosis susceptibility protein (CSE1) gene, exon 2	9e-027
2135	L06900	Human dystrophin gene, intron 1 containing pseudo exon.	7e-027
2136	U18271	Human thymopoietin (TMPO) gene, partial exon 6, complete exon 7, partial exon 8, and partial cds for	7e-027
2137	X05323	Human MRC OX-2 gene signal sequence	7e-027
2138	M99065	Rat core histone (MacroH2A.1) mRNA, complete cds.	7e-027
2139	X01037	Human 7SL RNA sequence	6e-027
2140	M22485	Human ring chromosome 21 [r(21)] breakpoint DNA.	2e-027
2141	D50494	Mouse mRNA for murine RCK, complete cds	2e-027
2142	M14292	Human L1Heg repetitive element from the intergenic region of the epsilon and G-gamma globin genes.	2e-027
2143	U72787	Homo sapiens cosmid clone U163C11 from Xp22.1-22.2, complete sequence [Homo sapiens]	7e-028
2144	NM_001030.1	Homo sapiens ribosomal protein S27 gb L19739 HUMMPSI Homo sapiens metalloproteinase (MPS1) mRNA, complete cds. > :: gb I60224 I60224 Sequence 1 from patent US	7e-028
2145	AC002186	Homo sapiens (subclone 1 fl2 from P1 H115) DNA	7e-028
2146	M22485	Human ring chromosome 21 [r(21)] breakpoint DNA.	3e-028
2147	Z95437	Human DNA sequence from cosmid A1 on chromosome 6 contains ESTs. HERV like retroviral sequence	2e-028
2148	NM_001025.1	Homo sapiens ribosomal protein S23 (RPS23) mRNA > :: dbj D14530 HUMRSPT Human homolog of yeast ribosomal protein S28, complete cds	2e-028
2149	Z95437	Human DNA sequence from cosmid A1 on chromosome 6 contains ESTs. HERV like retroviral sequence	2e-028
2150	Z62151	H.sapiens CpG island DNA genomic MseI fragment, clone 64c7, forward read cpg64c7.ft1a	1e-028
2151	Z62151	H.sapiens CpG island DNA genomic MseI fragment, clone 64c7, forward read cpg64c7.ft1a	8e-029
2152	X62996	H.sapiens mitochondrial genome (consensus sequence)	8e-029
2153	Z62151	H.sapiens CpG island DNA genomic MseI fragment, clone 64c7, forward read cpg64c7.ft1a	8e-029
2154	AC001518	Homo sapiens (subclone 2 b4 from P1 H49) DNA sequence	8e-029
2155	X56932	H.sapiens mRNA for 23 kD highly basic protein	8e-029
2156	U93563	Human L1 element L1.6 putative p150 gene, complete cds	8e-029
2157	Z96282	H.sapiens telomeric DNA sequence, clone 13QTEL058, read 13QTELO058.seq	8e-029
2158	NM_002892.1	Homo sapiens retinoblastoma-binding protein 1 (RBBP1) mRNA > :: gb S66427 S66427 RBP1=retinoblastoma binding protein 1 [human, Nalm-6 pre-B cell leukemia,	7e-029
2159	M12855	Human endogenous retrovirus DNA downstream of 5' LTR, clone HERV-K22.	3e-029

Table 2A Nearest Neighbor (BlastN vs. GenBank)

SEQ ID	ACCESSION	DESCRIPTION	P VALUE
2160	X86012	Human DNA sequence from intron 22 of the factor VIII gene, Xq28. Contains the end of a 9.5kb repeated region, int22h-1, involved in many cases of haemophilia	3e-029
2161	L81840	Homo sapiens (subclone 1_f8 from P1 H43) DNA sequence	3e-029
2162	Z11711	H.sapiens gene for alpha-2 macroglobulin, exon 1	3e-029
2163	X61453	M.musculus mRNA for H19 clone	3e-029
2164	NM_003389.1	Homo sapiens WD repeat domain 2 (WDR2) mRNA >	1e-029
2165	L81840	Homo sapiens (subclone 1_f8 from P1 H43) DNA sequence	9e-030
2166	L05173	Homo sapiens chromosome 21 DNA fragment with Alu, L1 and O repetitive elements.	8e-030
2167	M12855	Human endogenous retrovirus DNA downstream of 5' LTR, clone HERV-K22.	3e-030
2168	M12855	Human endogenous retrovirus DNA downstream of 5' LTR, clone HERV-K22.	3e-030
2169	J05211	Human desmoplakin mRNA, 3' end.	3e-030
2170	Z96167	H.sapiens telomeric DNA sequence, clone 10QTEL017, read 10QTELOO017.seq	3e-030
2171	M12855	Human endogenous retrovirus DNA downstream of 5' LTR, clone HERV-K22.	3e-030
2172	AC002186	Homo sapiens (subclone 1_f12 from P1 H115) DNA	3e-030
2173	L35657	Homo sapiens (subclone H8_5_a10 from P1 35 H5 C8) DNA	3e-030
2174	L35657	Homo sapiens (subclone H8_5_a10 from P1 35 H5 C8) DNA	3e-030
2175	L39061	Homo sapiens transcription factor SL1 mRNA, partial cds.	3e-030
2176	AF010313	Homo sapiens Pig8 (PIG8) mRNA, complete cds	1e-030
2177	AC001443	Homo sapiens (subclone 2_f10 from BAC 2913	1e-030
2178	Z62151	H.sapiens CpG island DNA genomic MseI fragment, clone 64c7, forward read cpg64c7.ft1a	3e-031
2179	AF010312	Homo sapiens Pig7 (PIG7) mRNA, complete cds	1e-031
2180	U77085	Human epithelial membrane protein (CL-20) mRNA,	1e-031
2181	D29805	Human mRNA for beta-1,4-galactosyltransferase, complete	1e-031
2182	Z95437	Human DNA sequence from cosmid A1 on chromosome 6 contains ESTs. HERV like retroviral sequence	1e-031
2183	X62996	H.sapiens mitochondrial genome (consensus sequence)	1e-031
2184	U80409	Lactococcus lactis cremoris glucose inhibited division protein homolog GidA (gidA) gene, partial cds	4e-032
2185	X00525	Mouse 28S ribosomal RNA	1e-032
2186	U35032	Human endogenous retrovirus clone c5.11, HERV-H multiply spliced subgenomic leader, protease and integrase	1e-032
2187	Z75894	Human DNA sequence from cosmid U61F10, between markers DXS366 and DXS87 on chromosome X contains	1e-032
2188	U22055	Human 100 kDa coactivator mRNA, complete cds.	1e-032
2189	M98509	Human NFB genomic fragment.	5e-033
2190	D38112	Human mitochondrial DNA, complete sequence	2e-033
2191	Z69364	Human DNA sequence from cosmid L96F8, Huntington's Disease Region, chromosome 4p16.3 contains EST and cDNA > :: emb Z69365 HSL96F8A Human DNA sequence from cosmid L96F8, Huntington's Disease Region, chromosome 4p16.3 contains EST and cDNA	5e-034
2192	U59695	Human apurinic/apyrimidinic endonuclease (HAP1) gene, 5' upstream region	5e-034
2193	L35657	Homo sapiens (subclone H8_5_a10 from P1 35 H5 C8) DNA	2e-034
2194	L78778	Homo sapiens (subclone 2_e10 from P1 H49) DNA	2e-034
2195	V00662	H.sapiens mitochondrial genome	5e-035

Table 2A Nearest Neighbor (BlastN vs. GenBank)

SEQ ID	ACCESSION	DESCRIPTION	P VALUE
2196	M30629	Human pregnancy-specific glycoprotein beta-1	5e-035
2197	NM_003134.1	Homo sapiens signal recognition particle 14kD (homologous Alu RNA-binding protein) (SRP14) mRNA > recognition	5e-035
2198	U93572	Human L1 element L1.25 p40 and putative p150 genes,	2e-035
2199	Z96176	H.sapiens telomeric DNA sequence, clone 10QTELO038, read 10QTELOO038.seq	6e-036
2200	V00710	Human mitochondrial genes for several tRNAs (Phe, Val, Leu) and 12S and 16S ribosomal RNAs	6e-036
2201	Z78715	H.sapiens flow-sorted chromosome 6 HindIII fragment,	5e-036
2202	U93574	Human L1 element L1.39 p40 and putative p150 genes,	2e-036
2203	S63912	D10S102=FBRNP [human, fetal brain, mRNA, 3043 nt]	1e-036
2204	AB011137	Homo sapiens mRNA for KIAA0565 protein, complete cds	1e-036
2205	Z55370	H.sapiens CpG island DNA genomic MseI fragment, clone 37a7, forward read cpg37a7.ft1a	7e-037
2206	L36720	Homo sapiens bystin mRNA, complete cds	7e-037
2207	S45936	HTS1=HeLa tumor suppressor gene [human, revertant clone F2, mRNA Partial, 2687 nt]	7e-037
2208	U36755	Human thrombin receptor (F2R) gene, 5' region and partial	6e-037
2209	D50694	Rattus norvegicus mRNA for proteasomal ATPase	3e-037
2210	AB001325	Human AQP3 gene for aquaporine 3 (water channel), partail	2e-037
2211	L35657	Homo sapiens (subclone H8_5_a10 from P1 35 H5 C8) DNA	2e-037
2212	U36445	Bos taurus calcium-activated chloride channel mRNA,	2e-037
2213	X66292	P.pygmaeus (OX3910-11) alphoid repetitive DNA	7e-038
2214	D38112	Human mitochondrial DNA, complete sequence	6e-038
2215	Z16571	H. sapiens (D12S80) DNA segment containing (CA) repeat; clone AFM102xd6; single read	6e-038
2216	D50561	Human DNA, replication enhancing element (REE1)	3e-038
2217	X66292	P.pygmaeus (OX3910-11) alphoid repetitive DNA	8e-039
2218	Z73360	Human DNA sequence from cosmid 92M18, BRCA2 gene region chromosome 13q12-13	7e-039
2219	M25718	Human rDNA and 4 Alu repeats.	4e-039
2220	NM_000397.1	Homo sapiens cytochrome b-245, beta polypeptide encoding mitochondrial protein, mRNA > :: emb X04011 HSXCGD Human mRNA of X-CGD gene involved in chronic granulomatous disease located on chromosome X	3e-039
2221	M13073	Human metallothionein I processed pseudogene, complete	2e-039
2222	Z78715	H.sapiens flow-sorted chromosome 6 HindIII fragment,	3e-040
2223	U72787	Homo sapiens cosmid clone U163C11 from Xp22.1-22.2, complete sequence [Homo sapiens]	3e-040
2224	Z12962	H.sapiens mRNA for homologue to yeast ribosomal protein	3e-040
2225	Z78715	H.sapiens flow-sorted chromosome 6 HindIII fragment,	9e-041
2226	AC001443	Homo sapiens (subclone 2_f10 from BAC 2913	4e-041
2227	Z73360	Human DNA sequence from cosmid 92M18, BRCA2 gene region chromosome 13q12-13	3e-041
2228	S72304	rah=ras-related homolog [mice, HT4 neural cell line,	3e-041
2229	AC001443	Homo sapiens (subclone 2_f10 from BAC 2913	1e-041
2230	U49974	Human mariner2 transposable element, complete consensus	1e-041
2231	L26507	Mouse myocyte nuclear factor (MNF) mRNA, complete cds.	1e-041
2232	U08191	Human R kappa B mRNA, complete cds.	1e-042
2233	D11078	Homo sapiens RGH2 gene, retrovirus-like element	1e-042
2234	U83908	Human nuclear antigen H731 mRNA, complete cds	1e-042
2235	X63209	B.taurus CI-ASHI mRNA for ubiquinone oxidoreductase	1e-042

Table 2A Nearest Neighbor (BlastN vs. GenBank)

SEQ ID	ACCESSION	DESCRIPTION	P VALUE
2236	NM_002743.1	Homo sapiens protein kinase C substrate 80K-H (PRKCSH) mRNA > :: gb J03075 HUMG19P1A Human 80K-H protein (kinase C substrate) mRNA, complete cds.	1e-042
2237	L78777	Homo sapiens (subclone 2_b8 from P1 H49) DNA sequence	4e-043
2238	Z59382	H.sapiens CpG island DNA genomic MseI fragment, clone 152b10, reverse read cpg152b10.rt1a	1e-043
2239	L12469	Gallus gallus (max) gene, complete cds.	1e-043
2240	U72789	Homo sapiens cosmid clone U197H5 from Xp22.1-22.2, complete sequence [Homo sapiens]	5e-044
2241	AF004161	Oryctolagus cuniculus peroxisomal Ca-dependent solute carrier mRNA, complete cds	5e-044
2242	M22485	Human ring chromosome 21 [r(21)] breakpoint DNA.	2e-044
2243	Z60212	H.sapiens CpG island DNA genomic MseI fragment, clone 195c8, forward read cpg195c8.ft1a	2e-045
2244	M22485	Human ring chromosome 21 [r(21)] breakpoint DNA.	2e-045
2245	AF004161	Oryctolagus cuniculus peroxisomal Ca-dependent solute carrier mRNA, complete cds	2e-045
2246	D38112	Human mitochondrial DNA, complete sequence	1e-045
2247	U72787	Homo sapiens cosmid clone U163C11 from Xp22.1-22.2, complete sequence [Homo sapiens]	6e-046
2248	Z69925	Human DNA sequence from cosmid cN116A5, on chromosome 22q12-qter contains exon trap	5e-046
2249	U12404	Human Csa-19 mRNA, complete cds.	5e-046
2250	Y07969	H.sapiens mRNA for APRIL protein	2e-046
2251	X90583	H.sapiens mRNA for rat translocon-associated protein delta	2e-046
2252	L35657	Homo sapiens (subclone H8 5_a10 from P1 35 H5 C8) DNA	2e-046
2253	NM_001762.1	Homo sapiens chaperonin containing T-complex subunit 6 (CCT6) mRNA > :: gb L27706 HUMTCP20 Human chaperonin protein (Tcp20) gene complete cds.	2e-046
2254	AF008563	Kluyveromyces lactis centromere-binding factor 5	7e-047
2255	NM_002137.1	Homo sapiens heterogeneous nuclear ribonucleoprotein A2/B1 (HNRPA2B1) mRNA > :: gb M29065 HUMRNP A2A Human hnRNP A2 protein	5e-047
2256	NM_001866.1	Homo sapiens cytochrome c oxidase subunit VIIb (COX7B), nuclear gene encoding mitochondrial protein, mRNA > :: emb Z14244 HSCOX7BM H.sapiens coxVIIb mRNA for cytochrome c oxidase subunit VIIb	3e-047
2257	Z55938	H.sapiens CpG island DNA genomic MseI fragment, clone 74a1, reverse read cpg74a1.rt1a	2e-047
2258	U31278	Homo sapiens mitotic feedback control protein Madp2 homolog mRNA, complete cds	2e-047
2259	U72787	Homo sapiens cosmid clone U163C11 from Xp22.1-22.2, complete sequence [Homo sapiens]	2e-047
2260	NM_003295.1	Homo sapiens tumor protein, translationally-controlled 1 (TPT1) mRNA > :: emb X16064 HSTUMP Human mRNA for translationally controlled tumor protein	7e-048
2261	NM_003503.1	Homo sapiens CDC7 (cell division cycle 7, S. cerevisiae, homolog)-like 1 (CDC7L1) mRNA, and translated products > :: gb AF015592 AF015592 Homo sapiens Cdc7	3e-048
2262	Z62151	H.sapiens CpG island DNA genomic MseI fragment, clone 64c7, forward read cpg64c7.ft1a	2e-048
2263	L11877	Homo sapiens dUTP nucleotidohydrolase mRNA, 5' end.	8e-049
2264	L40403	Homo sapiens (clone zap3) mRNA, 3' end of cds	3e-049

Table 2A Nearest Neighbor (BlastN vs. GenBank)

SEQ ID	ACCESSION	DESCRIPTION	P VALUE
2265	M81600	Human NAD(P)H:quinone oxireductase gene, exon 6 >	2e-049
2266	U72787	Homo sapiens cosmid clone U163C11 from Xp22.1-22.2, complete sequence [Homo sapiens]	8e-050
2267	M31004	Human nuclear phosphoprotein B23 mRNA, clone hpB2.	8e-050
2268	Z97207	Mus musculus mRNA for B-IND1 protein	8e-050
2269	AF007775	Rattus norvegicus aquaporin-pancreas and liver	3e-050
2270	U72787	Homo sapiens cosmid clone U163C11 from Xp22.1-22.2, complete sequence [Homo sapiens]	9e-051
2271	U72787	Homo sapiens cosmid clone U163C11 from Xp22.1-22.2, complete sequence [Homo sapiens]	9e-051
2272	X06683	Mouse mRNA for Cu-Zn superoxide dismutase (EC 1.15.1.1) > :: gb M35725 MUSCZSOD Mouse Cu-Zn superoxide dismutase mRNA, complete cds.	9e-051
2273	X93334	H.sapiens mitochondrial DNA, complete genome	3e-051
2274	U27197	Drosophila melanogaster pelota (pelo) mRNA, complete cds	3e-051
2275	D87953	Human mRNA for RTP, complete cds	1e-051
2276	L81869	Homo sapiens (subclone 1 c4 from P1 H55) DNA sequence	4e-052
2277	D63876	Human mRNA for KIAA0154 gene, partial cds	4e-052
2278	D14659	Human mRNA for KIAA0103 gene, complete cds	3e-052
2279	X93334	H.sapiens mitochondrial DNA, complete genome	4e-053
2280	D38112	Human mitochondrial DNA, complete sequence	4e-053
2281	U97519	Homo sapiens podocalyxin-like protein mRNA, complete	4e-053
2282	L35657	Homo sapiens (subclone H8 5 a10 from P1 35 H5 C8) DNA	4e-053
2283	D63876	Human mRNA for KIAA0154 gene, partial cds	4e-053
2284	D38112	Human mitochondrial DNA, complete sequence	1e-053
2285	Z57342	H.sapiens CpG island DNA genomic MseI fragment, clone 172a12, forward read cpg172a12.ft1a	1e-053
2286	Z64479	H.sapiens CpG island DNA genomic MseI fragment, clone 127c4, reverse read cpg127c4.rt1a	1e-053
2287	M28209	Homo sapiens GTP-binding protein (RAB1) mRNA,	1e-053
2288	S57803	Ro60 protein gene [human, mRNA Partial, 176 nt, segment	4e-054
2289	U01139	Mus musculus B6D2F1 clone 2C11B mRNA.	1e-054
2290	U72787	Homo sapiens cosmid clone U163C11 from Xp22.1-22.2, complete sequence [Homo sapiens]	1e-054
2291	M16553	Human tissue factor mRNA, complete cds, with an Alu repeat in the 3' untranslated region.	5e-055
2292	D10522	Homo sapiens mRNA for 80K-L protein, complete cds	5e-055
2293	Z71621	H.sapiens Wnt-13 mRNA	5e-055
2294	M81104	Human CD34 mRNA, complete cds.	4e-055
2295	D29805	Human mRNA for beta-1,4-galactosyltransferase, complete	2e-055
2296	X04299	Human mRNA for liver alcohol dehydrogenase (EC 1.1.1.1) gamma 2 subunit from ADH3 locus	2e-055
2297	U57715	Rattus norvegicus FGF receptor activating protein FRAG1 (FRAG1) mRNA, complete cds	2e-055
2298	NM_003150.1	Homo sapiens signal transducer and activator of transcription 3 (acute-phase response factor) (STAT3) mRNA > :: gb L29277 HUMAPRF Homo sapiens DNA-binding protein (APRF) mRNA, complete cds. > ::	2e-056
2299	X56974	M.musculus mRNA for external transcribed spacer	2e-057
2300	U62435	Human nicotinic acetylcholine receptor alpha6 subunit precursor, mRNA, complete cds	2e-057
2301	Z63454	H.sapiens CpG island DNA genomic MseI fragment, clone 84d2, reverse read cpg84d2.rt1a	6e-058

Table 2A Nearest Neighbor (BlastN vs. GenBank)

SEQ ID	ACCESSION	DESCRIPTION	P VALUE
2302	U34994	Human DNA-dependent protein kinase catalytic subunit	6e-058
2303	Z60432	H.sapiens CpG island DNA genomic MseI fragment, clone 22h4, reverse read cpg22h4.rt1a	2e-058
2304	U83590	Rattus norvegicus PAR interacting protein mRNA, complete	2e-058
2305	U83590	Rattus norvegicus PAR interacting protein mRNA, complete	2e-058
2306	M28449	Mouse Hox-1.7 protein mRNA, 3' end.	8e-059
2307	M18981	Human prolactin receptor-associated protein	3e-059
2308	NM_001866.1	Homo sapiens cytochrome c oxidase subunit VIIb (COX7B), nuclear gene encoding mitochondrial protein, mRNA > :: emb Z14244 HSCOX7BM H.sapiens coxVIIb mRNA for cytochrome c oxidase subunit VIIb	2e-059
2309	NM_003295.1	Homo sapiens tumor protein, translationally-controlled 1 (TPT1) mRNA > :: emb X16064 HSTUMP Human mRNA for translationally controlled tumor protein	2e-059
2310	D26067	Human mRNA for KIAA0033 gene, partial cds	9e-060
2311	NM_003130.1	Homo sapiens sorcin (SRI) mRNA > :: gb M32886 HUMSRICPA Human sorcin CP-22 mRNA,	9e-060
2312	X93334	H.sapiens mitochondrial DNA, complete genome	3e-060
2313	U12404	Human Csa-19 mRNA, complete cds.	2e-060
2314	AF070661	Homo sapiens HSPC005 mRNA, complete cds	1e-060
2315	U77665	Human RNaseP protein p30 (RPP30) mRNA, complete cds	1e-060
2316	L03558	Homo sapiens cystatin B mRNA, complete cds.	9e-061
2317	D14048	Rat mRNA for SP120, complete cds	3e-061
2318	NM_002450.1	Homo sapiens metallothionein 1L (MT1L) mRNA >	3e-061
2319	NM_001866.1	Homo sapiens cytochrome c oxidase subunit VIIb (COX7B), nuclear gene encoding mitochondrial protein, mRNA > :: emb Z14244 HSCOX7BM H.sapiens coxVIIb mRNA for cytochrome c oxidase subunit VIIb	4e-062
2320	AC001443	Homo sapiens (subclone 2_f10 from BAC 2913	3e-062
2321	NM_002156.1	Homo sapiens heat shock 60kD protein 1 chaperonin (HSP60) mRNA, complete cds.	3e-062
2322	Z97207	Mus musculus mRNA for B-IND1 protein	3e-062
2323	J01415	Human mitochondrion, complete genome	1e-062
2324	D83735	Homo sapiens mRNA for neutral calponin, complete cds	4e-063
2325	NM_001866.1	Homo sapiens cytochrome c oxidase subunit VIIb (COX7B), nuclear gene encoding mitochondrial protein, mRNA > :: emb Z14244 HSCOX7BM H.sapiens coxVIIb mRNA for cytochrome c oxidase subunit VIIb	4e-063
2326	X84694	H.sapiens mRNA for elongations factor Tu-mitochondrial	4e-063
2327	NM_001910.1	Homo sapiens cathepsin E (CTSE) mRNA > :: gb J05036 HUMCTSE Human cathepsin E mRNA, complete	4e-063
2328	AF007775	Rattus norvegicus aquaporin-pancreas and liver	3e-063
2329	AF007775	Rattus norvegicus aquaporin-pancreas and liver	3e-063
2330	AF007862	Mus musculus mm-Mago mRNA, complete cds	3e-063
2331	D38112	Human mitochondrial DNA, complete sequence	1e-063
2332	NM_003002.1	Homo sapiens succinate dehydrogenase complex, subunit D, integral membrane protein (SDHD) mRNA > :: dbj AB006202 AB006202 Homo sapiens mRNA for cytochrome b small subunit of complex II, complete cds	1e-063
2333	D38112	Human mitochondrial DNA, complete sequence	1e-063
2334	M12759	Human Ig J chain gene, exons 3 and 4.	1e-063
2335	U07802	Human Tis11d gene, complete cds.	1e-063
2336	D14659	Human mRNA for KIAA0103 gene, complete cds	1e-063

Table 2A

Table 2A Nearest Neighbor (BlastN vs. GenBank)

SEQ ID	ACCESSION	DESCRIPTION	P VALUE
2337	U38253	Rattus norvegicus initiation factor eIF-2B gamma subunit (eIF-2B gamma) mRNA, complete cds	6e-064
2338	M22146	Human scar protein mRNA, complete cds.	5e-064
2339	L20681	Rat proto-oncogene (Ets-1) mRNA, complete cds.	4e-064
2340	M14292	Human L1Heg repetitive element from the intergenic region of the epsilon and G-gamma globin genes.	4e-064
2341	NM_003257.1	Homo sapiens tight junction protein 1 (zona occludens 1) (TJP1) mRNA > :: gb L14837 HUMZO1A Human tight junction (zonula occludens) protein ZO-1 mRNA, complete	4e-064
2342	NM_003002.1	Homo sapiens succinate dehydrogenase complex, subunit D, integral membrane protein (SDHD) mRNA > :: dbj AB006202 AB006202 Homo sapiens mRNA for cytochrome b small subunit of complex II, complete cds	2e-064
2343	X12883	Human mRNA for cytokeratin 18	2e-064
2344	D42044	Human mRNA for KIAA0090 gene, partial cds	1e-064
2345	Z97207	Mus musculus mRNA for B-IND1 protein	1e-064
2346	X51867	H.sapiens MRP RNA gene encoding the RNA component of RNase MRP	7e-065
2347	X52104	Human mRNA for p68 protein	7e-065
2348	X74215	H.sapiens mRNA for Lon protease-like protein	6e-065
2349	U20796	Rattus norvegicus nuclear receptor Rev-ErbA-beta mRNA,	5e-065
2350	X79201	H.sapiens mRNA for SYT	5e-065
2351	U34584	Human Bcl-2 interacting killer (BIK) mRNA, complete cds	5e-065
2352	Z75894	Human DNA sequence from cosmid U61F10, between markers DXS366 and DXS87 on chromosome X contains	4e-065
2353	NM_002131.1	Homo sapiens high-mobility group (nonhistone chromosomal) protein isoforms I and Y (HMG1Y) mRNA > :: emb X14958 HSHMGY Human hmgI mRNA for high	2e-065
2354	AF007862	Mus musculus mm-Mago mRNA, complete cds	5e-068
2355	U74297	Oryctolagus cuniculus PiUS mRNA, complete cds	3e-069
2356	D11336	Sus scrofa mRNA for soluble angiotensin-binding protein, complete cds	2e-069
2357	AF007862	Mus musculus mm-Mago mRNA, complete cds	2e-069
2358	U74297	Oryctolagus cuniculus PiUS mRNA, complete cds	3e-071
2359	AF061260	Mus musculus immunosuperfamily protein BI2 mRNA,	5e-073
2360	U92949	Mus musculus kinesin motor protein KIFC2 mRNA,	2e-077
2361	AF007775	Rattus norvegicus aquaporin-pancreas and liver	6e-079
2362	AF007775	Rattus norvegicus aquaporin-pancreas and liver	8e-082
2363	U63840	Rattus norvegicus nucleoporin p54 mRNA, complete cds	6e-085
2364	U57344	Mus musculus homeobox protein Meis3 mRNA, complete	1e-085
2365	Z11886	M.musculus notch-1 mRNA	5e-087
2366	AF007862	Mus musculus mm-Mago mRNA, complete cds	2e-089
2367	AF007862	Mus musculus mm-Mago mRNA, complete cds	1e-092
2368	Y11092	M.musculus mRNA for map kinase interacting kinase, Mnk2	2e-097
2369	L77991	Gallus gallus cyclin-dependent kinase (cdk6) gene, complete	6e-098
2370	U42386	Mus musculus fibroblast growth factor inducible gene 14 (FIN14) mRNA, complete cds	e-163
2371	U42386	Mus musculus fibroblast growth factor inducible gene 14 (FIN14) mRNA, complete cds	e-160
2372	U42386	Mus musculus fibroblast growth factor inducible gene 14 (FIN14) mRNA, complete cds	e-144
2373	AJ000696	Rattus norvegicus mRNA for a novel kinesin-related protein,	e-106
2374	AJ000696	Rattus norvegicus mRNA for a novel kinesin-related protein,	e-101

Table 2A Nearest Neighbor (BlastN vs. GenBank)

SEQ ID	ACCESSION	DESCRIPTION	P VALUE
2375	AJ000696	Rattus norvegicus mRNA for a novel kinesin-related protein,	e-101
2376	Z97207	Mus musculus mRNA for B-IND1 protein	e-102
2377	AJ000696	Rattus norvegicus mRNA for a novel kinesin-related protein,	e-122
2378	AB000172	Porcine mRNA for endopeptidase 24.16, complete cds	e-118
2379	AB000171	Porcine mRNA for endopeptidase 24.16, complete cds	e-131
2380	U38253	Rattus norvegicus initiation factor eIF-2B gamma subunit (eIF-2B gamma) mRNA, complete cds	e-129
2381	X54352	M.domesticus MD6 mRNA	e-142
2382	X14678	Mouse TPA-induced TIS11 mRNA	e-121
2383	X82632	M.fascicularis mRNA for NAD+-isocitrate dehydrogenase	e-142
2384	U42385	Mus musculus fibroblast growth factor inducible gene 16 (FIN16) mRNA, complete cds	e-123
2385	U17901	Rattus norvegicus phospholipase A-2-activating protein (plap) mRNA, complete cds.	e-116
2386	U08215	Mus musculus Hsp70-related NST-1 (hsr.1) mRNA,	e-119
2387	X82632	M.fascicularis mRNA for NAD+-isocitrate dehydrogenase	e-148
2388	U63840	Rattus norvegicus nucleoporin p54 mRNA, complete cds	e-131
2389	U42385	Mus musculus fibroblast growth factor inducible gene 16 (FIN16) mRNA, complete cds	e-145
2390	U42385	Mus musculus fibroblast growth factor inducible gene 16 (FIN16) mRNA, complete cds	e-149
2391	U81045	Cricetulus griseus aldo-keto reductase mRNA, complete cds	e-114
2392	L77991	Gallus gallus cyclin-dependent kinase (cdk6) gene, complete	e-103
2393	U81045	Cricetulus griseus aldo-keto reductase mRNA, complete cds	e-115
2394	D30666	Rat mRNA for brain acyl-CoA synthetase II, complete cds	e-139
2395	U17901	Rattus norvegicus phospholipase A-2-activating protein (plap) mRNA, complete cds.	e-135
2396	D30666	Rat mRNA for brain acyl-CoA synthetase II, complete cds	e-126

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
1	734646					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis) (Colon Tumor Tissue vs. Colon Metastasis)	14	0	14.22	
		15,16 (Normal Colon vs. Colon Tumor Tissue) (Normal Colon vs. Colon Tumor Tissue)	0	14		13.25
2	400221					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	13	2	6.87	
3	205329					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	178	7	26.88	
		15,17 (Normal Colon Tissue vs. Colon Metastasis) (Normal Colon Tissue vs. Colon Metastasis)	178	1	191.06	
		18,19 (Normal Colon Tissue vs. Colon Tumor) (Normal Colon Tissue vs. Colon Tumor)	21	0	24	
		18,20 (Normal Colon Tissue vs. Colon Metastasis) (Normal Colon Tissue vs. Colon Metastasis)	21	0	17.95	
4	446680					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	29	84		2.7
		23,24 (Normal Lung Tissue vs. Lung Tumor Tissue) (Normal Lung Tissue vs. Lung Tumor Tissue)	40	94		2.33
5	1261					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	7		6.52
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	7		6.89
6	400258					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
7	450559					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	2	11		5.42
8	450959					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	1	9		8.51
9	451794					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	15	0	15.85	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	15	1	16.1	
10	415058					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
11	31506					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	20	77		3.64
		Low Met)	5	0	6.99	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	20	58		2.7
12	417155					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
13	448925					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	5	15		2.95
14	11329					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		19,20 (Colon Tumor Tissue vs. Colon Metastasis) (Colon Tumor Tissue vs. Colon Metastasis)	30	5	4.49	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	112	38	3.12	
15	650422					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	18	0	19.32	
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	18	6	3.17	
16	6863					
		01,02 (Colon, High Met vs. Colon, Low Met)	1	8		8.67
17	449690					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	3	17		5.58
18	724616					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	8		7.57
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	8	0	8.12	
19	549722					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
20	549722					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
21	448110					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	2	25		11.65
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	25		24.62
22	515631					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
23	11881					
		03,04 (Breast, High Met vs. Breast, Non-Met)	6	0	5.85	
24	650856					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
25	449701					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	17	1	17.26	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	1	17		16.08
26	651073					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	7	0	7.4	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
27	10340					
		03,04 (Breast, High Met vs. Breast, Non-Met)	6	0	5.85	
28	648310					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
29	730336					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	24		22.71
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	24	0	24.37	
30	3060					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	4	17		4.19
		15,16 (Normal Colon vs. Colon Tumor Tissue)	14	4	3.7	
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	11		11.27
31	453016					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
33	185461					
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	17		17.42
34	452530					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	10	2	5.28	
35	448925					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	5	15		2.95
36	1013					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
		01,02 (Colon, High Met vs. Colon, Low Met)	40	84		2.28
37	6545					
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	9		9.22
38	449891					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	8	1	8.46	
39	4045					
		01,02 (Colon, High Met vs. Colon, Low Met)	2	11		5.96
		03,04 (Breast, High Met vs. Breast, Non-Met)	10	1	9.76	
40	404475					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	11	2	5.59	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	19	2	10.2	
41	650297					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
42	650493					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
43	644884					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	11	0	11.81	
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
44	452212					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
45	402727					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	5	17		3.17
46	645194					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
47	447501					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	15	3	5.37	
48	556326					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	8		7.88
49	447035					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	8	1	8.12	
50	2551					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
51	736154					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
52	452028					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	7		6.52
53	447441					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	34	129		3.53
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	34	129		3.74
		19,20 (Colon Tumor Tissue vs. Colon Metastasis)	1	8		10.7
		23,24 (Normal Lung Tissue vs. Lung Tumor Tissue)	155	32	4.89	
54	11028					
		01,02 (Colon, High Met vs. Colon, Low Met) (Colon, High Met vs. Colon, Low Met)	0	6		6.5
55	640974					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	9	0	9.66	
56	555103					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	7		6.52
		23,24 (Normal Lung Tissue vs. Lung Tumor Tissue)	0	6		5.94
57	446789					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	16	5	3.38	
58	644884					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	11	0	11.81	
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
59	9029					
		01,02 (Colon, High Met vs. Colon, Low Met)	7	0	6.46	
60	419255					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	11	0	11.63	

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	11	1	11.81	
61	4309					
		01,02 (Colon, High Met vs. Colon, Low Met)	4	13		3.52
62	554069					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
63	4330					
		03,04 (Breast, High Met vs. Breast, Non-Met) (Breast, High Met vs. Breast, Non-Met)	13	3	4.23	
		01,02 (Colon, High Met vs. Colon, Low Met)	1	10		10.84
64	644903					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
65	549395					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	2	13		6.06
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	13		12.8
66	4974					
		01,02 (Colon, High Met vs. Colon, Low Met)	1	8		8.67
67	447466					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	155	5	32.77	
		18,19 (Normal Colon Tissue vs. Colon Tumor)	16	1	18.28	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	155	2	83.19	
		18,20 (Normal Colon Tissue vs. Colon Metastasis)	16	0	13.68	
68	645073					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
69	447978					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	8		7.45
70	607430					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
71	556198					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
72	450323					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	8		7.45
73	21205					
		03,04 (Breast, High Met vs. Breast, Non-Met)	1	9		9.22
74	561109					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	8		7.57
75	446673					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	8	1	8.12	
76	456026					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		15,16 (Normal Colon vs. Colon Tumor Tissue)	24	4	6.34	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	24	8	3.22	
77	449142					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	9	1	9.14	
78	5830					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
79	554109					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	15	2	7.93	
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	2	11		5.42
80	595506					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
81	453981					
		23,24 (Normal Lung Tissue vs. Lung Tumor Tissue)	43	258		5.94
		19,20 (Colon Tumor Tissue vs. Colon Metastasis)	2	110		73.53
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	590	6	99.86	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	68	6	12.16	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	68	590		8.21
		18,20 (Normal Colon Tissue vs. Colon Metastasis)	0	110		128.69
82	642461					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	14	0	15.03	
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	10	0	10.16	
83	556198					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
84	2082					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
		03,04 (Breast, High Met vs. Breast, Non-Met)	15	55		3.76
		08,09 (Lung, High Met vs. Lung, Low Met)	7	38		3.88
85	549435					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	14	2	7.4	
86	2286					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	5	28		5.3
		19,20 (Colon Tumor Tissue vs. Colon Metastasis)	13	2	4.86	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	5	19		3.54
		18,19 (Normal Colon Tissue vs. Colon Tumor)	3	13		3.79
87	2737					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	3	14		4.6
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	4	14		3.26
88	728115					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
89	650856					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
90	650476					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
91	535208					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
92	733849					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
93	447978					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	8		7.45
94	729483					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
95	12018					
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	6		6.15
96	4747					
		01,02 (Colon, High Met vs. Colon, Low Met)	2	10		5.42
97	4747					
		01,02 (Colon, High Met vs. Colon, Low Met)	2	10		5.42
98	185577					
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	8		8.2
99	4126					
		03,04 (Breast, High Met vs. Breast, Non-Met)	13	1	12.68	
100	11456					
		01,02 (Colon, High Met vs. Colon, Low Met)	0	6		6.5
101	729851					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
102	449849					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
103	2490					
		08,09 (Lung, High Met vs. Lung, Low Met)	7	1	9.78	
		01,02 (Colon, High Met vs. Colon, Low Met)	21	6	3.23	
		03,04 (Breast, High Met vs. Breast, Non-Met)	14	3	4.55	
104	549041					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
105	11881					
		03,04 (Breast, High Met vs. Breast, Non-Met)	6	0	5.85	
106	724296					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	128		121.1
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	128	0	129.99	
107	726173					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
108	2423					
		03,04 (Breast, High Met vs. Breast, Non-Met)	14	0	13.66	
109	556250					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	1	28		26.49
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	28	4	7.11	
110	643594					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	7	0	7.4	
111	11881					
		03,04 (Breast, High Met vs. Breast, Non-Met)	6	0	5.85	
112	7436					
		03,04 (Breast, High Met vs. Breast, Non-Met)	9	1	8.78	
113	2110					
		03,04 (Breast, High Met vs. Breast, Non-Met)	31	5	6.05	
114	10340					
		03,04 (Breast, High Met vs. Breast, Non-Met)	6	0	5.85	
115	643594					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	7	0	7.4	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
116	447035					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	8	1	8.12	
117	402707					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	1	9		8.38
118	645799					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
119	171511					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
120	451607					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	9		8.86

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
121	3138					
		03,04 (Breast, High Met vs. Breast, Non-Met)	1	10		10.25
122	2988					
		01,02 (Colon, High Met vs. Colon, Low Met)	2	11		5.96
123	447326					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
124	561734					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
125	454999					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	28	15	2	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	28	11	2.69	
126	185652					
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	7		7.17
127	6725					
		03,04 (Breast, High Met vs. Breast, Non-Met)	10	0	9.76	
128	726644					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	18		17.03
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	18	0	18.28	
129	11012					
		01,02 (Colon, High Met vs. Colon, Low Met)	0	6		6.5
130	726377					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
131	735326					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
132	650845					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
133	9048					
		01,02 (Colon, High Met vs. Colon, Low Met)	7	0	6.46	
134	732254					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
		23,24 (Normal Lung Tissue vs. Lung Tumor Tissue)	0	8		7.92
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
135	452052					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	8	1	8.59	
136	554079					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	2	10		4.92

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
137	9049					
		01,02 (Colon, High Met vs. Colon, Low Met)	7	0	6.46	
138	1307					
		03,04 (Breast, High Met vs. Breast, Non-Met)	14	89		6.52
139	139730					
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	9		9.22
140	7750					
		03,04 (Breast, High Met vs. Breast, Non-Met)	1	14		14.35
141	8050					
		01,02 (Colon, High Met vs. Colon, Low Met)	0	7		7.59
142	725222					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
143	3275					
		03,04 (Breast, High Met vs. Breast, Non-Met)	8	0	7.81	
144	7424					
		03,04 (Breast, High Met vs. Breast, Non-Met)	6	0	5.85	
145	8953					
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	13		13.32
146	8966					
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	7		7.17
147	530883					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
148	6725					
		03,04 (Breast, High Met vs. Breast, Non-Met)	10	0	9.76	
149	4439					
		08,09 (Lung, High Met vs. Lung, Low Met)	10	2	6.99	
		01,02 (Colon, High Met vs. Colon, Low Met)	15	2	6.92	
150	648472					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
151	735346					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
152	732121					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
153	650337					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
154	533588					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
155	649667					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
156	394436					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
157	649354					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
158	2022					
		03,04 (Breast, High Met vs. Breast, Non-Met)	5	15		3.07
		21,22 (Normal Prostate vs. Prostate Cancer)	0	6		6.1
159	561359					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	12	3	4.29	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	12	2	6.34	
160	7607					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	13	3	4.65	
		01,02 (Colon, High Met vs. Colon, Low Met)	0	7		7.59
		15,16 (Normal Colon vs. Colon Tumor Tissue)	13	4	3.44	
161	7750					
		03,04 (Breast, High Met vs. Breast, Non-Met)	1	14		14.35
162	410554					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
163	2315					
		03,04 (Breast, High Met vs. Breast, Non-Met)	7	118		17.28
		01,02 (Colon, High Met vs. Colon, Low Met)	25	4	5.76	
164	561734					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
165	4420					
		03,04 (Breast, High Met vs. Breast, Non-Met)	6	0	5.85	
		01,02 (Colon, High Met vs. Colon, Low Met)	1	10		10.84
166	559663					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	15	4	3.96	
167	7082					
		03,04 (Breast, High Met vs. Breast, Non-Met)	10	0	9.76	
168	2315					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		03,04 (Breast, High Met vs. Breast, Non-Met)	7	118		17.28
		01,02 (Colon, High Met vs. Colon, Low Met)	25	4	5.76	
169	650472					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
170	6482					
		01,02 (Colon, High Met vs. Colon, Low Met)	0	6		6.5
171	4584					
		01,02 (Colon, High Met vs. Colon, Low Met)	1	11		11.93
172	453846					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	11		10.25
173	650820					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	8	0	8.12	
174	642906					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
175	448805					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	20		3.28
176	649667					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
177	735786					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
178	121457					
		08,09 (Lung, High Met vs. Lung, Low Met)	91	359		2.82
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	2	11		5.12
179	372960					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	18		2.79
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	33		5.2
180	120049					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	10	2	5.37	
181	648996					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
182	3765					
		01,02 (Colon, High Met vs. Colon, Low Met)	19	6	2.92	
183	462642					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
184	727181					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
185	649259					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	7	0	7.4	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
186	649717					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
187	736860					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
188	729175					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
189	642906					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
190	4420					
		03,04 (Breast, High Met vs. Breast, Non-Met)	6	0	5.85	
		01,02 (Colon, High Met vs. Colon, Low Met)	1	10		10.84
191	2420					
		01,02 (Colon, High Met vs. Colon, Low Met)	28	11	2.35	
192	648109					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	8	0	8.59	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	8	1	8.46	
193	2334					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
194	639705					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	10	0	10.57	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	10	0	10.73	
195	551907					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	7	0	7.4	
196	561382					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	12	2	6.34	
197	595506					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
198	499424					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	8		7.57
199	735477					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
200	734370					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	11		10.41
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	11	0	11.17	
201	779					
		01,02 (Colon, High Met vs. Colon, Low Met)	27	54		2.17
		03,04 (Breast, High Met vs. Breast, Non-Met)	60	22	2.66	
202	649143					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
203	489					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	12	58		4.5
		15,16 (Normal Colon vs. Colon Tumor Tissue)	12	58		4.57
204	2994					
		01,02 (Colon, High Met vs. Colon, Low Met)	3	14		5.06
205	2994					
		01,02 (Colon, High Met vs. Colon, Low Met)	3	14		5.06
206	11147					
		01,02 (Colon, High Met vs. Colon, Low Met)	0	6		6.5
207	549395					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	2	13		6.06
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	13		12.8
208	559806					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
209	452238					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
210	225914					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
211	463480					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
212	184725					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	8	0	8.59	
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
213	557401					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	10	2	5.37	
214	455155					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	12	3	4.23	
215	551117					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
217	729295					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
218	450429					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	10	1	10.16	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	13	1	13.95	
219	450148					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
220	380412					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
221	446614					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
222	555911					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	2	21		9.78
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	21		20.68
223	450828					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	1	9		8.38
224	28					
		18,20 (Normal Colon Tissue vs. Colon Metastasis)	2	11		6.43
		18,19 (Normal Colon Tissue vs. Colon Tumor)	2	43		18.81
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	53	207		3.64
		03,04 (Breast, High Met vs. Breast, Non-Met)	697	1789		2.63
		19,20 (Colon Tumor Tissue vs. Colon Metastasis)	43	11	2.92	
225	446450					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	11	3	3.88	
226	452026					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	35	14	2.64	
227	643594					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	7	0	7.4	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
228	1905					
		01,02 (Colon, High Met vs. Colon, Low Met)	7	21		3.25
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	7		6.52
229	651073					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	7	0	7.4	
230	553705					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		15,16 (Normal Colon vs. Colon Tumor Tissue)	12	0	12.68	
231	521840					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
232	648689					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
233	447858					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	12	3	4.23	
234	556198					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
235	394436					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
236	639651					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
237	499424					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	8		7.57
238	468109					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
239	185701					
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	6		6.15
240	451811					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	10	2	5.37	
241	730670					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
242	172013					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
243	449142					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	9	1	9.14	
244	446964					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	1	10		9.32
245	414739					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	2	14		6.89
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	2	14		6.52
246	641124					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
247	555702					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	11	2	5.81	

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
248	549435					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	14	2	7.4	
249	643954					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
250	5984					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
251	560526					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	8		7.88
252	411113					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
253	7607					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	13	4	3.44	
		01,02 (Colon, High Met vs. Colon, Low Met)	0	7		7.59
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	13	3	4.65	
254	559409					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
255	650053					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	10	1	10.57	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	10	0	10.73	
256	448511					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	3	26		8.07
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	4	26		6.4
257	642142					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	11	0	11.17	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	2	11		5.2
258	470462					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
259	431601					
		18,20 (Normal Colon Tissue vs. Colon Metastasis)	9	0	7.69	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	28	9	3.34	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	28	6	4.93	
		08,09 (Lung, High Met vs. Lung, Low Met)	5	0	6.99	
260	421431					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	8	1	8.46	
261	284586					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
262	556198					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
263	431601					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		18,20 (Normal Colon Tissue vs. Colon Metastasis)	9	0	7.69	
		08,09 (Lung, High Met vs. Lung, Low Met)	5	0	6.99	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	28	6	4.93	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	28	9	3.34	
264	449891					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	8	1	8.46	
265	556561					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	10		9.32
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	10		9.85
266	554188					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
267	3247					
		01,02 (Colon, High Met vs. Colon, Low Met)	1	20		21.68
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	26		3.66
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	4	26		6.06
268	546705					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
269	560984					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
270	455820					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	7		6.89
271	643129					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
272	454653					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	3	17		5.28
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	5	17		3.35
273	456549					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	8		7.88
274	454806					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	10	2	5.28	
275	724296					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	128		121.1
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	128	0	129.99	
276	559280					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
277	171511					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
278	644242					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
279	734370					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	11		10.41
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	11	0	11.17	
280	639459					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	11	0	11.81	
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	9	0	9.14	
281	641679					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	8	0	8.59	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	8	0	8.46	
282	644611					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	7	0	7.4	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
283	550038					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	7		6.89
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	7		6.52
284	452567					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	3	14		4.6
		15,16 (Normal Colon vs. Colon Tumor Tissue)	21	3	7.4	
285	411113					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
286	650749					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
287	558899					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
288	452986					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	8	1	8.46	
289	393197					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
290	499424					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	8		7.57
291	21669					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	7		6.89
292	640590					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	9	0	9.66	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	9	1	9.51	
293	549936					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
294	448770					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
295	559280					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
296	648934					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	8	0	8.46	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	8	0	8.59	
297	452685					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	15	5	3.17	
298	456549					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	8		7.88
299	446614					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
300	559280					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
301	446673					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	8	1	8.12	
302	562550					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
303	467288					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
304	463824					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
305	393197					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
306	407077					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	8		7.45
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	8		7.88
307	499424					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	8		7.57
308	554500					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
309	730143					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
310	595506					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
311	2334					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
312	647444					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
313	380291					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
314	644849					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	8	0	8.59	
315	449457					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	7		6.52
316	446673					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	8	1	8.12	
317	549069					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	11	56		4.82
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	11	36		3.05
318	728884					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	8	0	8.12	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	8		7.57
319	415058					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
320	553955					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
321	455820					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	7		6.89
322	549617					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
323	449831					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	10		9.85
324	451580					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
325	558899					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
326	562292					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
327	5830					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
328	8953					
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	13		13.32
329	8012					
		03,04 (Breast, High Met vs. Breast, Non-Met)	7	0	6.83	
330	185718					
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	6		6.15
331	729851					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
332	185597					
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	8		8.2
333	9887					
		03,04 (Breast, High Met vs. Breast, Non-Met)	7	0	6.83	
334	725825					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	8		7.57
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	8	0	8.12	
335	6545					
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	9		9.22
336	21205					
		03,04 (Breast, High Met vs. Breast, Non-Met)	1	9		9.22
337	8867					
		03,04 (Breast, High Met vs. Breast, Non-Met)	6	0	5.85	
338	729295					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
339	730430					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	8		7.57
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	8	0	8.12	
340	7072					
		03,04 (Breast, High Met vs. Breast, Non-Met)	10	1	9.76	
341	730533					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
342	9121					
		01,02 (Colon, High Met vs. Colon, Low Met)	0	7		7.59
343	11131					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		01,02 (Colon, High Met vs. Colon, Low Met)	0	6		6.5
344	640116					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	19	4	5.02	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	19	0	20.39	
345	730282					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
346	550571					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
347	1183					
		01,02 (Colon, High Met vs. Colon, Low Met)	4	71		19.24
		03,04 (Breast, High Met vs. Breast, Non-Met)	32	15	2.08	
348	449437					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	14	3	4.93	
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	3	12		3.94
349	8966					
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	7		7.17
350	6134					
		18,20 (Normal Colon Tissue vs. Colon Metastasis)	22	5	3.76	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	142	40	3.81	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	142	42	3.57	
		19,20 (Colon Tumor Tissue vs. Colon Metastasis)	22	5	3.29	
351	95700					
		03,04 (Breast, High Met vs. Breast, Non-Met)	1	21		21.52
352	7066					
		01,02 (Colon, High Met vs. Colon, Low Met)	0	9		9.76
353	648310					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
354	730059					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
355	736014					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
356	646577					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
357	732254					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
		23,24 (Normal Lung Tissue vs. Lung Tumor Tissue)	0	8		7.92
358	7037					
		01,02 (Colon, High Met vs. Colon, Low Met)	0	9		9.76
359	7037					
		01,02 (Colon, High Met vs. Colon, Low Met)	0	9		9.76
360	6937					
		03,04 (Breast, High Met vs. Breast, Non-Met)	10	0	9.76	
361	7572					
		01,02 (Colon, High Met vs. Colon, Low Met)	0	8		8.67
362	388085					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	9	0	9.66	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	9	0	9.51	
363	2676					
		01,02 (Colon, High Met vs. Colon, Low Met)	2	17		9.22
364	639240					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	9	0	9.51	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	9	0	9.66	
365	650472					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
366	727789					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
367	2495					
		03,04 (Breast, High Met vs. Breast, Non-Met)	27	5	5.27	
		08,09 (Lung, High Met vs. Lung, Low Met)	13	2	9.08	
368	732254					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
		23,24 (Normal Lung Tissue vs. Lung Tumor Tissue)	0	8		7.92
369	5268					
		01,02 (Colon, High Met vs. Colon, Low Met)	0	15		16.26
370	11881					
		03,04 (Breast, High Met vs. Breast, Non-Met)	6	0	5.85	
371	448677					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	11	1	11.63	
372	1876					
		03,04 (Breast, High Met vs. Breast, Non-Met)	15	3	4.88	
373	3441					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		01,02 (Colon, High Met vs. Colon, Low Met)	4	13		3.52
		03,04 (Breast, High Met vs. Breast, Non-Met)	8	0	7.81	
374	726134					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	8		7.57
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	8	0	8.12	
375	9048					
		01,02 (Colon, High Met vs. Colon, Low Met)	7	0	6.46	
376	26489					
		03,04 (Breast, High Met vs. Breast, Non-Met)	1	8		8.2
377	644205					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	7	0	7.4	
378	468689					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
379	638971					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	8	0	8.59	
380	10274					
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	7		7.17
381	6725					
		03,04 (Breast, High Met vs. Breast, Non-Met)	10	0	9.76	
382	2488					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	8		7.45
383	8366					
		21,22 (Normal Prostate vs. Prostate Cancer) (Normal Prostate vs. Prostate Cancer)	2	15		7.63
		03,04 (Breast, High Met vs. Breast, Non-Met)	15	2	7.32	
384	502683					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
385	450914					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
386	21205					
		03,04 (Breast, High Met vs. Breast, Non-Met)	1	9		9.22
387	644205					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	7	0	7.4	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
388	5268					
		01,02 (Colon, High Met vs. Colon, Low Met)	0	15		16.26

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
389	8012					
		03,04 (Breast, High Met vs. Breast, Non-Met)	7	0	6.83	
390	11270					
		01,02 (Colon, High Met vs. Colon, Low Met)	0	6		6.5
391	10924					
		03,04 (Breast, High Met vs. Breast, Non-Met)	6	0	5.85	
393	3650					
		03,04 (Breast, High Met vs. Breast, Non-Met)	10	2	4.88	
394	1655					
		01,02 (Colon, High Met vs. Colon, Low Met)	67	2	30.9	
		21,22 (Normal Prostate vs. Prostate Cancer)	116	51	2.24	
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	58		59.45
395	3275					
		03,04 (Breast, High Met vs. Breast, Non-Met)	8	0	7.81	
396	3355					
		03,04 (Breast, High Met vs. Breast, Non-Met)	21	7	2.93	
397	2078					
		03,04 (Breast, High Met vs. Breast, Non-Met)	11	2	5.37	
398	4809					
		08,09 (Lung, High Met vs. Lung, Low Met)	3	27		6.44
		01,02 (Colon, High Met vs. Colon, Low Met)	15	1	13.84	
399	6402					
		03,04 (Breast, High Met vs. Breast, Non-Met)	10	0	9.76	
400	555244					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	11		10.83
401	548965					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	4	14		3.45
402	4747					
		01,02 (Colon, High Met vs. Colon, Low Met)	2	10		5.42
403	40208					
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	6		6.15
404	14596					
		08,09 (Lung, High Met vs. Lung, Low Met)	14	6	3.26	
		03,04 (Breast, High Met vs. Breast, Non-Met)	1	17		17.42
405	7110					
		03,04 (Breast, High Met vs. Breast, Non-Met)	4	19		4.87
406	7110					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		03,04 (Breast, High Met vs. Breast, Non-Met)	4	19		4.87
407	6592					
		03,04 (Breast, High Met vs. Breast, Non-Met)	12	1	11.71	
408	6455					
		03,04 (Breast, High Met vs. Breast, Non-Met)	6	0	5.85	
409	2738					
		03,04 (Breast, High Met vs. Breast, Non-Met)	15	4	3.66	
410	696					
		03,04 (Breast, High Met vs. Breast, Non-Met)	37	13	2.78	
		01,02 (Colon, High Met vs. Colon, Low Met)	24	87		3.93
411	379186					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
412	1588					
		03,04 (Breast, High Met vs. Breast, Non-Met)	15	95		6.49
		01,02 (Colon, High Met vs. Colon, Low Met)	45	19	2.18	
413	7007					
		01,02 (Colon, High Met vs. Colon, Low Met)	0	9		9.76
414	9025					
		01,02 (Colon, High Met vs. Colon, Low Met)	7	0	6.46	
415	650749					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
416	553158					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	8		7.88
417	641703					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	12	0	12.88	
418	833					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	12	3	4.23	
		08,09 (Lung, High Met vs. Lung, Low Met)	18	9	2.79	
		03,04 (Breast, High Met vs. Breast, Non-Met)	16	3	5.2	
419	649259					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	7	0	7.4	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
420	451179					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	1	9		8.38
421	9505					
		03,04 (Breast, High Met vs. Breast, Non-Met)	3	15		5.12
422	736728					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	

1. The first group of people who are interested in the study of the history of the United States are the people who are interested in the history of the United States.

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Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
438	448770					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
439	375380					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	1	9		8.38
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	9		8.86
440	726134					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	8	0	8.12	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	8		7.57
441	422687					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	10	0	10.16	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	10		9.46
442	448436					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	20	2	10.16	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	4	20		4.73
443	644893					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
444	559104					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
445	551172					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	1	10		9.46
446	724296					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	128		121.1
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	128	0	129.99	
447	735936					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	9		8.51
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	9	0	9.14	
448	556326					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	8		7.88
449	729699					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
450	550694					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	21	7	3.22	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	21	1	22.2	
451	734738					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
452	404502					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
453	554151					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	1	15		13.97
		15,16 (Normal Colon vs. Colon Tumor Tissue)	1	9		8.51
454	649852					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
455	734063					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
456	7279					
		01,02 (Colon, High Met vs. Colon, Low Met)	0	6		6.5
457	2676					
		01,02 (Colon, High Met vs. Colon, Low Met)	2	17		9.22
458	649148					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	8	0	8.59	
459	1953					
		03,04 (Breast, High Met vs. Breast, Non-Met)	4	48		12.3
		01,02 (Colon, High Met vs. Colon, Low Met)	39	13	2.77	
460	650108					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	9	0	9.66	
461	515350					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	14	0	14.8	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	14	3	5.01	
462	402494					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	3	13		4.1
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	13	3	4.4	
463	649148					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	8	0	8.59	
464	833					
		03,04 (Breast, High Met vs. Breast, Non-Met)	16	3	5.2	
		08,09 (Lung, High Met vs. Lung, Low Met)	18	9	2.79	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	12	3	4.23	
465	139730					
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	9		9.22
466	453079					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	8	1	8.12	
467	546705					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
468	644903					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
469	732254					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
		23,24 (Normal Lung Tissue vs. Lung Tumor Tissue)	0	8		7.92
470	561180					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	11	2	5.81	
471	732254					
		23,24 (Normal Lung Tissue vs. Lung Tumor Tissue)	0	8		7.92
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
472	449204					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	1	14		13.04
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	3	14		4.6
473	185651					
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	7		7.17
474	639029					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
475	452986					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	8	1	8.46	
476	729779					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	8		7.57
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	8	0	8.12	
477	646248					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
478	650448					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
479	642049					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
480	728273					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
481	446139					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	13	0	13.74	
		18,19 (Normal Colon Tissue vs. Colon Tumor)	12	0	13.71	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	13	0	13.95	
		18,20 (Normal Colon Tissue vs. Colon Metastasis)	12	0	10.26	
482	2783					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		03,04 (Breast, High Met vs. Breast, Non-Met)	5	40		8.2
		01,02 (Colon, High Met vs. Colon, Low Met)	27	6	4.15	
483	642906					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
484	8332					
		03,04 (Breast, High Met vs. Breast, Non-Met)	6	0	5.85	
485	453470					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	12	1	12.88	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	12	1	12.68	
486	552277					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	8		7.45
487	464029					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	9		8.86
489	649722					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	8	0	8.59	
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
490	612572					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
491	385980					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	27	12	2.28	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	2	12		5.59
		15,16 (Normal Colon vs. Colon Tumor Tissue)	2	27		12.77
492	141185					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	8	0	8.46	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	8	0	8.59	
493	463824					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
494	446139					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	13	0	13.74	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	13	0	13.95	
		18,19 (Normal Colon Tissue vs. Colon Tumor)	12	0	13.71	
		18,20 (Normal Colon Tissue vs. Colon Metastasis)	12	0	10.26	
495	725994					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
496	736679					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
497	551718					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	8		7.45
498	640525					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	7	0	7.4	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
499	645210					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	10	1	10.57	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	10	0	10.73	
500	6567					
		03,04 (Breast, High Met vs. Breast, Non-Met)	10	0	9.76	
501	646146					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	8	0	8.59	
502	4934					
		01,02 (Colon, High Met vs. Colon, Low Met)	1	9		9.76
503	450791					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	18	6	3.17	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	18	3	6.44	
504	227936					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	8		7.57
505	9436					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	4	15		3.69
506	2557					
		01,02 (Colon, High Met vs. Colon, Low Met)	23	8	2.65	
507	11356					
		01,02 (Colon, High Met vs. Colon, Low Met)	0	6		6.5
508	7571					
		01,02 (Colon, High Met vs. Colon, Low Met)	0	8		8.67
509	558116					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
510	216574					
		18,20 (Normal Colon Tissue vs. Colon Metastasis)	15	2	6.41	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	107	29	3.96	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	107	29	3.9	
511	455145					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
512	649148					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	8	0	8.59	
513	648996					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
514	304253					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
515	649717					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
516	5838					
		01,02 (Colon, High Met vs. Colon, Low Met)	1	9		9.76
517	454050					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	8	1	8.59	
518	557903					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	9		8.51
519	1724					
		03,04 (Breast, High Met vs. Breast, Non-Met)	6	24		4.1
520	734803					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
521	557948					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	11		10.83
522	5838					
		01,02 (Colon, High Met vs. Colon, Low Met)	1	9		9.76
523	2334					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
524	450953					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	2	14		6.52
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	14		13.79
525	4840					
		03,04 (Breast, High Met vs. Breast, Non-Met)	18	6	2.93	
526	728421					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
527	4747					
		01,02 (Colon, High Met vs. Colon, Low Met)	2	10		5.42
528	648934					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	8	0	8.46	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	8	0	8.59	
529	1787					
		01,02 (Colon, High Met vs. Colon, Low Met)	17	36		2.3

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
530	558098					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
531	1655					
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	58		59.45
		21,22 (Normal Prostate vs. Prostate Cancer)	116	51	2.24	
		01,02 (Colon, High Met vs. Colon, Low Met)	67	2	30.9	
532	158601					
		03,04 (Breast, High Met vs. Breast, Non-Met)	1	10		10.25
533	185486					
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	13		13.32
534	7110					
		03,04 (Breast, High Met vs. Breast, Non-Met)	4	19		4.87
535	2543					
		01,02 (Colon, High Met vs. Colon, Low Met)	23	7	3.03	
536	115762					
		21,22 (Normal Prostate vs. Prostate Cancer)	16	5	3.15	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	7		6.52
537	696					
		01,02 (Colon, High Met vs. Colon, Low Met)	24	87		3.93
		03,04 (Breast, High Met vs. Breast, Non-Met)	37	13	2.78	
538	1948					
		03,04 (Breast, High Met vs. Breast, Non-Met)	37	15	2.41	
539	696					
		01,02 (Colon, High Met vs. Colon, Low Met)	24	87		3.93
		03,04 (Breast, High Met vs. Breast, Non-Met)	37	13	2.78	
540	696					
		03,04 (Breast, High Met vs. Breast, Non-Met)	37	13	2.78	
		01,02 (Colon, High Met vs. Colon, Low Met)	24	87		3.93
541	380477					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
542	638799					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	10	0	10.73	
543	551982					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
544	551982					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
545	521840					

Table 5

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
546	561180					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	11	2	5.81	
547	556245					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
548	449792					
		19,20 (Colon Tumor Tissue vs. Colon Metastasis)	0	5		6.68
		15,16 (Normal Colon vs. Colon Tumor Tissue)	3	13		4.1
549	549722					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
550	612572					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
551	551235					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	7		6.89
552	449701					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	17	1	17.26	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	1	17		16.08
553	375380					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	9		8.86
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	1	9		8.38
554	56940					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	8		7.45
555	549160					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	7		6.52
556	554151					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	1	15		13.97
		15,16 (Normal Colon vs. Colon Tumor Tissue)	1	9		8.51
557	727331					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
558	551502					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	22	7	3.32	
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	19		2.67
559	612572					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
560	701221					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
561	378041					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	13	4	3.3	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	13		12.3
562	503491					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
563	452833					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	7		6.52
564	640974					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	9	0	9.66	
565	735326					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
566	555944					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
567	447532					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	11	0	11.63	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	11	1	11.81	
568	455598					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
569	555734					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	10		9.32
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	10		9.85
570	446663					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	32		5.25
		18,20 (Normal Colon Tissue vs. Colon Metastasis)	1	8		9.36
		19,20 (Colon Tumor Tissue vs. Colon Metastasis)	0	8		10.7
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	14	32		2.13
571	449862					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	7		6.52
572	549591					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	24		3.38
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	2	24		11.18
573	553877					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	8		7.88
574	553501					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	14	1	14.8	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	14	3	5.01	
575	1905					
		01,02 (Colon, High Met vs. Colon, Low Met)	7	21		3.25
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	7		6.52

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
576	446599					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	13	2	6.87	
577	559409					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
578	551982					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
579	559057					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	7		6.52
580	446760					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	22	7	3.19	
581	551502					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	19		2.67
		15,16 (Normal Colon vs. Colon Tumor Tissue)	22	7	3.32	
582	446531					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
583	506744					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	7	0	7.4	
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	8		7.88
584	401849					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	7	0	7.4	
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	15		14.77
585	453848					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	2	14		6.62
586	456764					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	10	1	10.16	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	14	1	15.03	
587	446371					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
588	406413					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	9		8.86
589	555103					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	7		6.52
		23,24 (Normal Lung Tissue vs. Lung Tumor Tissue)	0	6		5.94
590	735292					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	9		8.51
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	9	0	9.14	
591	558534					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	7		6.89

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
592	727181					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
593	551117					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
594	464040					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
595	446371					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
596	728408					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	12	0	12.19	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	12		11.35
597	649259					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	7	0	7.4	
598	15414					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	1	9		8.38
599	639240					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	9	0	9.66	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	9	0	9.51	
600	549722					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
601	561499					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	8		7.88
		15,16 (Normal Colon vs. Colon Tumor Tissue)	8	1	8.46	
602	639029					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
603	449512					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	4	14		3.26
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	14		13.79
604	446987					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	10	0	10.73	
605	466302					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	9	1	9.51	
606	553802					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	1	9		8.38
607	639662					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		15,16 (Normal Colon vs. Colon Tumor Tissue)	7	0	7.4	
608	551527					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	7		6.52
609	730389					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	9	0	9.14	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	9		8.51
610	640974					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	9	0	9.66	
611	417155					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
612	417155					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
613	451784					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	7		6.89
614	649152					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
615	450867					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	7	0	7.4	
616	143436					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	21	9	2.5	
617	549395					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	13		12.8
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	2	13		6.06
618	639273					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	9	0	9.51	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	9	0	9.66	
619	506744					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	7	0	7.4	
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	8		7.88
620	736595					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
621	230995					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
622	451784					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	7		6.89
623	226324					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
624	449617					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	18		2.53
625	451092					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	9		8.86
626	546642					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	11	0	11.17	
627	553736					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	2	10		4.92
628	394413					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	113	3	39.81	
		18,20 (Normal Colon Tissue vs. Colon Metastasis)	21	0	17.95	
		18,19 (Normal Colon Tissue vs. Colon Tumor)	21	2	12	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	113	0	121.29	
629	556326					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	8		7.88
630	448606					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	3	20		6.21
631	394413					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	113	0	121.29	
		18,19 (Normal Colon Tissue vs. Colon Tumor)	21	2	12	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	113	3	39.81	
		18,20 (Normal Colon Tissue vs. Colon Metastasis)	21	0	17.95	
632	645633					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
633	551634					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
634	556326					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	8		7.88
635	540787					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	7	0	7.4	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
636	648872					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
637	643804					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
638	446139					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	13	0	13.95	

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		18,19 (Normal Colon Tissue vs. Colon Tumor)	12	0	13.71	
		18,20 (Normal Colon Tissue vs. Colon Metastasis)	12	0	10.26	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	13	0	13.74	
639	640356					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	10	0	10.73	
640	379186					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
641	454927					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	3	14		4.6
642	401849					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	15		14.77
		15,16 (Normal Colon vs. Colon Tumor Tissue)	7	0	7.4	
643	452414					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	17	0	17.97	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	17	0	18.25	
644	446789					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	16	5	3.38	
645	189561					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	9		8.51
		08,09 (Lung, High Met vs. Lung, Low Met)	1	14		10.02
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	9		8.38
646	640323					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	8	0	8.59	
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
647	558116					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
648	468109					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
649	481441					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	12	0	12.19	
650	449956					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	10	1	10.16	
651	727224					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	8	0	8.12	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	8		7.57
652	551907					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	7	0	7.4	
653	447532					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	11	0	11.63	

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	11	1	11.81	
654	447532					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	11	1	11.81	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	11	0	11.63	
655	558454					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	7		6.52
656	502683					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
657	446909					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	2	12		5.91
658	452506					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	7	0	7.4	
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
659	449792					
		19,20 (Colon Tumor Tissue vs. Colon Metastasis)	0	5		6.68
		15,16 (Normal Colon vs. Colon Tumor Tissue)	3	13		4.1
660	549395					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	2	13		6.06
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	13		12.8
661	234653					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	18		2.95
662	453911					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
663	452071					
		18,20 (Normal Colon Tissue vs. Colon Metastasis)	14	0	11.97	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	109	1	115.21	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	109	0	117	
		18,19 (Normal Colon Tissue vs. Colon Tumor)	14	0	16	
664	451032					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
665	446680					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	29	84		2.7
		23,24 (Normal Lung Tissue vs. Lung Tumor Tissue)	40	94		2.33
666	641884					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	8	0	8.59	
667	452800					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	3	13		4.04
668	461835					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		15,16 (Normal Colon vs. Colon Tumor Tissue)	7	0	7.4	
669	548965					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	4	14		3.45
670	734793					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	9		8.51
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	9	0	9.14	
671	539955					
		23,24 (Normal Lung Tissue vs. Lung Tumor Tissue)	3	47		15.51
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	24	0	24.37	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	11	0	11.81	
672	561892					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	7		6.52
673	562292					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
674	420686					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	8		7.88
675	9436					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	4	15		3.69
676	1013					
		01,02 (Colon, High Met vs. Colon, Low Met)	40	84		2.28
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
677	412364					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
678	44424					
		08,09 (Lung, High Met vs. Lung, Low Met)	4	40		7.16
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	25	90		3.35
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	41	90		2.16
679	394413					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	113	0	121.29	
		18,19 (Normal Colon Tissue vs. Colon Tumor)	21	2	12	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	113	3	39.81	
		18,20 (Normal Colon Tissue vs. Colon Metastasis)	21	0	17.95	
680	449617					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	18		2.53
681	455032					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
682	185400					
		03,04 (Breast, High Met vs. Breast, Non-Met)	1	62		63.55

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	9		8.86
683	453911					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
684	650297					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
685	185400					
		03,04 (Breast, High Met vs. Breast, Non-Met)	1	62		63.55
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	9		8.86
686	449512					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	4	14		3.26
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	14		13.79
687	44424					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	41	90		2.16
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	25	90		3.35
		08,09 (Lung, High Met vs. Lung, Low Met)	4	40		7.16
688	556216					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	7		6.89
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	7		6.52
689	448677					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	11	1	11.63	
690	375380					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	1	9		8.38
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	9		8.86
691	379341					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	3	14		4.35
		08,09 (Lung, High Met vs. Lung, Low Met)	2	21		7.51
692	376988					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	8		7.88
693	559806					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
694	550195					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	11		10.83
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	2	11		5.12
695	562221					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	8	0	8.46	
696	211					
		01,02 (Colon, High Met vs. Colon, Low Met)	109	206		2.05
		03,04 (Breast, High Met vs. Breast, Non-Met)	121	43	2.75	
697	6751					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	11		11.27
		08,09 (Lung, High Met vs. Lung, Low Met)	5	0	6.99	
698	6751					
		08,09 (Lung, High Met vs. Lung, Low Met)	5	0	6.99	
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	11		11.27
700	2883					
		03,04 (Breast, High Met vs. Breast, Non-Met)	9	21		2.39
701	9784					
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	6		6.15
702	649722					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	8	0	8.59	
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
704	10340					
		03,04 (Breast, High Met vs. Breast, Non-Met)	6	0	5.85	
705	1649					
		03,04 (Breast, High Met vs. Breast, Non-Met)	15	1	14.63	
706	4325					
		03,04 (Breast, High Met vs. Breast, Non-Met)	7	0	6.83	
707	10882					
		03,04 (Breast, High Met vs. Breast, Non-Met)	6	20		3.42
708	10342					
		03,04 (Breast, High Met vs. Breast, Non-Met)	7	0	6.83	
709	6474					
		01,02 (Colon, High Met vs. Colon, Low Met)	0	6		6.5
710	10340					
		03,04 (Breast, High Met vs. Breast, Non-Met)	6	0	5.85	
711	734723					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	9	0	9.14	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	9		8.51
712	452142					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	1	10		9.46
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	10	2	5.08	
713	185432					
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	26		26.65
714	11456					
		01,02 (Colon, High Met vs. Colon, Low Met)	0	6		6.5
715	508892					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	1	10		9.32

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	2	10		4.92
716	67					
		03,04 (Breast, High Met vs. Breast, Non-Met)	23	0	22.44	
		01,02 (Colon, High Met vs. Colon, Low Met)	0	32		34.69
717	2636					
		08,09 (Lung, High Met vs. Lung, Low Met)	7	1	9.78	
		01,02 (Colon, High Met vs. Colon, Low Met)	8	19		2.57
718	735028					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
719	1924					
		01,02 (Colon, High Met vs. Colon, Low Met)	8	21		2.85
720	640116					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	19	4	5.02	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	19	0	20.39	
721	6546					
		01,02 (Colon, High Met vs. Colon, Low Met)	0	9		9.76
722	730866					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	8	0	8.12	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	8		7.57
723	4829					
		01,02 (Colon, High Met vs. Colon, Low Met)	0	7		7.59
724	546632					
		23,24 (Normal Lung Tissue vs. Lung Tumor Tissue)	3	34		11.22
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	15	0	15.23	
725	549934					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	11	3	3.88	
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	3	20		6.56
		21,22 (Normal Prostate vs. Prostate Cancer)	8	0	7.87	
726	649655					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	12	0	12.19	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
727	62016					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
728	2783					
		01,02 (Colon, High Met vs. Colon, Low Met)	27	6	4.15	
		03,04 (Breast, High Met vs. Breast, Non-Met)	5	40		8.2
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
729	3876					
		21,22 (Normal Prostate vs. Prostate Cancer)	9	26		2.94

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	3	14		4.35
730	20036					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	1	13		12.11
731	644032					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	124	0	125.92	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	7	124		16.76
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
732	451636					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	8		7.88
733	3428					
		03,04 (Breast, High Met vs. Breast, Non-Met)	20	0	19.51	
734	643954					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
735	456506					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	17	7	2.61	
736	449269					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	26	7	3.99	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	26	5	5.5	
737	732712					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
738	696					
		01,02 (Colon, High Met vs. Colon, Low Met)	24	87		3.93
		03,04 (Breast, High Met vs. Breast, Non-Met)	37	13	2.78	
739	456528					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
740	4043					
		01,02 (Colon, High Met vs. Colon, Low Met)	1	9		9.76
741	3639					
		03,04 (Breast, High Met vs. Breast, Non-Met)	12	3	3.9	
742	1024					
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	292		299.28
		08,09 (Lung, High Met vs. Lung, Low Met)	41	11	5.21	
743	1247					
		03,04 (Breast, High Met vs. Breast, Non-Met)	51	15	3.32	
744	4934					
		01,02 (Colon, High Met vs. Colon, Low Met)	1	9		9.76
745	901					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		03,04 (Breast, High Met vs. Breast, Non-Met)	56	5	10.93	
746	452726					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	8	1	8.12	
747	725825					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	8	0	8.12	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	8		7.57
748	456808					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	7	42		5.68
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	42	1	42.65	
749	729295					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
750	551907					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	7	0	7.4	
751	551527					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	7		6.52
752	7098					
		03,04 (Breast, High Met vs. Breast, Non-Met)	10	0	9.76	
753	4589					
		01,02 (Colon, High Met vs. Colon, Low Met)	14	2	6.46	
754	554812					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	8		7.45
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	8		7.88
755	3114					
		03,04 (Breast, High Met vs. Breast, Non-Met)	9	1	8.78	
756	6031					
		01,02 (Colon, High Met vs. Colon, Low Met)	9	1	8.3	
757	185628					
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	6		6.15
758	24719					
		03,04 (Breast, High Met vs. Breast, Non-Met)	4	26		6.66
		21,22 (Normal Prostate vs. Prostate Cancer)	4	14		3.56
759	3428					
		03,04 (Breast, High Met vs. Breast, Non-Met)	20	0	19.51	
760	2676					
		01,02 (Colon, High Met vs. Colon, Low Met)	2	17		9.22
761	649148					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	8	0	8.59	

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
762	234605					
		23,24 (Normal Lung Tissue vs. Lung Tumor Tissue)	17	5	3.43	
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	39	14	2.83	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	32	14	2.45	
763	2224					
		03,04 (Breast, High Met vs. Breast, Non-Met)	44	8	5.37	
764	185642					
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	7		7.17
765	649655					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	12	0	12.19	
766	2854					
		03,04 (Breast, High Met vs. Breast, Non-Met)	31	3	10.08	
767	453470					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	12	1	12.68	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	12	1	12.88	
768	11012					
		01,02 (Colon, High Met vs. Colon, Low Met)	0	6		6.5
769	535208					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
770	448606					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	3	20		6.21
771	12304					
		03,04 (Breast, High Met vs. Breast, Non-Met)	5	17		3.48
772	2756					
		01,02 (Colon, High Met vs. Colon, Low Met)	28	8	3.23	
773	367					
		08,09 (Lung, High Met vs. Lung, Low Met)	30	99		2.36
		03,04 (Breast, High Met vs. Breast, Non-Met)	105	24	4.27	
		01,02 (Colon, High Met vs. Colon, Low Met)	19	97		5.53
		15,16 (Normal Colon vs. Colon Tumor Tissue)	13	4	3.44	
774	11351					
		01,02 (Colon, High Met vs. Colon, Low Met)	0	6		6.5
775	6858					
		01,02 (Colon, High Met vs. Colon, Low Met)	0	8		8.67
776	7750					
		03,04 (Breast, High Met vs. Breast, Non-Met)	1	14		14.35
777	6923					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		03,04 (Breast, High Met vs. Breast, Non-Met)	6	0	5.85	
778	11552					
		03,04 (Breast, High Met vs. Breast, Non-Met)	6	0	5.85	
779	12448					
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	7		7.17
781	10342					
		03,04 (Breast, High Met vs. Breast, Non-Met)	7	0	6.83	
782	9026					
		01,02 (Colon, High Met vs. Colon, Low Met)	7	0	6.46	
783	10342					
		03,04 (Breast, High Met vs. Breast, Non-Met)	7	0	6.83	
784	6455					
		03,04 (Breast, High Met vs. Breast, Non-Met)	6	0	5.85	
785	6455					
		03,04 (Breast, High Met vs. Breast, Non-Met)	6	0	5.85	
786	3416					
		01,02 (Colon, High Met vs. Colon, Low Met)	1	11		11.93
787	3416					
		01,02 (Colon, High Met vs. Colon, Low Met)	1	11		11.93
788	2889					
		01,02 (Colon, High Met vs. Colon, Low Met)	8	19		2.57
789	7393					
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	8		8.2
790	14390					
		03,04 (Breast, High Met vs. Breast, Non-Met)	2	43		22.04
791	661					
		03,04 (Breast, High Met vs. Breast, Non-Met)	77	10	7.51	
		08,09 (Lung, High Met vs. Lung, Low Met)	0	10		7.16
792	452992					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
793	1943					
		03,04 (Breast, High Met vs. Breast, Non-Met)	16	4	3.9	
		01,02 (Colon, High Met vs. Colon, Low Met)	9	29		3.49
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	19		3
794	2027					
		03,04 (Breast, High Met vs. Breast, Non-Met)	12	35		2.99
795	5482					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		01,02 (Colon, High Met vs. Colon, Low Met)	1	8		8.67
796	650493					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
797	640318					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
798	646309					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
799	4316					
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	6		6.15
800	449701					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	17	1	17.26	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	1	17		16.08
801	560367					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	9		8.51
802	9997					
		03,04 (Breast, High Met vs. Breast, Non-Met)	7	0	6.83	
803	649106					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
804	461835					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	7	0	7.4	
805	640590					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	9	0	9.66	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	9	1	9.51	
806	648340					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
807	554812					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	8		7.45
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	8		7.88
808	447035					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	8	1	8.12	
809	1208					
		03,04 (Breast, High Met vs. Breast, Non-Met)	13	0	12.68	
810	3114					
		03,04 (Breast, High Met vs. Breast, Non-Met)	9	1	8.78	
811	3114					
		03,04 (Breast, High Met vs. Breast, Non-Met)	9	1	8.78	
812	734078					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
813	450323					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	8		7.45
814	11567					
		03,04 (Breast, High Met vs. Breast, Non-Met)	7	0	6.83	
815	11567					
		03,04 (Breast, High Met vs. Breast, Non-Met)	7	0	6.83	
816	6660					
		01,02 (Colon, High Met vs. Colon, Low Met)	7	0	6.46	
817	9026					
		01,02 (Colon, High Met vs. Colon, Low Met)	7	0	6.46	
818	185539					
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	10		10.25
819	3224					
		01,02 (Colon, High Met vs. Colon, Low Met)	17	2	7.84	
820	95700					
		03,04 (Breast, High Met vs. Breast, Non-Met)	1	21		21.52
821	4439					
		08,09 (Lung, High Met vs. Lung, Low Met)	10	2	6.99	
		01,02 (Colon, High Met vs. Colon, Low Met)	15	2	6.92	
822	3428					
		03,04 (Breast, High Met vs. Breast, Non-Met)	20	0	19.51	
823	1456					
		01,02 (Colon, High Met vs. Colon, Low Met)	9	22		2.65
		03,04 (Breast, High Met vs. Breast, Non-Met)	50	9	5.42	
824	11343					
		01,02 (Colon, High Met vs. Colon, Low Met)	0	6		6.5
825	729206					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	10		9.46
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	10	0	10.16	
826	558371					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	10	2	5.28	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	10	2	5.37	
827	451589					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	7		6.52
828	404475					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	11	2	5.59	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	19	2	10.2	
829	734582					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
830	729779					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	8		7.57
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	8	0	8.12	
831	555244					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	11		10.83
832	449269					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	26	7	3.99	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	26	5	5.5	
833	4609					
		01,02 (Colon, High Met vs. Colon, Low Met)	2	12		6.5
834	640318					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
835	729851					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
836	11028					
		01,02 (Colon, High Met vs. Colon, Low Met)	0	6		6.5
837	643924					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
838	630259					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	7	0	7.4	
839	11286					
		01,02 (Colon, High Met vs. Colon, Low Met)	0	6		6.5
840	185651					
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	7		7.17
841	7379					
		01,02 (Colon, High Met vs. Colon, Low Met)	0	6		6.5
842	728408					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	12		11.35
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	12	0	12.19	
843	646309					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
844	405073					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
845	185489					
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	12		12.3
846	447326					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
847	11006					
		01,02 (Colon, High Met vs. Colon, Low Met)	0	6		6.5
848	6863					
		01,02 (Colon, High Met vs. Colon, Low Met)	1	8		8.67
849	11351					
		01,02 (Colon, High Met vs. Colon, Low Met)	0	6		6.5
850	401553					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	8	0	8.59	
851	504513					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
852	645979					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
853	6923					
		03,04 (Breast, High Met vs. Breast, Non-Met)	6	0	5.85	
854	1924					
		01,02 (Colon, High Met vs. Colon, Low Met)	8	21		2.85
855	5838					
		01,02 (Colon, High Met vs. Colon, Low Met)	1	9		9.76
856	2062					
		13,14 (bFGF Treated HMVEC vs. VEGF-Treated HMVEC) (bFGF Treated HMVEC vs. VEGF-Treated HMVEC)	0	7		6.88
		03,04 (Breast, High Met vs. Breast, Non-Met)	8	19		2.43
		01,02 (Colon, High Met vs. Colon, Low Met)	9	39		4.7
857	447388					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	142	4	38.1	
		18,19 (Normal Colon Tissue vs. Colon Tumor)	18	0	20.57	
		18,20 (Normal Colon Tissue vs. Colon Metastasis)	18	0	15.39	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	142	2	75.05	
858	12419					
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	15		15.37
859	3224					
		01,02 (Colon, High Met vs. Colon, Low Met)	17	2	7.84	

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
860	5474					
		03,04 (Breast, High Met vs. Breast, Non-Met)	5	17		3.48
		01,02 (Colon, High Met vs. Colon, Low Met)	1	8		8.67
861	3522					
		01,02 (Colon, High Met vs. Colon, Low Met)	3	12		4.34
862	731785					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
863	3765					
		01,02 (Colon, High Met vs. Colon, Low Met)	19	6	2.92	
864	640323					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	8	0	8.59	
865	379105					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	8		7.57
866	448029					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	10	1	10.16	
867	650476					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
868	640525					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	7	0	7.4	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
869	390124					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	18		2.79
		19,20 (Colon Tumor Tissue vs. Colon Metastasis)	8	0	5.98	
		18,19 (Normal Colon Tissue vs. Colon Tumor)	0	8		7
870	464029					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	9		8.86
871	468109					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
872	21669					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	7		6.89
873	651088					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
874	2737					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	3	14		4.6
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	4	14		3.26
875	556421					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		15,16 (Normal Colon vs. Colon Tumor Tissue)	12	1	12.68	
876	452245					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	12		11.82
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	1	12		11.18
877	447539					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	8	0	8.59	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	8	1	8.46	
878	546642					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	11	0	11.17	
879	236368					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	271	16	17.9	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	271	0	290.88	
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	16	0	16.25	
		18,19 (Normal Colon Tissue vs. Colon Tumor)	9	1	10.29	
		18,20 (Normal Colon Tissue vs. Colon Metastasis)	9	0	7.69	
880	644523					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
881	729173					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	8	0	8.12	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	8		7.57
882	8315					
		03,04 (Breast, High Met vs. Breast, Non-Met)	6	0	5.85	
883	450463					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	31	13	2.52	
884	650856					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
885	648109					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	8	1	8.46	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	8	0	8.59	
886	726644					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	18	0	18.28	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	18		17.03
887	727224					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	8	0	8.12	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	8		7.57
888	557906					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	12	3	4.23	
889	502683					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
890	728408					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	12		11.35
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	12	0	12.19	
891	647952					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
892	639991					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
893	735346					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
894	102655					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	14	0	14.8	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	14	0	15.03	
		03,04 (Breast, High.Met vs. Breast, Non-Met)	4	33		8.46
895	553629					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	4	17		4.19
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	4	17		3.96
896	1609					
		01,02 (Colon, High Met vs. Colon, Low Met)	3	58		20.96
		03,04 (Breast, High Met vs. Breast, Non-Met)	10	2	4.88	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	15	3	5.37	
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	14	3	4.74	
897	641884					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	8	0	8.59	
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
898	648872					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
899	644242					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
900	63559					
		03,04 (Breast, High Met vs. Breast, Non-Met)	2	12		6.15
901	550108					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	37		5.75
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	19		3
902	374306					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	1	10		9.32
903	5838					
		01,02 (Colon, High Met vs. Colon, Low Met)	1	9		9.76

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
904	645530					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	10	0	10.73	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	10	2	5.28	
905	649732					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
906	649143					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
907	7571					
		01,02 (Colon, High Met vs. Colon, Low Met)	0	8		8.67
908	4572					
		03,04 (Breast, High Met vs. Breast, Non-Met)	2	11		5.64
909	2147					
		01,02 (Colon, High Met vs. Colon, Low Met)	31	6	4.77	
		03,04 (Breast, High Met vs. Breast, Non-Met)	12	2	5.85	
910	462659					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	7	0	7.4	
911	727723					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
912	2636					
		08,09 (Lung, High Met vs. Lung, Low Met)	7	1	9.78	
		01,02 (Colon, High Met vs. Colon, Low Met)	8	19		2.57
913	500959					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	8	0	8.59	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	8	0	8.46	
914	3428					
		03,04 (Breast, High Met vs. Breast, Non-Met)	20	0	19.51	
915	734929					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
916	453592					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	19	6	3.35	
917	15414					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	1	9		8.38
918	648959					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	7	0	7.4	

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
919	453470					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	12	1	12.88	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	12	1	12.68	
920	649272					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	8	0	8.12	
921	1699					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	1	10		9.46
		03,04 (Breast, High Met vs. Breast, Non-Met)	37	12	3.01	
922	649719					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
923	562805					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
924	452204					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	8		7.88
		23,24 (Normal Lung Tissue vs. Lung Tumor Tissue)	3	13		4.29
		15,16 (Normal Colon vs. Colon Tumor Tissue)	9	1	9.51	
925	549178					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	10		9.85
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	1	10		9.32
926	639177					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
927	562550					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
928	561807					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	8		7.88
929	641373					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	15	0	16.1	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	15	3	5.28	
930	514418					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	9		8.86
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	1	9		8.38
931	567078					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	11	1	11.17	
932	643061					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	8	0	8.59	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	8	1	8.46	
933	549160					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	7		6.52
934	449269					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	26	7	3.99	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	26	5	5.5	
935	453082					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
936	418135					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	23		3.77
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	1	23		21.43
937	2783					
		01,02 (Colon, High Met vs. Colon, Low Met)	27	6	4.15	
		03,04 (Breast, High Met vs. Breast, Non-Met)	5	40		8.2
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
938	549435					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	14	2	7.4	
939	446614					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
940	449477					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	2	12		5.59
941	454380					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	3	14		4.42
942	450914					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
943	736860					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
944	727224					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	8		7.57
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	8	0	8.12	
945	644242					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
946	562550					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
947	649148					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	8	0	8.59	
948	375889					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	7		6.52
949	449437					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		15,16 (Normal Colon vs. Colon Tumor Tissue)	14	3	4.93	
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	3	12		3.94
950	449044					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	9	0	9.14	
951	555318					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	2	12		5.91
952	456764					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	10	1	10.16	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	14	1	15.03	
953	11567					
		03,04 (Breast, High Met vs. Breast, Non-Met)	7	0	6.83	
954	3522					
		01,02 (Colon, High Met vs. Colon, Low Met)	3	12		4.34
955	456528					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
956	639142					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	8	0	8.59	
957	446371					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
958	554742					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
959	448029					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	10	1	10.16	
960	551380					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	4	14		3.45
961	551527					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	7		6.52
962	729295					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
963	349744					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
964	648996					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
965	447126					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	19	5	4.02	

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	5	20		3.94
966	730866					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	8	0	8.12	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	8		7.57
967	420686					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	8		7.88
968	451753					
		23,24 (Normal Lung Tissue vs. Lung Tumor Tissue)	1	12		11.88
		15,16 (Normal Colon vs. Colon Tumor Tissue)	4	15		3.55
969	451380					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	20	7	3.02	
970	645530					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	10	2	5.28	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	10	0	10.73	
971	554703					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	9		8.86
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	9		8.38
972	562835					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	9		8.38
973	732764					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
974	556216					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	7		6.89
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	7		6.52
975	728779					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
976	414739					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	2	14		6.89
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	2	14		6.52
977	551514					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	13		12.8
		15,16 (Normal Colon vs. Colon Tumor Tissue)	8	1	8.46	
978	550107					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	36	14	2.72	
979	726786					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	8		7.57
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	8	0	8.12	
980	456747					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
981	562550					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
982	549722					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
983	640525					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	7	0	7.4	
984	455542					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
985	9436					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	4	15		3.69
986	380284					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	9	0	9.51	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	9	1	9.66	
987	556260					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
988	650476					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
989	554500					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
990	422375					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	2	11		5.12
991	456528					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
992	644190					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
993	554080					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	9		8.86
994	546705					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
995	558337					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
996	449269					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	26	7	3.99	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	26	5	5.5	
997	645799					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
998	456506					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	17	7	2.61	
999	218416					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
1000	455820					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	7		6.89
1001	554703					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	9		8.86
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	9		8.38
1002	650204					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	11	0	11.81	
1003	456808					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	7	42		5.68
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	42	1	42.65	
1004	420686					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	8		7.88
1005	378373					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	7		6.89
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	7		6.52
1006	463824					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
1007	24939					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	8		7.57
1008	556561					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	10		9.85
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	10		9.32
1009	380406					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	3	12		3.94
		15,16 (Normal Colon vs. Colon Tumor Tissue)	16	3	5.64	
1010	456764					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	14	1	15.03	
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	10	1	10.16	
1011	725703					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	9		8.51
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	9	0	9.14	
1012	185465					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		03,04 (Breast, High Met vs. Breast, Non-Met)	2	14		7.17
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	4	14		3.45
		23,24 (Normal Lung Tissue vs. Lung Tumor Tissue)	25	9	2.81	
1013	5830					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
1014	539955					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	24	0	24.37	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	11	0	11.81	
		23,24 (Normal Lung Tissue vs. Lung Tumor Tissue)	3	47		15.51
1015	640747					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
1016	500630					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
1017	448511					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	4	26		6.4
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	3	26		8.07
1018	405073					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
1019	641439					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
1020	406092					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	12	3	4.29	
1021	559806					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
1022	380284					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	9	0	9.51	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	9	1	9.66	
1023	560700					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
1024	552879					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	2	14		6.89
		15,16 (Normal Colon vs. Colon Tumor Tissue)	11	2	5.81	
1025	640590					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	9	0	9.66	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	9	1	9.51	
1026	641683					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	8	0	8.46	

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	8	0	8.59	
1027	648934					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	8	0	8.46	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	8	0	8.59	
1028	557948					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	11		10.83
1029	377094					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	10	2	5.28	
1030	449617					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	18		2.53
1031	978					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	67	20	3.6	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	67	28	2.53	
		03,04 (Breast, High Met vs. Breast, Non-Met)	78	23	3.31	
1032	607430					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
1033	641837					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	16	0	17.17	
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	31	0	31.48	
1034	449750					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	28		27.57
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	4	28		6.52
1035	646780					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	10	0	10.73	
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
1036	546642					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	11	0	11.17	
1037	642906					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
1038	552879					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	2	14		6.89
		15,16 (Normal Colon vs. Colon Tumor Tissue)	11	2	5.81	
1039	644205					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	7	0	7.4	
1040	506744					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	8		7.88
		15,16 (Normal Colon vs. Colon Tumor Tissue)	7	0	7.4	
1041	557797					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	3	16		5.25
1042	640356					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	10	0	10.73	
1043	462659					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	7	0	7.4	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
1044	645633					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
1045	237288					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	7	0	7.4	
1046	454343					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	10	0	10.16	
1047	386543					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	3	23		7.55
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	3	23		7.14
1048	446404					
		18,20 (Normal Colon Tissue vs. Colon Metastasis)	23	0	19.66	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	73	0	78.36	
		18,19 (Normal Colon Tissue vs. Colon Tumor)	23	0	26.28	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	73	1	77.16	
1049	456528					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
1050	456528					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
1051	452781					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	2	11		5.12
1052	551671					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	7		6.89
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	7		6.52
1053	644242					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
1054	561892					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	7		6.52
1055	450429					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	10	1	10.16	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	13	1	13.95	
1056	533588					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
1057	553877					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	8		7.88
1058	650195					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
1059	193486					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	7		6.52
1060	650195					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
1061	562835					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	9		8.38
1062	736816					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	9	0	9.14	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	9		8.51
1063	403632					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	2	11		5.12
1064	390124					
		18,19 (Normal Colon Tissue vs. Colon Tumor)	0	8		7
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	18		2.79
		19,20 (Colon Tumor Tissue vs. Colon Metastasis)	8	0	5.98	
1065	390124					
		18,19 (Normal Colon Tissue vs. Colon Tumor)	0	8		7
		19,20 (Colon Tumor Tissue vs. Colon Metastasis)	8	0	5.98	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	18		2.79
1066	422687					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	10		9.46
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	10	0	10.16	
1067	394413					
		18,19 (Normal Colon Tissue vs. Colon Tumor)	21	2	12	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	113	3	39.81	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	113	0	121.29	
		18,20 (Normal Colon Tissue vs. Colon Metastasis)	21	0	17.95	
1068	549178					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	10		9.85
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	1	10		9.32
1069	453079					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	8	1	8.12	
1070	463824					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
1071	736595					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
1072	102655					
		03,04 (Breast, High Met vs. Breast, Non-Met)	4	33		8.46
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	14	0	15.03	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	14	0	14.8	
1073	448606					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	3	20		6.21
1074	504513					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
1075	20036					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	1	13		12.11
1076	530883					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
1077	447126					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	19	5	4.02	
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	5	20		3.94
1078	556561					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	10		9.32
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	10		9.85
1079	455096					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	2	10		4.92
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	1	10		9.32
1080	549320					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	7		6.52
1081	560984					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
1082	450791					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	18	6	3.17	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	18	3	6.44	
1083	16556					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	12	3	4.23	
1084	402707					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	1	9		8.38
1085	557903					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	9		8.51

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
1086	451243					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	7		6.52
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
1087	452506					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	7	0	7.4	
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
1088	554703					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	9		8.38
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	9		8.86
1089	449580					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	16	4	4.23	
1090	3316					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
1091	97507					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	1	9		8.51
1092	556216					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	7		6.89
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	7		6.52
1093	185401					
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	63		64.57
1094	3758					
		03,04 (Breast, High Met vs. Breast, Non-Met)	17	5	3.32	
1095	95700					
		03,04 (Breast, High Met vs. Breast, Non-Met)	1	21		21.52
1096	2478					
		03,04 (Breast, High Met vs. Breast, Non-Met)	17	5	3.32	
1097	550267					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	15	4	4.03	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	15	1	15.85	
1098	185652					
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	7		7.17
1099	55798					
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	9		9.22
1100	5078					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
1101	9784					
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	6		6.15
1102	2245					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		03,04 (Breast, High Met vs. Breast, Non-Met)	13	1	12.68	
		01,02 (Colon, High Met vs. Colon, Low Met)	12	27		2.44
1103	11606					
		03,04 (Breast, High Met vs. Breast, Non-Met)	6	0	5.85	
1104	2245					
		03,04 (Breast, High Met vs. Breast, Non-Met)	13	1	12.68	
		01,02 (Colon, High Met vs. Colon, Low Met)	12	27		2.44
1105	551172					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	1	10		9.46
1106	729175					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
1107	6317					
		01,02 (Colon, High Met vs. Colon, Low Met)	0	6		6.5
1108	2478					
		03,04 (Breast, High Met vs. Breast, Non-Met)	17	5	3.32	
1109	4727					
		03,04 (Breast, High Met vs. Breast, Non-Met)	19	0	18.54	
1110	185598					
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	8		8.2
1111	736349					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
1113	189561					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	9		8.51
		08,09 (Lung, High Met vs. Lung, Low Met)	1	14		10.02
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	9		8.38
1114	728131					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
1115	560984					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
1116	549945					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	12	2	6.44	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	12	2	6.34	
1117	554785					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	8		7.88
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	8		7.45
1118	554785					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	8		7.45
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	8		7.88
1119	551235					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	7		6.89
1120	2634					
		03,04 (Breast, High Met vs. Breast, Non-Met)	48	0	46.83	
1121	548858					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	11		10.83
1122	15625					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	17	0	18.25	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	17	1	17.97	
1123	649259					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	7	0	7.4	
1124	550267					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	15	1	15.85	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	15	4	4.03	
1125	7436					
		03,04 (Breast, High Met vs. Breast, Non-Met)	9	1	8.78	
1126	451794					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	15	0	15.85	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	15	1	16.1	
1127	5744					
		01,02 (Colon, High Met vs. Colon, Low Met)	0	6		6.5
1128	3516					
		01,02 (Colon, High Met vs. Colon, Low Met)	5	17		3.69
1129	730555					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
1130	3085					
		03,04 (Breast, High Met vs. Breast, Non-Met)	2	11		5.64
1131	638854					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	32	11	3.07	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	32	0	34.35	
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	11	0	11.17	
1132	7379					
		01,02 (Colon, High Met vs. Colon, Low Met)	0	6		6.5
1133	185562					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	9		9.22
1134	452491					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	12	3	4.23	
1135	646248					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
1136	6056					
		03,04 (Breast, High Met vs. Breast, Non-Met)	7	0	6.83	
1137	643103					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	7	0	7.4	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
1138	6923					
		03,04 (Breast, High Met vs. Breast, Non-Met)	6	0	5.85	
1139	6923					
		03,04 (Breast, High Met vs. Breast, Non-Met)	6	0	5.85	
1140	901					
		03,04 (Breast, High Met vs. Breast, Non-Met)	56	5	10.93	
1141	901					
		03,04 (Breast, High Met vs. Breast, Non-Met)	56	5	10.93	
1142	367					
		08,09 (Lung, High Met vs. Lung, Low Met)	30	99		2.36
		15,16 (Normal Colon vs. Colon Tumor Tissue)	13	4	3.44	
		03,04 (Breast, High Met vs. Breast, Non-Met)	105	24	4.27	
		01,02 (Colon, High Met vs. Colon, Low Met)	19	97		5.53
1143	4043					
		01,02 (Colon, High Met vs. Colon, Low Met)	1	9		9.76
1144	3299					
		08,09 (Lung, High Met vs. Lung, Low Met)	10	1	13.97	
		03,04 (Breast, High Met vs. Breast, Non-Met)	20	3	6.5	
1145	11881					
		03,04 (Breast, High Met vs. Breast, Non-Met)	6	0	5.85	
1146	9113					
		01,02 (Colon, High Met vs. Colon, Low Met)	0	7		7.59
1147	185460					
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	16		16.4
1148	185716					
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	6		6.15
1149	5753					
		01,02 (Colon, High Met vs. Colon, Low Met)	0	10		10.84

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
1150	24939					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	8		7.57
1151	649684					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	10	0	10.73	
1152	642109					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
1153	15035					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	8	0	8.46	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	8	1	8.59	
1154	649354					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
1155	4465					
		01,02 (Colon, High Met vs. Colon, Low Met)	4	14		3.79
1156	647952					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
1157	455601					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	8	0	8.12	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	10	0	10.73	
1158	641901					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
1159	446878					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	12		11.82
1160	7436					
		03,04 (Breast, High Met vs. Breast, Non-Met)	9	1	8.78	
1161	2245					
		01,02 (Colon, High Met vs. Colon, Low Met)	12	27		2.44
		03,04 (Breast, High Met vs. Breast, Non-Met)	13	1	12.68	
1162	3531					
		01,02 (Colon, High Met vs. Colon, Low Met)	3	17		6.14
1163	9625					
		03,04 (Breast, High Met vs. Breast, Non-Met)	1	12		12.3
1164	727489					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	9	0	9.14	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	9		8.51
1165	159925					
		03,04 (Breast, High Met vs. Breast, Non-Met)	1	22		22.55

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
1166	645210					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	10	1	10.57	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	10	0	10.73	
1167	157629					
		03,04 (Breast, High Met vs. Breast, Non-Met)	3	18		6.15
1168	8375					
		03,04 (Breast, High Met vs. Breast, Non-Met)	7	0	6.83	
1169	4319					
		03,04 (Breast, High Met vs. Breast, Non-Met)	14	0	13.66	
		01,02 (Colon, High Met vs. Colon, Low Met)	0	6		6.5
1170	4045					
		01,02 (Colon, High Met vs. Colon, Low Met)	2	11		5.96
		03,04 (Breast, High Met vs. Breast, Non-Met)	10	1	9.76	
1171	185642					
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	7		7.17
1172	7436					
		03,04 (Breast, High Met vs. Breast, Non-Met)	9	1	8.78	
1173	3531					
		01,02 (Colon, High Met vs. Colon, Low Met)	3	17		6.14
1174	644776					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	9	0	9.14	
1175	8354					
		03,04 (Breast, High Met vs. Breast, Non-Met)	7	0	6.83	
1176	2099					
		03,04 (Breast, High Met vs. Breast, Non-Met)	27	7	3.76	
1177	449956					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	10	1	10.16	
1178	649106					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
1179	452414					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	17	0	17.97	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	17	0	18.25	
1180	732712					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
1181	185562					
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	9		9.22
1182	3516					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		01,02 (Colon, High Met vs. Colon, Low Met)	5	17		3.69
1183	185562					
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	9		9.22
1184	185460					
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	16		16.4
1185	10947					
		03,04 (Breast, High Met vs. Breast, Non-Met)	8	0	7.81	
1186	452856					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
1187	558767					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	8	1	8.46	
1188	15035					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	8	1	8.59	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	8	0	8.46	
1189	556421					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	12	1	12.68	
1190	7082					
		03,04 (Breast, High Met vs. Breast, Non-Met)	10	0	9.76	
1191	452523					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	10	2	5.37	
1192	3242					
		01,02 (Colon, High Met vs. Colon, Low Met)	2	17		9.22
1193	6660					
		01,02 (Colon, High Met vs. Colon, Low Met)	7	0	6.46	
1194	547					
		01,02 (Colon, High Met vs. Colon, Low Met)	35	67		2.08
		03,04 (Breast, High Met vs. Breast, Non-Met)	90	30	2.93	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	1	10		9.46
1195	121213					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	8	0	8.12	
1196	4378					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	2	11		5.42
		03,04 (Breast, High Met vs. Breast, Non-Met)	1	8		8.2
		15,16 (Normal Colon vs. Colon Tumor Tissue)	11	2	5.81	
1197	185554					
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	9		9.22
1198	185482					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	13		13.32
1200	66017					
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	8		8.2
1201	403111					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
1202	3224					
		01,02 (Colon, High Met vs. Colon, Low Met)	17	2	7.84	
1203	966					
		01,02 (Colon, High Met vs. Colon, Low Met)	22	47		2.32
		03,04 (Breast, High Met vs. Breast, Non-Met)	50	19	2.57	
1204	3639					
		03,04 (Breast, High Met vs. Breast, Non-Met)	12	3	3.9	
1205	5388					
		03,04 (Breast, High Met vs. Breast, Non-Met)	5	21		4.3
1206	3299					
		08,09 (Lung, High Met vs. Lung, Low Met)	10	1	13.97	
		03,04 (Breast, High Met vs. Breast, Non-Met)	20	3	6.5	
1207	23760					
		03,04 (Breast, High Met vs. Breast, Non-Met)	4	34		8.71
1208	729384					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
1209	46559					
		03,04 (Breast, High Met vs. Breast, Non-Met)	2	30		15.37
		15,16 (Normal Colon vs. Colon Tumor Tissue)	10	2	5.28	
1210	449750					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	4	28		6.52
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	28		27.57
1211	735936					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	9	0	9.14	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	9		8.51
1212	607430					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
1213	452856					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
1214	557903					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	9		8.51
1215	453112					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	3	13		4.27
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	3	13		4.04
1216	645900					
		23,24 (Normal Lung Tissue vs. Lung Tumor Tissue)	7	0	7.07	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	9	0	9.66	
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	9	0	9.14	
1217	415114					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	10	0	10.57	
1218	418763					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	9	0	9.66	
1219	2245					
		03,04 (Breast, High Met vs. Breast, Non-Met)	13	1	12.68	
		01,02 (Colon, High Met vs. Colon, Low Met)	12	27		2.44
1220	403668					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	13	3	4.4	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	2	13		6.15
1221	15427					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	7		6.52
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	8		7.57
1222	555714					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	23	11	2.21	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	23	7	3.53	
1223	555830					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	16	2	8.59	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	16	2	8.46	
1224	4620					
		03,04 (Breast, High Met vs. Breast, Non-Met)	7	0	6.83	
1225	171511					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
1226	451401					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	9	1	9.66	
1227	447501					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	15	3	5.37	
1228	460445					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
1229	375814					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	8	1	8.59	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	8	0	8.46	

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
1230	449356					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	21		2.79
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	4	21		5.17
1231	468736					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
1232	548858					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	11		10.83
1233	3693					
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	6		6.15
1234	642973					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
1235	561180					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	11	2	5.81	
1236	453708					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	19		18.71
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	1	19		17.7
1237	645305					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
1238	463487					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	8	1	8.59	
1239	11131					
		01,02 (Colon, High Met vs. Colon, Low Met)	0	6		6.5
1240	561807					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	8		7.88
1241	452800					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	3	13		4.04
1242	372960					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	18		2.79
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	33		5.2
1243	449317					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	5	20		3.73
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	8	20		2.46
1244	730759					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
1245	9113					
		01,02 (Colon, High Met vs. Colon, Low Met)	0	7		7.59
1246	630259					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		15,16 (Normal Colon vs. Colon Tumor Tissue)	7	0	7.4	
1247	3516					
		01,02 (Colon, High Met vs. Colon, Low Met)	5	17		3.69
1248	447494					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	26	8	3.44	
1249	554500					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
1250	639662					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	7	0	7.4	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
1251	421					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	7		6.52
1252	736014					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
1253	643061					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	8	0	8.59	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	8	1	8.46	
1254	9113					
		01,02 (Colon, High Met vs. Colon, Low Met)	0	7		7.59
1255	650856					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
1256	476223					
		23,24 (Normal Lung Tissue vs. Lung Tumor Tissue)	2	19		9.4
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
1257	737088					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
1258	449512					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	4	14		3.26
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	14		13.79
1259	449457					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	7		6.52
1260	521901					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
1261	175799					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	14	3	4.93	
		23,24 (Normal Lung Tissue vs. Lung Tumor Tissue)	1	9		8.91

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
1262	550108					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	19		3
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	37		5.75
1263	203605					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	17	7	2.57	
1264	450429					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	13	1	13.95	
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	10	1	10.16	
1265	2478					
		03,04 (Breast, High Met vs. Breast, Non-Met)	17	5	3.32	
1266	644099					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
1267	552614					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	7		6.89
1268	452523					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	10	2	5.37	
1269	446789					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	16	5	3.38	
1270	515631					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
1271	452523					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	10	2	5.37	
1272	640116					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	19	0	20.39	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	19	4	5.02	
1273	9113					
		01,02 (Colon, High Met vs. Colon, Low Met)	0	7		7.59
1274	562221					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	8	0	8.46	
1275	455972					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
1276	449137					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	3	18		5.68
1277	5078					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
1278	5078					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
1279	4016					
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	6		6.15
		01,02 (Colon, High Met vs. Colon, Low Met)	5	14		3.04
1280	403111					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
1281	562292					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
1282	403111					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
1283	403111					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
1284	500959					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	8	0	8.59	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	8	0	8.46	
1285	763					
		01,02 (Colon, High Met vs. Colon, Low Met)	29	77		2.88
		03,04 (Breast, High Met vs. Breast, Non-Met)	42	10	4.1	
1286	763					
		03,04 (Breast, High Met vs. Breast, Non-Met)	42	10	4.1	
		01,02 (Colon, High Met vs. Colon, Low Met)	29	77		2.88
1287	500959					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	8	0	8.59	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	8	0	8.46	
1288	452071					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	109	0	117	
		18,20 (Normal Colon Tissue vs. Colon Metastasis)	14	0	11.97	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	109	1	115.21	
		18,19 (Normal Colon Tissue vs. Colon Tumor)	14	0	16	
1289	468672					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	8		7.88
1290	455492					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	8	1	8.46	
1291	639667					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	9	0	9.14	
1292	549829					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
1293	553158					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	8		7.88
1294	561485					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	7		6.52
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	7		6.89
1295	639352					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	7	0	7.4	
1296	451401					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	9	1	9.66	
1297	643103					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	7	0	7.4	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
1298	468736					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
1299	218416					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
1300	447501					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	15	3	5.37	
1301	558371					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	10	2	5.37	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	10	2	5.28	
1302	561794					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
1303	645065					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
1304	451269					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	13	3	4.58	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	13	4	3.49	
1305	401553					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	8	0	8.59	
1306	555276					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
1307	551617					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	9	0	9.51	
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	7		6.89
1308	463480					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
1309	549178					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	1	10		9.32
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	10		9.85
1310	374450					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	7	0	7.4	
1311	562835					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	9		8.38
1312	730555					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
1313	732978					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
1314	1609					
		01,02 (Colon, High Met vs. Colon, Low Met)	3	58		20.96
		03,04 (Breast, High Met vs. Breast, Non-Met)	10	2	4.88	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	15	3	5.37	
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	14	3	4.74	
1315	18591					
		08,09 (Lung, High Met vs. Lung, Low Met)	8	0	11.18	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	30	8	3.96	
1316	553158					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	8		7.88
1317	470602					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	9		8.86
		15,16 (Normal Colon vs. Colon Tumor Tissue)	12	1	12.68	
1318	639662					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	7	0	7.4	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
1319	644721					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
1320	453202					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	11		10.83
1321	554655					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
1322	641988					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
1323	453112					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	3	13		4.27
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	3	13		4.04
1324	550694					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	21	1	22.2	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	21	7	3.22	
1325	649106					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
1326	638973					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	12	0	12.19	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
1327	549911					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
1328	648774					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
1329	549911					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
1330	639662					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	7	0	7.4	
1331	560455					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	7		6.52
1332	735805					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
1333	732712					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
1334	446663					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	14	32		2.13
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	32		5.25
		19,20 (Colon Tumor Tissue vs. Colon Metastasis)	0	8		10.7
		18,20 (Normal Colon Tissue vs. Colon Metastasis)	1	8		9.36
1335	226324					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
1336	453016					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
1337	550998					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
1338	452414					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	17	0	17.97	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	17	0	18.25	
1339	129535					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	41	1	44.01	
		08,09 (Lung, High Met vs. Lung, Low Met)	2	22		7.87
		15,16 (Normal Colon vs. Colon Tumor Tissue)	41	5	8.67	
1340	447089					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	8		7.88
1341	447850					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
1342	556216					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	7		6.52
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	7		6.89
1343	452523					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	10	2	5.37	
1344	44424					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	41	90		2.16
		08,09 (Lung, High Met vs. Lung, Low Met)	4	40		7.16
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	25	90		3.35
1345	648872					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
1346	451636					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	8		7.88
1347	5078					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
1348	403111					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
1349	648959					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	7	0	7.4	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
1350	380291					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
1351	380291					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
1352	230995					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
1353	562221					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	8	0	8.46	
1354	450959					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	1	9		8.51
1355	452833					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	7		6.52
1356	550195					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	11		10.83
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	2	11		5.12
1357	448927					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	2	12		5.59
1358	551514					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	13		12.8
		15,16 (Normal Colon vs. Colon Tumor Tissue)	8	1	8.46	
1359	549829					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
1360	551514					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	8	1	8.46	
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	13		12.8
1361	561485					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	7		6.89
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	7		6.52
1362	453846					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	11		10.25
1363	69863					
		08,09 (Lung, High Met vs. Lung, Low Met)	3	23		5.49
		03,04 (Breast, High Met vs. Breast, Non-Met)	3	21		7.17
1364	727181					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
1365	454050					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	8	1	8.59	
1366	725994					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
1367	1495					
		03,04 (Breast, High Met vs. Breast, Non-Met)	31	12	2.52	
1368	5665					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		03,04 (Breast, High Met vs. Breast, Non-Met)	13	0	12.68	
1369	5665					
		03,04 (Breast, High Met vs. Breast, Non-Met)	13	0	12.68	
1370	646146					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	8	0	8.59	
1371	8371					
		01,02 (Colon, High Met vs. Colon, Low Met)	0	6		6.5
1372	73812					
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	12		12.3
1373	4242					
		03,04 (Breast, High Met vs. Breast, Non-Met)	17	0	16.59	
1374	5482					
		01,02 (Colon, High Met vs. Colon, Low Met)	1	8		8.67
1375	5474					
		01,02 (Colon, High Met vs. Colon, Low Met)	1	8		8.67
		03,04 (Breast, High Met vs. Breast, Non-Met)	5	17		3.48
1376	5448					
		01,02 (Colon, High Met vs. Colon, Low Met)	1	10		10.84
1377	7607					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	13	3	4.65	
		01,02 (Colon, High Met vs. Colon, Low Met)	0	7		7.59
		15,16 (Normal Colon vs. Colon Tumor Tissue)	13	4	3.44	
1378	555928					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
1379	4046					
		01,02 (Colon, High Met vs. Colon, Low Met)	4	14		3.79
1380	554080					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	9		8.86
1381	451092					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	9		8.86
1382	551380					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	4	14		3.45
1383	546642					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	11	0	11.17	
1384	1764					
		03,04 (Breast, High Met vs. Breast, Non-Met)	27	4	6.59	
		01,02 (Colon, High Met vs. Colon, Low Met)	25	8	2.88	

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
1385	650773					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
1386	644205					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	7	0	7.4	
1387	185718					
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	6		6.15
1388	5538					
		01,02 (Colon, High Met vs. Colon, Low Met)	0	8		8.67
		03,04 (Breast, High Met vs. Breast, Non-Met)	6	0	5.85	
1389	7546					
		01,02 (Colon, High Met vs. Colon, Low Met)	8	0	7.38	
1390	727789					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
1391	3837					
		03,04 (Breast, High Met vs. Breast, Non-Met)	9	1	8.78	
1392	380477					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
1393	3299					
		03,04 (Breast, High Met vs. Breast, Non-Met)	20	3	6.5	
		08,09 (Lung, High Met vs. Lung, Low Met)	10	1	13.97	
1394	448853					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	1	10		9.46
1395	736701					
		23,24 (Normal Lung Tissue vs. Lung Tumor Tissue)	10	0	10.1	
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
1396	735296					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
1397	13666					
		03,04 (Breast, High Met vs. Breast, Non-Met)	1	9		9.22
1398	732712					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
1399	3765					
		01,02 (Colon, High Met vs. Colon, Low Met)	19	6	2.92	
1400	185596					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	8		8.2
1401	1943					
		03,04 (Breast, High Met vs. Breast, Non-Met)	16	4	3.9	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	19		3
		01,02 (Colon, High Met vs. Colon, Low Met)	9	29		3.49
1402	448193					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	10	2	5.08	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	1	10		9.46
1403	1793					
		01,02 (Colon, High Met vs. Colon, Low Met)	13	27		2.25
		03,04 (Breast, High Met vs. Breast, Non-Met)	35	13	2.63	
1404	2475					
		03,04 (Breast, High Met vs. Breast, Non-Met)	5	35		7.17
1405	730866					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	8	0	8.12	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	8		7.57
1406	730389					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	9		8.51
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	9	0	9.14	
1407	641884					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	8	0	8.59	
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
1408	463487					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	8	1	8.59	
1409	5156					
		01,02 (Colon, High Met vs. Colon, Low Met)	1	8		8.67
1410	728408					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	12		11.35
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	12	0	12.19	
1411	73812					
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	12		12.3
1412	1662					
		01,02 (Colon, High Met vs. Colon, Low Met)	7	34		5.27
		03,04 (Breast, High Met vs. Breast, Non-Met)	31	5	6.05	
1413	736556					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	8	0	8.12	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	8		7.57
1414	5240					
		08,09 (Lung, High Met vs. Lung, Low Met)	18	10	2.52	

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		03,04 (Breast, High Met vs. Breast, Non-Met)	12	2	5.85	
1415	6184					
		01,02 (Colon, High Met vs. Colon, Low Met)	0	8		8.67
1416	446404					
		18,19 (Normal Colon Tissue vs. Colon Tumor)	23	0	26.28	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	73	0	78.36	
		18,20 (Normal Colon Tissue vs. Colon Metastasis)	23	0	19.66	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	73	1	77.16	
1417	646825					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	10	0	10.73	
1418	734929					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
1419	648851					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
1420	640135					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	8	0	8.59	
1421	7443					
		03,04 (Breast, High Met vs. Breast, Non-Met)	9	0	8.78	
1422	454050					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	8	1	8.59	
1423	3765					
		01,02 (Colon, High Met vs. Colon, Low Met)	19	6	2.92	
1424	648320					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
1425	451269					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	13	4	3.49	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	13	3	4.58	
1426	535208					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
1427	728115					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
1428	5240					
		03,04 (Breast, High Met vs. Breast, Non-Met)	12	2	5.85	
		08,09 (Lung, High Met vs. Lung, Low Met)	18	10	2.52	
1429	909					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		08,09 (Lung, High Met vs. Lung, Low Met)	34	4	11.88	
		03,04 (Breast, High Met vs. Breast, Non-Met)	54	18	2.93	
1430	447697					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	2	11		5.2
1431	447737					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	19	6	3.35	
1432	651100					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
1433	735477					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
1434	3774					
		01,02 (Colon, High Met vs. Colon, Low Met)	1	12		13.01
1435	646146					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	8	0	8.59	
1436	643931					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
1437	463487					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	8	1	8.59	
1438	650097					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
1439	554469					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	24	3	8.59	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	24	8	3.17	
1440	476223					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
		23,24 (Normal Lung Tissue vs. Lung Tumor Tissue)	2	19		9.4
1441	8738					
		03,04 (Breast, High Met vs. Breast, Non-Met)	6	0	5.85	
1442	403978					
		23,24 (Normal Lung Tissue vs. Lung Tumor Tissue)	23	50		2.15
		15,16 (Normal Colon vs. Colon Tumor Tissue)	7	19		2.57
1443	185539					
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	10		10.25
1444	451811					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	10	2	5.37	
1445	140731					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
1446	734582					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
1447	463487					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	8	1	8.59	
1448	558719					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	18	6	3.17	
1449	21669					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	7		6.89
1450	470462					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
1451	3316					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
1452	553728					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	11		10.83
1453	736014					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
1454	237288					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	7	0	7.4	
1455	11141					
		01,02 (Colon, High Met vs. Colon, Low Met)	0	6		6.5
1456	556421					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	12	1	12.68	
1457	549435					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	14	2	7.4	
1458	448927					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	2	12		5.59
1459	379105					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	8		7.57
1460	552614					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	7		6.89
1461	470602					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	12	1	12.68	
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	9		8.86

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
1462	557039					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	2	16		7.88
		15,16 (Normal Colon vs. Colon Tumor Tissue)	11	2	5.81	
1463	549864					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
1464	449836					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	8	1	8.59	
1465	554812					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	8		7.88
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	8		7.45
1466	3316					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
1467	649852					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
1468	453592					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	19	6	3.35	
1469	455096					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	1	10		9.32
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	2	10		4.92
1470	446199					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	8		7.88
1471	558427					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	4	15		3.55
1472	450255					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
1473	452026					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	35	14	2.64	
1474	374971					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	8		7.88
		08,09 (Lung, High Met vs. Lung, Low Met)	0	16		11.45
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	8		7.45
1475	446404					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	73	0	78.36	
		18,20 (Normal Colon Tissue vs. Colon Metastasis)	23	0	19.66	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	73	1	77.16	
		18,19 (Normal Colon Tissue vs. Colon Tumor)	23	0	26.28	
1476	549591					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	24		3.38
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	2	24		11.18

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
1477	640135					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	8	0	8.59	
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
1478	646248					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
1479	639705					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	10	0	10.73	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	10	0	10.57	
1480	483084					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
1481	464029					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	9		8.86
1482	428005					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	8		7.45
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	8		7.88
1483	91178					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	7		6.52
1484	550571					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
1485	735028					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
1486	559409					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
1487	551172					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	1	10		9.46
1488	648872					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
1489	446404					
		18,19 (Normal Colon Tissue vs. Colon Tumor)	23	0	26.28	
		18,20 (Normal Colon Tissue vs. Colon Metastasis)	23	0	19.66	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	73	1	77.16	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	73	0	78.36	
1490	734063					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
1491	467991					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	7	0	7.4	

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
1492	454050					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	8	1	8.59	
1493	734646					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	14		13.25
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	14	0	14.22	
1494	450192					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	7		6.89
1495	403978					
		23,24 (Normal Lung Tissue vs. Lung Tumor Tissue)	23	50		2.15
		15,16 (Normal Colon vs. Colon Tumor Tissue)	7	19		2.57
1496	734209					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	9	0	9.14	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	9		8.51
1497	14805					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	2	10		4.92
1498	230995					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
1499	120049					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	10	2	5.37	
1500	642142					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	11	0	11.17	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	2	11		5.2
1501	403978					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	7	19		2.57
		23,24 (Normal Lung Tissue vs. Lung Tumor Tissue)	23	50		2.15
1502	386543					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	3	23		7.14
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	3	23		7.55
1503	379105					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	8		7.57
1504	450255					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
1505	730143					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
1506	734209					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	9		8.51
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	9	0	9.14	
1507	401553					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	8	0	8.59	
1508	72979					
		18,19 (Normal Colon Tissue vs. Colon Tumor)	1	36		31.5
		19,20 (Colon Tumor Tissue vs. Colon Metastasis)	36	4	6.73	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	46	311		6.3
		08,09 (Lung, High Met vs. Lung, Low Met)	18	0	25.15	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	46	193		3.97
1509	726307					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
1510	230995					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
1511	3524					
		01,02 (Colon, High Met vs. Colon, Low Met)	21	6	3.23	
1512	8112					
		03,04 (Breast, High Met vs. Breast, Non-Met)	8	0	7.81	
1513	5240					
		08,09 (Lung, High Met vs. Lung, Low Met)	18	10	2.52	
		03,04 (Breast, High Met vs. Breast, Non-Met)	12	2	5.85	
1514	447326					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
1515	2676					
		01,02 (Colon, High Met vs. Colon, Low Met)	2	17		9.22
1516	736701					
		23,24 (Normal Lung Tissue vs. Lung Tumor Tissue)	10	0	10.1	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
1517	736701					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
		23,24 (Normal Lung Tissue vs. Lung Tumor Tissue)	10	0	10.1	
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
1518	8371					
		01,02 (Colon, High Met vs. Colon, Low Met)	0	6		6.5
1520	185542					
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	10		10.25
1521	448046					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	12		11.18
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	3	12		3.94
1522	185422					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	32		32.8
1523	650448					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
1524	5753					
		01,02 (Colon, High Met vs. Colon, Low Met)	0	10		10.84
1526	1644					
		03,04 (Breast, High Met vs. Breast, Non-Met)	27	57		2.16
		01,02 (Colon, High Met vs. Colon, Low Met)	11	33		3.25
1527	4453					
		03,04 (Breast, High Met vs. Breast, Non-Met)	10	2	4.88	
1528	454152					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	11	3	3.88	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	11	1	11.81	
1529	9913					
		03,04 (Breast, High Met vs. Breast, Non-Met)	7	0	6.83	
1530	1350					
		01,02 (Colon, High Met vs. Colon, Low Met)	3	44		15.9
1531	188					
		03,04 (Breast, High Met vs. Breast, Non-Met)	129	309		2.46
		21,22 (Normal Prostate vs. Prostate Cancer)	71	166		2.38
1532	4471					
		03,04 (Breast, High Met vs. Breast, Non-Met)	10	1	9.76	
1533	2622					
		03,04 (Breast, High Met vs. Breast, Non-Met)	7	31		4.54
1534	185465					
		23,24 (Normal Lung Tissue vs. Lung Tumor Tissue)	25	9	2.81	
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	4	14		3.45
		03,04 (Breast, High Met vs. Breast, Non-Met)	2	14		7.17
1535	19205					
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	6		6.15
1536	185635					
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	7		7.17
1537	5289					
		03,04 (Breast, High Met vs. Breast, Non-Met)	19	2	9.27	
1538	779					
		01,02 (Colon, High Met vs. Colon, Low Met)	27	54		2.17
		03,04 (Breast, High Met vs. Breast, Non-Met)	60	22	2.66	
1539	779					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		01,02 (Colon, High Met vs. Colon, Low Met)	27	54		2.17
		03,04 (Breast, High Met vs. Breast, Non-Met)	60	22	2.66	
1540	5289					
		03,04 (Breast, High Met vs. Breast, Non-Met)	19	2	9.27	
1541	456808					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	7	42		5.68
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	42	1	42.65	
1543	546642					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	11	0	11.17	
1544	649732					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
1545	5240					
		03,04 (Breast, High Met vs. Breast, Non-Met)	12	2	5.85	
		08,09 (Lung, High Met vs. Lung, Low Met)	18	10	2.52	
1546	448046					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	12		11.18
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	3	12		3.94
1547	650476					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
1548	379341					
		08,09 (Lung, High Met vs. Lung, Low Met)	2	21		7.51
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	3	14		4.35
1549	401849					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	15		14.77
		15,16 (Normal Colon vs. Colon Tumor Tissue)	7	0	7.4	
1550	11452					
		01,02 (Colon, High Met vs. Colon, Low Met)	0	6		6.5
1551	185417					
		08,09 (Lung, High Met vs. Lung, Low Met)	8	56		5.01
		03,04 (Breast, High Met vs. Breast, Non-Met)	4	32		8.2
1552	4471					
		03,04 (Breast, High Met vs. Breast, Non-Met)	10	1	9.76	
1553	2557					
		01,02 (Colon, High Met vs. Colon, Low Met)	23	8	2.65	
1554	3656					
		01,02 (Colon, High Met vs. Colon, Low Met)	2	12		6.5
1555	2327					
		03,04 (Breast, High Met vs. Breast, Non-Met)	8	19		2.43
		08,09 (Lung, High Met vs. Lung, Low Met)	10	2	6.99	

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
1556	449026					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	10	2	5.37	
1557	730227					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
1558	650864					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	8	0	8.46	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	8	0	8.59	
1559	530774					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	5	16		2.98
1560	395341					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
1561	557906					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	12	3	4.23	
1562	452531					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	2	11		5.2
1563	559057					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	7		6.52
1564	448046					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	12		11.18
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	3	12		3.94
1565	553547					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
1566	4636					
		03,04 (Breast, High Met vs. Breast, Non-Met)	3	15		5.12
1567	455601					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	10	0	10.73	
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	8	0	8.12	
1568	172013					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
1569	552597					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	7		6.52
1570	446531					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
1571	639352					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	7	0	7.4	
1572	642604					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	10	0	10.73	
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	13	0	13.2	
1573	558534					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	7		6.89
1574	556421					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	12	1	12.68	
1575	735477					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
1576	640703					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	10	0	10.16	
1577	643878					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	8	0	8.59	
1578	557797					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	3	16		5.25
1579	557200					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	10		9.85
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	1	10		9.32
1580	729531					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
1581	734554					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
1582	418008					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	7		6.52
1583	558614					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	9		8.86
1584	452245					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	1	12		11.18
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	12		11.82
1585	449891					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	8	1	8.46	
1587	6162					
		03,04 (Breast, High Met vs. Breast, Non-Met)	13	0	12.68	
1588	6162					
		03,04 (Breast, High Met vs. Breast, Non-Met)	13	0	12.68	
1589	4809					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		08,09 (Lung, High Met vs. Lung, Low Met)	3	27		6.44
		01,02 (Colon, High Met vs. Colon, Low Met)	15	1	13.84	
1590	3926					
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	9		9.22
1591	185693					
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	6		6.15
1592	641683					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	8	0	8.59	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	8	0	8.46	
1593	11351					
		01,02 (Colon, High Met vs. Colon, Low Met)	0	6		6.5
1594	650864					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	8	0	8.59	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	8	0	8.46	
1595	460445					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
1596	447669					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	4	16		3.78
1597	227936					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	8		7.57
1598	639459					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	9	0	9.14	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	11	0	11.81	
1599	650195					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
1600	734793					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	9	0	9.14	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	9		8.51
1601	540787					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	7	0	7.4	
1602	400654					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	8		7.88
1603	731467					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
1604	4045					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		03,04 (Breast, High Met vs. Breast, Non-Met)	10	1	9.76	
		01,02 (Colon, High Met vs. Colon, Low Met)	2	11		5.96
1605	447669					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	4	16		3.78
1606	11351					
		01,02 (Colon, High Met vs. Colon, Low Met)	0	6		6.5
1607	648931					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	9	0	9.66	
1608	726786					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	8	0	8.12	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	8		7.57
1609	4508					
		01,02 (Colon, High Met vs. Colon, Low Met)	1	12		13.01
1610	415058					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
1611	450633					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	34	13	2.76	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	34	7	5.21	
1612	736955					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	13		12.3
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	13	0	13.2	
1613	729851					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
1614	2512					
		03,04 (Breast, High Met vs. Breast, Non-Met)	7	0	6.83	
1615	452704					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	10	1	10.57	
1616	4589					
		01,02 (Colon, High Met vs. Colon, Low Met)	14	2	6.46	
1617	4727					
		03,04 (Breast, High Met vs. Breast, Non-Met)	19	0	18.54	
1618	454380					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	3	14		4.42
1619	553912					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	7		6.89
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	7		6.52
1620	450004					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	13		12.3
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	13	2	6.6	
1621	448193					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	10	2	5.08	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	1	10		9.46
1622	549591					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	2	24		11.18
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	24		3.38
1623	448511					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	3	26		8.07
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	4	26		6.4
1624	335					
		13,14 (bFGF Treated HMVEC vs. VEGF-Treated HMVEC)	3	15		4.92
		15,16 (Normal Colon vs. Colon Tumor Tissue)	12	38		3
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	12	41		3.18
		18,19 (Normal Colon Tissue vs. Colon Tumor)	0	29		25.38
		19,20 (Colon Tumor Tissue vs. Colon Metastasis)	29	4	5.42	
		12,14 (Untreated HMVEC vs. VEGF-Treated HMVEC) (Untreated HMVEC vs. VEGF-Treated HMVEC)	1	15		14.69
1625	561382					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	12	2	6.34	
1626	3447					
		08,09 (Lung, High Met vs. Lung, Low Met)	0	13		9.3
		01,02 (Colon, High Met vs. Colon, Low Met)	2	16		8.67
1627	639896					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	8	0	8.12	
1628	1353					
		01,02 (Colon, High Met vs. Colon, Low Met)	39	13	2.77	
		03,04 (Breast, High Met vs. Breast, Non-Met)	37	17	2.12	
1629	3031					
		01,02 (Colon, High Met vs. Colon, Low Met)	7	18		2.79
1630	557928					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
1631	4727					
		03,04 (Breast, High Met vs. Breast, Non-Met)	19	0	18.54	
1632	4046					
		01,02 (Colon, High Met vs. Colon, Low Met)	4	14		3.79
1633	10882					
		03,04 (Breast, High Met vs. Breast, Non-Met)	6	20		3.42
1634	646283					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	9	0	9.66	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	9	0	9.51	
1635	646283					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	9	0	9.51	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	9	0	9.66	
1636	139516					
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	7		7.17
1637	6184					
		01,02 (Colon, High Met vs. Colon, Low Met)	0	8		8.67
1638	6184					
		01,02 (Colon, High Met vs. Colon, Low Met)	0	8		8.67
1639	454653					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	5	17		3.35
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	3	17		5.28
1640	3309					
		03,04 (Breast, High Met vs. Breast, Non-Met)	9	0	8.78	
		08,09 (Lung, High Met vs. Lung, Low Met)	10	38		2.72
1641	1037					
		03,04 (Breast, High Met vs. Breast, Non-Met)	4	22		5.64
1642	450665					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
1643	726307					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
1644	447669					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	4	16		3.78
1645	639651					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
1646	736860					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
1647	553705					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	12	0	12.68	
1648	451375					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	2	11		5.2
1649	204862					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
1650	530883					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
1651	447539					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	8	1	8.46	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	8	0	8.59	
1652	455096					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	2	10		4.92
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	1	10		9.32
1654	449142					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	9	1	9.14	
1655	557401					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	10	2	5.37	
1656	418763					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	9	0	9.66	
1657	17649					
		03,04 (Breast, High Met vs. Breast, Non-Met)	6	0	5.85	
1658	2078					
		03,04 (Breast, High Met vs. Breast, Non-Met)	11	2	5.37	
1659	640370					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
1660	449269					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	26	7	3.99	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	26	5	5.5	
1661	639029					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
1662	448677					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	11	1	11.63	
1663	349					
		01,02 (Colon, High Met vs. Colon, Low Met)	69	138		2.17
		03,04 (Breast, High Met vs. Breast, Non-Met)	77	1	75.13	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	7		6.52
1664	447494					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	26	8	3.44	
1665	551433					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	8		7.88
1666	414739					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	2	14		6.52
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	2	14		6.89
1667	640525					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	7	0	7.4	
1668	640525					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	7	0	7.4	
1669	233108					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	11	0	11.81	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	11	0	11.63	
1670	643594					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	7	0	7.4	
1671	1642					
		03,04 (Breast, High Met vs. Breast, Non-Met)	28	5	5.46	
1672	643804					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
1673	449701					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	1	17		16.08
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	17	1	17.26	
1674	185695					
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	6		6.15
1675	555830					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	16	2	8.46	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	16	2	8.59	
1676	227936					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	8		7.57
1677	1609					
		01,02 (Colon, High Met vs. Colon, Low Met)	3	58		20.96
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	15	3	5.37	
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	14	3	4.74	
		03,04 (Breast, High Met vs. Breast, Non-Met)	10	2	4.88	
1678	643938					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	7	0	7.4	
1679	3656					
		01,02 (Colon, High Met vs. Colon, Low Met)	2	12		6.5
1680	16576					
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	8		8.2
1681	9784					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	6		6.15
1682	2557					
		01,02 (Colon, High Met vs. Colon, Low Met)	23	8	2.65	
1683	4620					
		03,04 (Breast, High Met vs. Breast, Non-Met)	7	0	6.83	
1684	43642					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
1685	555103					
		23,24 (Normal Lung Tissue vs. Lung Tumor Tissue)	0	6		5.94
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	7		6.52
1686	643341					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	8	0	8.46	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	8	0	8.59	
1687	185531					
		03,04 (Breast, High Met vs. Breast, Non-Met)	1	9		9.22
		08,09 (Lung, High Met vs. Lung, Low Met)	0	13		9.3
1688	4045					
		01,02 (Colon, High Met vs. Colon, Low Met)	2	11		5.96
		03,04 (Breast, High Met vs. Breast, Non-Met)	10	1	9.76	
1689	400258					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
1690	96618					
		03,04 (Breast, High Met vs. Breast, Non-Met)	4	13		3.33
1691	646060					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	13	0	13.95	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	13	3	4.58	
1692	5665					
		03,04 (Breast, High Met vs. Breast, Non-Met)	13	0	12.68	
1693	149265					
		03,04 (Breast, High Met vs. Breast, Non-Met)	1	16		16.4
1694	727314					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
1695	736349					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
1696	648931					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	9	0	9.66	
1697	553881					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		15,16 (Normal Colon vs. Colon Tumor Tissue)	15	4	3.96	
1698	7444					
		03,04 (Breast, High Met vs. Breast, Non-Met)	9	0	8.78	
1699	150					
		03,04 (Breast, High Met vs. Breast, Non-Met)	51	24	2.07	
		08,09 (Lung, High Met vs. Lung, Low Met)	5	0	6.99	
1700	2889					
		01,02 (Colon, High Met vs. Colon, Low Met)	8	19		2.57
1701	730670					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
1702	560984					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
1703	453708					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	19		18.71
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	1	19		17.7
1704	48977					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	8		7.45
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	8		7.88
1707	97507					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	1	9		8.51
1708	735966					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
		23,24 (Normal Lung Tissue vs. Lung Tumor Tissue)	7	0	7.07	
1709	35					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	2	12		5.59
		03,04 (Breast, High Met vs. Breast, Non-Met)	386	1967		5.22
		08,09 (Lung, High Met vs. Lung, Low Met)	868	11	110.27	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	2	14		6.62
1710	650195					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
1711	639705					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	10	0	10.57	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	10	0	10.73	
1712	185465					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	4	14		3.45
		03,04 (Breast, High Met vs. Breast, Non-Met)	2	14		7.17
		23,24 (Normal Lung Tissue vs. Lung Tumor Tissue)	25	9	2.81	

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
1713	378525					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	9	1	9.14	
1714	2889					
		01,02 (Colon, High Met vs. Colon, Low Met)	8	19		2.57
1715	557686					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
1716	735786					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
1717	455145					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
1718	639667					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	9	0	9.14	
1719	446913					
		18,19 (Normal Colon Tissue vs. Colon Tumor)	10	0	11.43	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	63	0	67.62	
		18,20 (Normal Colon Tissue vs. Colon Metastasis)	10	0	8.55	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	63	1	66.59	
1720	402494					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	3	13		4.1
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	13	3	4.4	
1721	734256					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
1722	734256					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
1723	559362					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	8		7.88
1724	639651					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
1725	419774					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	2	12		5.59
1726	555318					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	2	12		5.91
1727	449956					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	10	1	10.16	
1728	558427					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		15,16 (Normal Colon vs. Colon Tumor Tissue)	4	15		3.55
1729	7531					
		01,02 (Colon, High Met vs. Colon, Low Met)	1	8		8.67
1730	446514					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	8	1	8.12	
1731	456808					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	42	1	42.65	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	7	42		5.68
1732	447035					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	8	1	8.12	
1733	446913					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	63	1	66.59	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	63	0	67.62	
		18,19 (Normal Colon Tissue vs. Colon Tumor)	10	0	11.43	
		18,20 (Normal Colon Tissue vs. Colon Metastasis)	10	0	8.55	
1734	446900					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	2	11		5.42
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	1	11		10.25
1735	504513					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
1736	380477					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
1738	8259					
		01,02 (Colon, High Met vs. Colon, Low Met)	10	0	9.22	
		08,09 (Lung, High Met vs. Lung, Low Met)	13	49		2.7
1739	8259					
		01,02 (Colon, High Met vs. Colon, Low Met)	10	0	9.22	
		08,09 (Lung, High Met vs. Lung, Low Met)	13	49		2.7
1740	552968					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	9		8.86
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	9		8.38
1741	650845					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
1742	648594					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	10	0	10.73	
1743	648594					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	10	0	10.73	
1744	2796					
		03,04 (Breast, High Met vs. Breast, Non-Met)	8	37		4.74

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
1745	5753					
		01,02 (Colon, High Met vs. Colon, Low Met)	0	10		10.84
1746	734256					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
1747	449580					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	16	4	4.23	
1748	553705					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	12	0	12.68	
1749	730670					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
1750	15035					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	8	0	8.46	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	8	1	8.59	
1751	394436					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
1752	726810					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
1753	352763					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	10		9.85
1754	3506					
		03,04 (Breast, High Met vs. Breast, Non-Met)	1	10		10.25
1755	726377					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
1756	562111					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	2	13		6.4
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	2	13		6.06
1757	404475					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	11	2	5.59	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	19	2	10.2	
1758	13824					
		03,04 (Breast, High Met vs. Breast, Non-Met)	6	0	5.85	
1759	558222					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
1760	2834					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		01,02 (Colon, High Met vs. Colon, Low Met)	8	22		2.98
1761	453470					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	12	1	12.68	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	12	1	12.88	
1762	558682					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	3	12		3.94
1763	641710					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
1764	640221					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	8	0	8.59	
1765	559057					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	7		6.52
1766	551433					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	8		7.88
1767	5729					
		01,02 (Colon, High Met vs. Colon, Low Met)	1	10		10.84
1768	352763					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	10		9.85
1769	375651					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	8	0	8.12	
1770	644032					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	124	0	125.92	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	7	124		16.76
1771	185562					
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	9		9.22
1772	736349					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
1773	638870					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	11	0	11.17	
1774	649719					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
1775	62016					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
1776	2889					
		01,02 (Colon, High Met vs. Colon, Low Met)	8	19		2.57
1777	647135					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
1778	8283					
		01,02 (Colon, High Met vs. Colon, Low Met)	0	8		8.67
1779	732121					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
1780	532307					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	7		6.89
1781	6589					
		01,02 (Colon, High Met vs. Colon, Low Met)	1	9		9.76
1782	554678					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	10	2	5.28	
1783	450410					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	7		6.89
1784	643924					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
1785	453719					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	9		8.86
1786	451811					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	10	2	5.37	
1787	453059					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	9	0	9.66	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	9	1	9.51	
1788	453457					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	8		7.88
1789	558454					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	7		6.52
1790	417467					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	7		6.52
1791	447850					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
1792	557948					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	11		10.83
1793	452685					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	15	5	3.17	
1794	446964					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	1	10		9.32
1795	550318					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	15	3	5.28	
1796	407077					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	8		7.45
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	8		7.88
1797	650864					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	8	0	8.46	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	8	0	8.59	
1798	644721					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
1799	485431					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
1800	651073					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	7	0	7.4	
1801	725811					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
1802	645139					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	9	0	9.14	
1803	185478					
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	14		14.35
1804	1441					
		01,02 (Colon, High Met vs. Colon, Low Met)	9	40		4.82
		03,04 (Breast, High Met vs. Breast, Non-Met)	38	16	2.32	
1805	640005					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	20	6	3.52	
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	20	0	21.47	
1806	728273					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
1807	185579					
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	8		8.2
1808	724473					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
		21,22 (Normal Prostate vs. Prostate Cancer)	5	16		3.25

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
1809	559674					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	7		6.52
1810	456026					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	24	4	6.34	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	24	8	3.22	
1811	549320					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	7		6.52
1812	447338					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
1813	560700					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
1814	3070					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
1815	3070					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
1816	380477					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
1817	735040					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
1818	378525					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	9	1	9.14	
1819	284586					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
1820	640276					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	8	0	8.12	
1821	3344					
		01,02 (Colon, High Met vs. Colon, Low Met)	7	17		2.63
1822	555830					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	16	2	8.46	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	16	2	8.59	
1823	726307					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
1824	416					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	8	23		2.72
		21,22 (Normal Prostate vs. Prostate Cancer)	11	31		2.87
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	8	22		2.56

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
1825	2543					
		01,02 (Colon, High Met vs. Colon, Low Met)	23	7	3.03	
1826	639352					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	7	0	7.4	
1827	453592					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	19	6	3.35	
1828	450633					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	34	13	2.76	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	34	7	5.21	
1829	448383					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	13	1	13.95	
1830	648719					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	9	0	9.66	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	9	1	9.51	
1831	730655					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
1832	141185					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	8	0	8.46	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	8	0	8.59	
1833	640498					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
1834	9029					
		01,02 (Colon, High Met vs. Colon, Low Met)	7	0	6.46	
1835	559674					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	7		6.52
1836	555734					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	10		9.32
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	10		9.85
1837	1943					
		03,04 (Breast, High Met vs. Breast, Non-Met)	16	4	3.9	
		01,02 (Colon, High Met vs. Colon, Low Met)	9	29		3.49
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	19		3
1838	648320					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
1839	558098					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
1840	468672					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	8		7.88
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
1841	456596					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	12		11.82
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	2	12		5.59
1842	649722					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	8	0	8.59	
1843	550708					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	8		7.88
1844	643931					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
1845	726927					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	11	0	11.17	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	11		10.41
1846	459012					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
1847	397773					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	12	0	12.88	
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	9	0	9.14	
1848	450004					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	13		12.3
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	13	2	6.6	
1849	649732					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
1850	553955					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
1851	646309					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
1852	402727					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	5	17		3.17
1853	468736					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
1854	650422					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	18	6	3.17	
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	18	0	19.32	

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
1855	730533					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
1856	726307					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
1857	450311					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	8	1	8.46	
1858	450940					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	1	9		8.38
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	9		8.86
1859	726786					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	8		7.57
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	8	0	8.12	
1860	7634					
		03,04 (Breast, High Met vs. Breast, Non-Met)	6	0	5.85	
1861	230995					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
1862	374770					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	8	0	8.59	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	8	0	8.46	
1863	9275					
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	6		6.15
1864	553860					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	9		8.38
1865	452010					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	13	3	4.4	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	3	13		4.1
1866	649560					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
1867	452704					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	10	1	10.57	
1868	447594					
		18,19 (Normal Colon Tissue vs. Colon Tumor)	11	2	6.29	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	20		3.11
1869	555444					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	22	4	5.59	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	2	22		10.41
1870	736556					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	8	0	8.12	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	8		7.57
1871	5289					
		03,04 (Breast, High Met vs. Breast, Non-Met)	19	2	9.27	
1872	732121					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
1873	452567					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	3	14		4.6
		15,16 (Normal Colon vs. Colon Tumor Tissue)	21	3	7.4	
1874	551634					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
1875	644099					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
1876	726788					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
1877	638802					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
1878	646283					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	9	0	9.66	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	9	0	9.51	
1879	8403					
		03,04 (Breast, High Met vs. Breast, Non-Met)	6	0	5.85	
1880	2224					
		03,04 (Breast, High Met vs. Breast, Non-Met)	44	8	5.37	
1881	650053					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	10	0	10.73	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	10	1	10.57	
1882	380477					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
1883	450867					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	7	0	7.4	
1884	456764					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	10	1	10.16	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	14	1	15.03	
1885	641373					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	15	3	5.28	

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	15	0	16.1	
1886	555882					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	9		8.86
1887	644046					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	9	0	9.66	
1888	447250					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
1889	456596					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	2	12		5.59
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	12		11.82
1890	2218					
		01,02 (Colon, High Met vs. Colon, Low Met)	2	21		11.38
		03,04 (Breast, High Met vs. Breast, Non-Met)	27	8	3.29	
		08,09 (Lung, High Met vs. Lung, Low Met)	5	0	6.99	
1891	446450					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	11	3	3.88	
1892	640889					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
1893	530774					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	5	16		2.98
1894	649062					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
1895	12808					
		03,04 (Breast, High Met vs. Breast, Non-Met)	6	0	5.85	
1896	468672					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	8		7.88
1897	650773					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
1898	732237					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
1899	650773					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
1900	550216					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	7		6.52
1901	639189					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
1902	3447					
		01,02 (Colon, High Met vs. Colon, Low Met)	2	16		8.67
		08,09 (Lung, High Met vs. Lung, Low Met)	0	13		9.3
1903	2012					
		03,04 (Breast, High Met vs. Breast, Non-Met)	20	58		2.97
		01,02 (Colon, High Met vs. Colon, Low Met)	13	29		2.42
1904	642876					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	10	0	10.73	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	10	2	5.28	
1905	449690					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	3	17		5.58
1906	451208					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	14	3	5.01	
1907	725811					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
1908	1256					
		08,09 (Lung, High Met vs. Lung, Low Met)	35	110		2.25
		03,04 (Breast, High Met vs. Breast, Non-Met)	14	31		2.27
1909	446599					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	13	2	6.87	
1910	446537					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	9	1	9.51	
1911	726281					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
1912	11286					
		01,02 (Colon, High Met vs. Colon, Low Met)	0	6		6.5
1913	556082					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	10		9.85
1914	97507					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	1	9		8.51
1915	535955					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	10		9.85
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	1	10		9.32
1916	728251					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
1917	733849					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
1918	447574					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
1919	7607					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	13	3	4.65	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	13	4	3.44	
		01,02 (Colon, High Met vs. Colon, Low Met)	0	7		7.59
1920	644032					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	7	124		16.76
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	124	0	125.92	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
1921	454087					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	14	3	4.93	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	14	1	15.03	
1922	412364					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
1923	535208					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
1924	644609					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
1925	645073					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
1926	417467					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	7		6.52
1927	554188					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
1928	647185					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
1929	736679					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
1930	553547					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
1931	641524					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
1932	649717					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
1933	451041					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
1934	3483					
		01,02 (Colon, High Met vs. Colon, Low Met)	3	20		7.23
1935	500959					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	8	0	8.46	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	8	0	8.59	
1936	500959					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	8	0	8.46	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	8	0	8.59	
1937	697					
		03,04 (Breast, High Met vs. Breast, Non-Met)	30	72		2.46
		21,22 (Normal Prostate vs. Prostate Cancer)	10	2	4.92	
1938	736955					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	13	0	13.2	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	13		12.3
1939	554742					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
1940	642973					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
1941	449437					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	14	3	4.93	
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	3	12		3.94
1942	467991					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	7	0	7.4	
1943	650204					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	11	0	11.81	
1944	640618					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
1945	452366					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
1946	640276					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	8	0	8.12	
1947	554101					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
1948	185432					
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	26		26.65
1949	455598					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
1950	649354					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
1951	4408					
		03,04 (Breast, High Met vs. Breast, Non-Met)	4	17		4.36
		08,09 (Lung, High Met vs. Lung, Low Met)	21	3	9.78	
1952	452366					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
1953	452366					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
1954	727331					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
1955	644853					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
1956	554079					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	2	10		4.92
1957	556245					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
1958	557388					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	13	2	6.6	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	13		12.3
1959	449468					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	2	11		5.12
1960	556245					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
1961	455327					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	1	12		11.18
		15,16 (Normal Colon vs. Colon Tumor Tissue)	1	10		9.46
1962	546632					
		23,24 (Normal Lung Tissue vs. Lung Tumor Tissue)	3	34		11.22

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	15	0	15.23	
1963	558762					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	7		6.89
1964	550818					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	8		7.88
1965	554079					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	2	10		4.92
1966	452430					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
1967	452430					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
1968	556082					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	10		9.85
1969	514418					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	9		8.86
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	1	9		8.38
1970	426895					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	2	18		8.38
1971	560803					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	7		6.89
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	7		6.52
1972	447737					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	19	6	3.35	
1973	373432					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	23	78		3.16
		15,16 (Normal Colon vs. Colon Tumor Tissue)	23	53		2.18
		08,09 (Lung, High Met vs. Lung, Low Met)	3	49		11.69
1974	779					
		03,04 (Breast, High Met vs. Breast, Non-Met)	60	22	2.66	
		01,02 (Colon, High Met vs. Colon, Low Met)	27	54		2.17
1975	455327					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	1	10		9.46
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	1	12		11.18
1976	554742					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
1977	455327					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	1	10		9.46
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	1	12		11.18
1978	11043					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		01,02 (Colon, High Met vs. Colon, Low Met)	0	6		6.5
1979	727447					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
1980	552905					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	7		6.52
1981	446900					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	2	11		5.42
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	1	11		10.25
1982	644190					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
1983	455327					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	1	10		9.46
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	1	12		11.18
1984	422375					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	2	11		5.12
1985	422375					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	2	11		5.12
1986	530774					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	5	16		2.98
1987	554101					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
1988	5268					
		01,02 (Colon, High Met vs. Colon, Low Met)	0	15		16.26
1989	642461					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	14	0	15.03	
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	10	0	10.16	
1990	770					
		03,04 (Breast, High Met vs. Breast, Non-Met)	47	9	5.1	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	11	1	11.81	
1991	3837					
		03,04 (Breast, High Met vs. Breast, Non-Met)	9	1	8.78	
1992	561382					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	12	2	6.34	
1993	4408					
		08,09 (Lung, High Met vs. Lung, Low Met)	21	3	9.78	
		03,04 (Breast, High Met vs. Breast, Non-Met)	4	17		4.36
1994	5686					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		03,04 (Breast, High Met vs. Breast, Non-Met)	16	3	5.2	
1995	374609					
		21,22 (Normal Prostate vs. Prostate Cancer)	1	9		9.15
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
1996	734793					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	9	0	9.14	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	9		8.51
1997	452430					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
1998	450940					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	9		8.86
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	1	9		8.38
1999	460445					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
2000	549041					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
2001	555276					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
2002	426895					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	2	18		8.38
2003	1833					
		01,02 (Colon, High Met vs. Colon, Low Met)	9	25		3.01
2004	446450					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	11	3	3.88	
2005	650517					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
2006	554785					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	8		7.88
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	8		7.45
2007	607430					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
2008	446673					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	8	1	8.12	
2009	734685					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
2010	11630					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		21,22 (Normal Prostate vs. Prostate Cancer)	1	12		12.2
		03,04 (Breast, High Met vs. Breast, Non-Met)	3	13		4.44
2011	2930					
		01,02 (Colon, High Met vs. Colon, Low Met)	3	14		5.06
2012	44424					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	41	90		2.16
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	25	90		3.35
		08,09 (Lung, High Met vs. Lung, Low Met)	4	40		7.16
2013	452052					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	8	1	8.59	
2014	449356					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	21		2.79
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	4	21		5.17
2015	726225					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
2016	453708					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	19		18.71
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	1	19		17.7
2017	447858					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	12	3	4.23	
2018	451613					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	4	14		3.26
2019	650337					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
2020	62016					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
2021	447250					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
2022	3837					
		03,04 (Breast, High Met vs. Breast, Non-Met)	9	1	8.78	
2023	640614					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	13	0	13.2	
2024	729531					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
2025	729531					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
2026	647952					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
2027	446913					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	63	1	66.59	
		18,20 (Normal Colon Tissue vs. Colon Metastasis)	10	0	8.55	
		18,19 (Normal Colon Tissue vs. Colon Tumor)	10	0	11.43	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	63	0	67.62	
2028	2675					
		03,04 (Breast, High Met vs. Breast, Non-Met)	12	2	5.85	
2029	643481					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
2030	1345					
		21,22 (Normal Prostate vs. Prostate Cancer)	18	6	2.95	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
		08,09 (Lung, High Met vs. Lung, Low Met)	44	27	2.28	
		03,04 (Breast, High Met vs. Breast, Non-Met)	25	11	2.22	
2031	26					
		03,04 (Breast, High Met vs. Breast, Non-Met)	62	0	60.49	
		01,02 (Colon, High Met vs. Colon, Low Met)	0	28		30.36
2032	945					
		01,02 (Colon, High Met vs. Colon, Low Met)	10	21		2.28
2033	449169					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	16	2	8.46	
2034	394193					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
2035	452212					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
2036	394193					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
2037	1310					
		03,04 (Breast, High Met vs. Breast, Non-Met)	42	16	2.56	
		21,22 (Normal Prostate vs. Prostate Cancer)	15	2	7.38	
2038	734094					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	8	0	8.12	
		23,24 (Normal Lung Tissue vs. Lung Tumor Tissue)	6	0	6.06	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	8		7.57
2039	646579					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
2040	4471					
		03,04 (Breast, High Met vs. Breast, Non-Met)	10	1	9.76	
2041	729173					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	8	0	8.12	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	8		7.57
2042	450323					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	8		7.45
2043	4652					
		03,04 (Breast, High Met vs. Breast, Non-Met)	16	2	7.81	
2044	553316					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	12	3	4.23	
2045	642604					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	10	0	10.73	
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	13	0	13.2	
2046	553316					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	12	3	4.23	
2047	4097					
		03,04 (Breast, High Met vs. Breast, Non-Met)	20	43		2.2
2048	6818					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	24	8	3.22	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	24	10	2.54	
2049	395341					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
2050	649143					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
2051	649143					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
2052	648310					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
2053	447574					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
2054	648931					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	9	0	9.66	
2055	6878					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		03,04 (Breast, High Met vs. Breast, Non-Met)	2	11		5.64
2056	452238					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
2057	1870					
		01,02 (Colon, High Met vs. Colon, Low Met)	11	31		3.06
		03,04 (Breast, High Met vs. Breast, Non-Met)	12	3	3.9	
2058	559259					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	17	5	3.59	
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	5	21		4.14
2059	453457					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	8		7.88
2060	8868					
		08,09 (Lung, High Met vs. Lung, Low Met)	5	0	6.99	
		03,04 (Breast, High Met vs. Breast, Non-Met)	9	1	8.78	
2061	453059					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	9	0	9.66	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	9	1	9.51	
2062	236368					
		18,19 (Normal Colon Tissue vs. Colon Tumor)	9	1	10.29	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	271	0	290.88	
		18,20 (Normal Colon Tissue vs. Colon Metastasis)	9	0	7.69	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	271	16	17.9	
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	16	0	16.25	
2063	453059					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	9	1	9.51	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	9	0	9.66	
2064	549979					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	7		6.89
2065	515631					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
2066	2235					
		03,04 (Breast, High Met vs. Breast, Non-Met)	36	12	2.93	
2067	448193					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	1	10		9.46
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	10	2	5.08	
2068	530774					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	5	16		2.98
2069	650204					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	11	0	11.81	
2070	644240					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
2071	552614					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	7		6.89
2072	727331					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
2073	185457					
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	18		18.45
2074	454531					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	9		8.86
2075	643485					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	9	1	9.51	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	9	0	9.66	
2076	733669					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
2077	452344					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
2078	63602					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
2079	454155					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	12	2	6.34	
2080	549903					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	8		7.88
2081	515631					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
2082	6878					
		03,04 (Breast, High Met vs. Breast, Non-Met)	2	11		5.64
2083	2977					
		03,04 (Breast, High Met vs. Breast, Non-Met)	15	4	3.66	
2084	553823					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	24	7	3.62	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	24	6	4.29	
2085	3070					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
2086	728884					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	8		7.57

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	8	0	8.12	
2087	8166					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
2088	644190					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
2089	733669					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
2090	728273					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
2091	406499					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
2092	557720					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
2093	732050					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	8	0	8.12	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	8		7.57
2094	450867					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	7	0	7.4	
2095	650297					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
2096	448064					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	11	3	3.88	
2097	452530					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	10	2	5.28	
2098	7592					
		01,02 (Colon, High Met vs. Colon, Low Met)	0	7		7.59
2099	733669					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
2100	11028					
		01,02 (Colon, High Met vs. Colon, Low Met)	0	6		6.5
2101	1013					
		01,02 (Colon, High Met vs. Colon, Low Met)	40	84		2.28
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
2102	549265					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		15,16 (Normal Colon vs. Colon Tumor Tissue)	11	3	3.88	
2103	376600					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
2104	643804					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
2105	454927					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	3	14		4.6
2106	446528					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	10	0	10.57	
2107	2218					
		01,02 (Colon, High Met vs. Colon, Low Met)	2	21		11.38
		08,09 (Lung, High Met vs. Lung, Low Met)	5	0	6.99	
		03,04 (Breast, High Met vs. Breast, Non-Met)	27	8	3.29	
2108	452704					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	10	1	10.57	
2109	84895					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	46	120		2.57
		08,09 (Lung, High Met vs. Lung, Low Met)	0	12		8.59
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	24	120		4.66
2110	157629					
		03,04 (Breast, High Met vs. Breast, Non-Met)	3	18		6.15
2111	2930					
		01,02 (Colon, High Met vs. Colon, Low Met)	3	14		5.06
2112	7037					
		01,02 (Colon, High Met vs. Colon, Low Met)	0	9		9.76
2113	559806					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
2114	452076					
		23,24 (Normal Lung Tissue vs. Lung Tumor Tissue)	11	1	11.11	
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	20	7	2.9	
2115	454869					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
2116	559674					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	7		6.52
2117	2235					
		03,04 (Breast, High Met vs. Breast, Non-Met)	36	12	2.93	
2118	7545					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		01,02 (Colon, High Met vs. Colon, Low Met)	9	0	8.3	
2119	729173					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	8		7.57
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	8	0	8.12	
2120	650448					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
2121	172013					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
2122	651088					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
2123	651088					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
2124	726810					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
2125	406499					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
2126	556325					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	8		7.88
2127	644836					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	8	0	8.46	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	8	0	8.59	
2128	649062					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
2129	454776					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	5	20		3.78
2130	377579					
		21,22 (Normal Prostate vs. Prostate Cancer)	25	53		2.16
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	2	13		6.06
2131	728131					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
2132	475203					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	1	14		13.04
		15,16 (Normal Colon vs. Colon Tumor Tissue)	1	12		11.35
2133	727314					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
2134	552025					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	19	6	3.35	
2135	561382					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	12	2	6.34	
2136	732579					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
2137	167					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	7	19		2.57
2138	185585					
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	8		8.2
2139	728131					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
2140	475203					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	1	14		13.04
		15,16 (Normal Colon vs. Colon Tumor Tissue)	1	12		11.35
2141	724616					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	8	0	8.12	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	8		7.57
2143	645222					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	11	0	11.17	
2144	400362					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	35	117		3.29
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	21	117		5.19
2145	646583					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
2146	475203					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	1	14		13.04
		15,16 (Normal Colon vs. Colon Tumor Tissue)	1	12		11.35
2147	550001					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	10	2	5.08	
2148	640703					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	10	0	10.16	
2149	646583					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
2150	449468					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	2	11		5.12
2151	449468					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	2	11		5.12
2152	551628					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	38	5	8.03	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	38	13	3.14	
2153	449468					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	2	11		5.12
2154	417259					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	14		13.79
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	4	14		3.26
2155	448029					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	10	1	10.16	
2156	524363					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
2157	446531					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
2158	561359					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	12	2	6.34	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	12	3	4.29	
2159	711297					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	1	11		10.41
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	11	0	11.17	
2160	650097					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
2161	495715					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	8		7.88
2162	734685					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
2163	560515					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
2164	3441					
		03,04 (Breast, High Met vs. Breast, Non-Met)	8	0	7.81	
		01,02 (Colon, High Met vs. Colon, Low Met)	4	13		3.52
2165	729273					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	7	0	7.11	

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
2166	557039					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	2	16		7.88
		15,16 (Normal Colon vs. Colon Tumor Tissue)	11	2	5.81	
2167	711297					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	1	11		10.41
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	11	0	11.17	
2168	711297					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	1	11		10.41
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	11	0	11.17	
2169	2860					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	1	13		12.3
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	1	13		12.11
		03,04 (Breast, High Met vs. Breast, Non-Met)	1	48		49.2
		01,02 (Colon, High Met vs. Colon, Low Met)	23	9	2.36	
2170	558534					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	7		6.89
2171	711297					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	11	0	11.17	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	1	11		10.41
2172	378457					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	1	9		8.51
2173	646583					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
2174	646583					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
2175	1996					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	13	4	3.3	
		03,04 (Breast, High Met vs. Breast, Non-Met)	34	139		4.19
		15,16 (Normal Colon vs. Colon Tumor Tissue)	2	13		6.15
		08,09 (Lung, High Met vs. Lung, Low Met)	20	13	2.15	
2176	7962					
		03,04 (Breast, High Met vs. Breast, Non-Met)	7	0	6.83	
2177	645139					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	9	0	9.14	
2178	449468					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	2	11		5.12
2179	9898					
		03,04 (Breast, High Met vs. Breast, Non-Met)	4	14		3.59
2180	406499					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
2181	1257					
		01,02 (Colon, High Met vs. Colon, Low Met)	46	20	2.12	
		21,22 (Normal Prostate vs. Prostate Cancer)	6	42		7.12
2182	549903					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	8		7.88
2183	557906					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	12	3	4.23	
2184	3538					
		01,02 (Colon, High Met vs. Colon, Low Met)	18	5	3.32	
2185	3114					
		03,04 (Breast, High Met vs. Breast, Non-Met)	9	1	8.78	
2186	426895					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	2	18		8.38
2187	923					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	7	23		3.11
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	23	9	2.6	
2188	645194					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
2189	550161					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	4	15		3.55
2190	650119					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
2191	642142					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	11	0	11.17	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	2	11		5.2
2192	419255					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	11	1	11.81	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	11	0	11.63	
2193	552905					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	7		6.52
2194	511997					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
2195	551434					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	40	13	3.25	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	40	6	7.16	
2196	727447					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
2197	378786					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	9		8.86
2198	649152					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
2199	18853					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
2200	643481					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
2201	644417					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
2202	726788					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
2203	206					
		08,09 (Lung, High Met vs. Lung, Low Met)	19	4	6.64	
		03,04 (Breast, High Met vs. Breast, Non-Met)	166	79	2.05	
2204	395930					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
2205	185589					
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	9		9.22
2206	1441					
		01,02 (Colon, High Met vs. Colon, Low Met)	9	40		4.82
		03,04 (Breast, High Met vs. Breast, Non-Met)	38	16	2.32	
2207	14522					
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	8		8.2
2208	203605					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	17	7	2.57	
2209	551527					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	7		6.52
2210	4509					
		08,09 (Lung, High Met vs. Lung, Low Met)	36	22	2.29	
		03,04 (Breast, High Met vs. Breast, Non-Met)	1	40		41
2211	447737					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	19	6	3.35	
2212	447388					
		18,20 (Normal Colon Tissue vs. Colon Metastasis)	18	0	15.39	

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		15,16 (Normal Colon vs. Colon Tumor Tissue)	142	2	75.05	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	142	4	38.1	
		18,19 (Normal Colon Tissue vs. Colon Tumor)	18	0	20.57	
2213	451932					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	28	4	7.51	
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	15	4	3.81	
2214	559043					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	11	50		4.48
		15,16 (Normal Colon vs. Colon Tumor Tissue)	54	11	5.19	
2215	380634					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	3	14		4.6
2216	495715					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	8		7.88
2217	451932					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	28	4	7.51	
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	15	4	3.81	
2218	447939					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	14	1	14.8	
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	8		7.88
2219	1181					
		03,04 (Breast, High Met vs. Breast, Non-Met)	17	58		3.5
2220	376600					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	7		6.62
2221	234761					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	8	0	8.59	
2222	644417					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
2223	639048					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
2224	11452					
		01,02 (Colon, High Met vs. Colon, Low Met)	0	6		6.5
2225	452076					
		23,24 (Normal Lung Tissue vs. Lung Tumor Tissue)	11	1	11.11	
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	20	7	2.9	
2226	644523					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
2227	554678					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	10	2	5.28	
2228	3550					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		03,04 (Breast, High Met vs. Breast, Non-Met)	31	5	6.05	
2229	450311					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	8	1	8.46	
2230	647280					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	8	0	8.12	
2231	548858					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	11		10.83
2232	4204					
		01,02 (Colon, High Met vs. Colon, Low Met)	16	2	7.38	
2233	540690					
		23,24 (Normal Lung Tissue vs. Lung Tumor Tissue)	0	8		7.92
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	11	0	11.17	
2234	404774					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	11	3	3.88	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	11	1	11.81	
2235	557823					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	9		8.86
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	9		8.38
2236	1458					
		03,04 (Breast, High Met vs. Breast, Non-Met)	20	3	6.5	
2237	485431					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
2238	2245					
		03,04 (Breast, High Met vs. Breast, Non-Met)	13	1	12.68	
		01,02 (Colon, High Met vs. Colon, Low Met)	12	27		2.44
2239	3242					
		01,02 (Colon, High Met vs. Colon, Low Met)	2	17		9.22
2240	648747					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
2241	3805					
		01,02 (Colon, High Met vs. Colon, Low Met)	17	3	5.23	
2242	475203					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	1	12		11.35
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	1	14		13.04
2243	12018					
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	6		6.15
2244	475203					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		15,16 (Normal Colon vs. Colon Tumor Tissue)	1	12		11.35
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	1	14		13.04
2245	3805					
		01,02 (Colon, High Met vs. Colon, Low Met)	17	3	5.23	
2246	496132					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
2247	650600					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
2248	650749					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
2249	223148					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	1	9		8.38
2250	449					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	3	14		4.35
		15,16 (Normal Colon vs. Colon Tumor Tissue)	3	14		4.42
2251	735620					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
2252	650600					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
2253	218					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	1	11		10.25
		03,04 (Breast, High Met vs. Breast, Non-Met)	127	49	2.53	
2254	4161					
		08,09 (Lung, High Met vs. Lung, Low Met)	31	2	21.66	
		01,02 (Colon, High Met vs. Colon, Low Met)	13	1	11.99	
2255	373202					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	5	22		4.1
2256	724339					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
2257	113291					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	2	15		6.99
2258	736753					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	11		10.41
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	11	0	11.17	
2259	650600					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
2260	451569					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	8		7.45
2261	1297					
		03,04 (Breast, High Met vs. Breast, Non-Met)	30	14	2.09	
2263	63602					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	0	6		5.91
2264	2757					
		03,04 (Breast, High Met vs. Breast, Non-Met)	4	16		4.1
2265	373128					
		08,09 (Lung, High Met vs. Lung, Low Met)	4	29		5.19
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	4	14		3.26
2266	641479					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	8	0	8.12	
2267	450380					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	4	31		7.22
		15,16 (Normal Colon vs. Colon Tumor Tissue)	4	23		5.44
2268	133512					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	7		6.52
		18,19 (Normal Colon Tissue vs. Colon Tumor)	0	8		7
2269	447211					
		18,20 (Normal Colon Tissue vs. Colon Metastasis)	9	0	7.69	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	46	0	49.38	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	46	0	48.62	
		18,19 (Normal Colon Tissue vs. Colon Tumor)	9	0	10.29	
2270	645222					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	11	0	11.17	
2271	645222					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	11	0	11.17	
2272	17372					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
2273	451619					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	24	9	2.82	
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	9	39		4.27
2274	2510					
		03,04 (Breast, High Met vs. Breast, Non-Met)	13	1	12.68	
2275	643974					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	16	3	5.64	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	16	0	17.17	
2276	500630					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
2277	3101					
		01,02 (Colon, High Met vs. Colon, Low Met)	4	19		5.15
2278	446938					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	8	1	8.46	
2279	554469					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	24	3	8.59	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	24	8	3.17	
2280	554469					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	24	3	8.59	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	24	8	3.17	
2281	2894					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
		03,04 (Breast, High Met vs. Breast, Non-Met)	22	4	5.37	
		08,09 (Lung, High Met vs. Lung, Low Met)	5	20		2.86
2282	650600					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
2283	3101					
		01,02 (Colon, High Met vs. Colon, Low Met)	4	19		5.15
2284	554469					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	24	3	8.59	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	24	8	3.17	
2285	9910					
		03,04 (Breast, High Met vs. Breast, Non-Met)	6	0	5.85	
2286	400608					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	21	7	3.22	
2287	555051					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	8		7.45
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	9		8.51
2288	185400					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	1	9		8.86
		03,04 (Breast, High Met vs. Breast, Non-Met)	1	62		63.55
2289	3059					
		03,04 (Breast, High Met vs. Breast, Non-Met)	16	3	5.2	
2290	647185					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
2291	1669					
		21,22 (Normal Prostate vs. Prostate Cancer)	0	34		34.57

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		03,04 (Breast, High Met vs. Breast, Non-Met)	40	0	39.03	
		01,02 (Colon, High Met vs. Colon, Low Met)	11	29		2.86
2292	7158					
		03,04 (Breast, High Met vs. Breast, Non-Met)	6	0	5.85	
2293	496132					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
2294	378623					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	3	33		10.25
		15,16 (Normal Colon vs. Colon Tumor Tissue)	3	24		7.57
		08,09 (Lung, High Met vs. Lung, Low Met)	1	16		11.45
2295	1257					
		01,02 (Colon, High Met vs. Colon, Low Met)	46	20	2.12	
		21,22 (Normal Prostate vs. Prostate Cancer)	6	42		7.12
2296	648499					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	10	0	10.73	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	10	2	5.28	
2297	185627					
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	7		7.17
2298	640005					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	20	6	3.52	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	20	0	21.47	
2299	553462					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	6	0	6.34	
2300	649852					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
2301	422375					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	2	11		5.12
2302	10910					
		01,02 (Colon, High Met vs. Colon, Low Met)	0	6		6.5
2303	2737					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	3	14		4.6
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	4	14		3.26
2304	3438					
		01,02 (Colon, High Met vs. Colon, Low Met)	5	14		3.04
2305	3438					
		01,02 (Colon, High Met vs. Colon, Low Met)	5	14		3.04
2306	3763					
		01,02 (Colon, High Met vs. Colon, Low Met)	19	6	2.92	

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
2307	648966					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
2308	724339					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
2309	451569					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	8		7.45
2310	554109					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	15	2	7.93	
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	2	11		5.42
2311	380339					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	166	57	3.08	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	166	51	3.49	
		19,20 (Colon Tumor Tissue vs. Colon Metastasis)	9	0	6.73	
		18,20 (Normal Colon Tissue vs. Colon Metastasis)	18	0	15.39	
2312	729903					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
2313	45					
		08,09 (Lung, High Met vs. Lung, Low Met)	374	1067		2.04
		15,16 (Normal Colon vs. Colon Tumor Tissue)	40	119		2.81
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	40	209		4.87
		18,19 (Normal Colon Tissue vs. Colon Tumor)	0	29		25.38
		18,20 (Normal Colon Tissue vs. Colon Metastasis)	0	11		12.87
		03,04 (Breast, High Met vs. Breast, Non-Met)	649	1876		2.96
2314	454653					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	3	17		5.28
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	5	17		3.35
2315	11536					
		03,04 (Breast, High Met vs. Breast, Non-Met)	6	0	5.85	
2316	373134					
		08,09 (Lung, High Met vs. Lung, Low Met)	2	45		16.1
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	24	73		2.83
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	28	73		2.57
2317	185691					
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	6		6.15
2318	234761					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	8	0	8.59	
2319	724339					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
2320	732740					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
2321	35895					
		21,22 (Normal Prostate vs. Prostate Cancer)	6	19		3.22
		15,16 (Normal Colon vs. Colon Tumor Tissue)	1	13		12.3
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	13	0	13.2	
2322	133512					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	7		6.52
		18,19 (Normal Colon Tissue vs. Colon Tumor)	0	8		7
2323	2974					
		01,02 (Colon, High Met vs. Colon, Low Met)	22	7	2.9	
2324	500					
		03,04 (Breast, High Met vs. Breast, Non-Met)	89	22	3.95	
		01,02 (Colon, High Met vs. Colon, Low Met)	34	114		3.64
2325	376919					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	24	61		2.5
		21,22 (Normal Prostate vs. Prostate Cancer)	4	13		3.3
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	21	61		2.71
2326	8403					
		03,04 (Breast, High Met vs. Breast, Non-Met)	6	0	5.85	
2327	3643					
		01,02 (Colon, High Met vs. Colon, Low Met)	6	19		3.43
2328	447211					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	46	0	48.62	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	46	0	49.38	
		18,19 (Normal Colon Tissue vs. Colon Tumor)	9	0	10.29	
		18,20 (Normal Colon Tissue vs. Colon Metastasis)	9	0	7.69	
2329	447211					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	46	0	49.38	
		18,19 (Normal Colon Tissue vs. Colon Tumor)	9	0	10.29	
		18,20 (Normal Colon Tissue vs. Colon Metastasis)	9	0	7.69	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	46	0	48.62	
2330	14929					
		08,09 (Lung, High Met vs. Lung, Low Met)	23	16	2.01	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	2	13		6.15
2331	648934					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	8	0	8.46	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	8	0	8.59	
2332	731785					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
2333	639908					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	13	4	3.44	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	13	0	13.95	
2334	344577					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	28	2	14.22	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	38	2	20.39	
2335	2906					
		01,02 (Colon, High Met vs. Colon, Low Met)	10	25		2.71
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	7		6.52
		03,04 (Breast, High Met vs. Breast, Non-Met)	2	15		7.69
2336	446938					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	8	1	8.46	
2337	2493					
		03,04 (Breast, High Met vs. Breast, Non-Met)	33	9	3.58	
2338	38					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	40	118		2.79
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	40	259		6.03
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	118	259		2.16
		19,20 (Colon Tumor Tissue vs. Colon Metastasis)	88	6	10.97	
		18,19 (Normal Colon Tissue vs. Colon Tumor)	3	88		25.67
2339	13818					
		03,04 (Breast, High Met vs. Breast, Non-Met)	6	0	5.85	
2340	8371					
		01,02 (Colon, High Met vs. Colon, Low Met)	0	6		6.5
2341	402494					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	3	13		4.1
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	13	3	4.4	
2342	731785					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
2343	4621					
		03,04 (Breast, High Met vs. Breast, Non-Met)	11	1	10.73	
2344	9750					
		01,02 (Colon, High Met vs. Colon, Low Met)	0	6		6.5
2345	133512					
		18,19 (Normal Colon Tissue vs. Colon Tumor)	0	8		7
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	7		6.52
2346	162626					
		03,04 (Breast, High Met vs. Breast, Non-Met)	1	12		12.3

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
2347	730059					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	6		5.68
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	6	0	6.09	
2348	2069					
		01,02 (Colon, High Met vs. Colon, Low Met)	26	8	3	
		08,09 (Lung, High Met vs. Lung, Low Met)	21	6	4.89	
		03,04 (Breast, High Met vs. Breast, Non-Met)	1	47		48.17
2349	5868					
		03,04 (Breast, High Met vs. Breast, Non-Met)	10	2	4.88	
2350	2683					
		01,02 (Colon, High Met vs. Colon, Low Met)	3	22		7.95
		03,04 (Breast, High Met vs. Breast, Non-Met)	13	2	6.34	
2351	380409					
		16,17 (Colon Tumor Tissue vs. Colon Metastasis)	10	2	5.08	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	0	10		9.46
2352	639991					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	6	0	6.44	
2353	535					
		03,04 (Breast, High Met vs. Breast, Non-Met)	87	13	6.53	
2354	14929					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	2	13		6.15
		08,09 (Lung, High Met vs. Lung, Low Met)	23	16	2.01	
2355	134702					
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	7		7.17
2356	642477					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	7	0	7.4	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
2357	14929					
		08,09 (Lung, High Met vs. Lung, Low Met)	23	16	2.01	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	2	13		6.15
2358	134702					
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	7		7.17
2359	185649					
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	7		7.17
2360	10702					
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	15		15.37
2361	643955					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	12	0	12.88	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	12	0	12.68	

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
2362	643955					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	12	0	12.88	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	12	0	12.68	
2363	4455					
		03,04 (Breast, High Met vs. Breast, Non-Met)	13	1	12.68	
2364	185567					
		03,04 (Breast, High Met vs. Breast, Non-Met)	0	9		9.22
2365	9115					
		01,02 (Colon, High Met vs. Colon, Low Met)	0	7		7.59
2366	14929					
		08,09 (Lung, High Met vs. Lung, Low Met)	23	16	2.01	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	2	13		6.15
2367	14929					
		08,09 (Lung, High Met vs. Lung, Low Met)	23	16	2.01	
		15,16 (Normal Colon vs. Colon Tumor Tissue)	2	13		6.15
2368	4181					
		03,04 (Breast, High Met vs. Breast, Non-Met)	15	3	4.88	
2369	5206					
		03,04 (Breast, High Met vs. Breast, Non-Met)	7	0	6.83	
2370	825					
		03,04 (Breast, High Met vs. Breast, Non-Met)	70	25	2.73	
		08,09 (Lung, High Met vs. Lung, Low Met)	13	3	6.06	
2371	825					
		08,09 (Lung, High Met vs. Lung, Low Met)	13	3	6.06	
		03,04 (Breast, High Met vs. Breast, Non-Met)	70	25	2.73	
2372	825					
		03,04 (Breast, High Met vs. Breast, Non-Met)	70	25	2.73	
		08,09 (Lung, High Met vs. Lung, Low Met)	13	3	6.06	
2373	2748					
		01,02 (Colon, High Met vs. Colon, Low Met)	2	26		14.09
		03,04 (Breast, High Met vs. Breast, Non-Met)	15	4	3.66	
2374	2748					
		03,04 (Breast, High Met vs. Breast, Non-Met)	15	4	3.66	
		01,02 (Colon, High Met vs. Colon, Low Met)	2	26		14.09
2375	2748					
		01,02 (Colon, High Met vs. Colon, Low Met)	2	26		14.09
		03,04 (Breast, High Met vs. Breast, Non-Met)	15	4	3.66	
2376	133512					
		18,19 (Normal Colon Tissue vs. Colon Tumor)	0	8		7

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	0	7		6.52
2377	2748					
		03,04 (Breast, High Met vs. Breast, Non-Met)	15	4	3.66	
		01,02 (Colon, High Met vs. Colon, Low Met)	2	26		14.09
2378	642477					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	7	0	7.4	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
2379	642477					
		15,16 (Normal Colon vs. Colon Tumor Tissue)	7	0	7.4	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	7	0	7.51	
2380	2493					
		03,04 (Breast, High Met vs. Breast, Non-Met)	33	9	3.58	
2381	5796					
		08,09 (Lung, High Met vs. Lung, Low Met)	5	0	6.99	
		03,04 (Breast, High Met vs. Breast, Non-Met)	14	3	4.55	
2382	3782					
		03,04 (Breast, High Met vs. Breast, Non-Met)	21	0	20.49	
2383	884					
		03,04 (Breast, High Met vs. Breast, Non-Met)	51	20	2.49	
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	1	10		9.32
		21,22 (Normal Prostate vs. Prostate Cancer)	20	7	2.81	
		08,09 (Lung, High Met vs. Lung, Low Met)	10	63		4.51
2384	5860					
		03,04 (Breast, High Met vs. Breast, Non-Met)	10	2	4.88	
2385	5275					
		01,02 (Colon, High Met vs. Colon, Low Met)	11	2	5.07	
2386	3932					
		03,04 (Breast, High Met vs. Breast, Non-Met)	13	1	12.68	
2387	884					
		08,09 (Lung, High Met vs. Lung, Low Met)	10	63		4.51
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	1	10		9.32
		03,04 (Breast, High Met vs. Breast, Non-Met)	51	20	2.49	
		21,22 (Normal Prostate vs. Prostate Cancer)	20	7	2.81	
2388	4455					
		03,04 (Breast, High Met vs. Breast, Non-Met)	13	1	12.68	
2389	5860					
		03,04 (Breast, High Met vs. Breast, Non-Met)	10	2	4.88	
2390	5860					
		03,04 (Breast, High Met vs. Breast, Non-Met)	10	2	4.88	
2391	372791					

Table 5

SEQ	CLST	Library Pair A,B	A	B	A/B	B/A
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	12	0	12.88	
2392	5206					
		03,04 (Breast, High Met vs. Breast, Non-Met)	7	0	6.83	
2393	372791					
		15,17 (Normal Colon Tissue vs. Colon Metastasis)	12	0	12.88	
2394	2846					
		01,02 (Colon, High Met vs. Colon, Low Met)	8	19		2.57
2395	5275					
		01,02 (Colon, High Met vs. Colon, Low Met)	11	2	5.07	
2396	2846					
		01,02 (Colon, High Met vs. Colon, Low Met)	8	19		2.57

Table 7

Table 7 ES #	CMCC#	ATCC Deposit#
85	5175	PTA-1313
86	5176	PTA-1314
87	5177	PTA-1315
88	5178	PTA-1316
89	5179	PTA-1317
90	5180	PTA-1318
91	5181	PTA-1319
92	5182	PTA-1320
93	5183	PTA-1321
94	5184	PTA-1322
95	5185	PTA-1323
96	5186	PTA-1324
97	5187	PTA-1325
98	5188	PTA-1326
99	5189	PTA-1327
100	5190	PTA-1328
101	5191	PTA-1329
102	5192	PTA-1330
103	5193	PTA-1331
104	5194	PTA-1332
105	5195	PTA-1333
106	5196	PTA-1334
107	5197	PTA-1335
108	5198	PTA-1336
109	5199	PTA-1372
110	5200	PTA-1373
111	5201	PTA-1374
112	5202	PTA-1375
113	5203	PTA-1376
114	5204	PTA-1377
115	5205	PTA-1378
116	5206	PTA-1379
117	5207	PTA-1380
118	5208	PTA-1381
122	5212	PTA-1382
123	5213	PTA-1383
124	5214	PTA-1384
125	5215	PTA-1385
126	5216	PTA-1386
127	5217	PTA-1387
128	5218	PTA-1388
129	5219	PTA-1389
130	5220	PTA-1390
131	5221	PTA-1391
132	5222	PTA-1392
133	5223	PTA-1393
134	5209	PTA-1431
135	5210	PTA-1432
136	5238	PTA-1497

Table 8			
ES No.	Clone Name	ES No.	Clone Name
ES 85	M00057077B:D02	ES 109	M00027658B:G03
ES 85	M00057078D:C12	ES 109	M00027660C:E03
ES 85	M00057079D:E09	ES 109	M00027660C:E03
ES 85	M00057080C:C02	ES 109	M00027665B:D01
ES 85	M00057085A:A03	ES 109	M00027681D:D02
ES 85	M00057088B:C02	ES 109	M00027699D:D02
ES 85	M00057091A:C03	ES 109	M00027717C:G05
ES 85	M00057091A:C04	ES 109	M00027733D:D05
ES 85	M00057091C:E12	ES 109	M00027742C:B01
ES 85	M00057093B:F09	ES 109	M00027742C:B01
ES 85	M00057099C:C08	ES 109	M00027747D:D01
ES 85	M00057100C:E09	ES 109	M00027757A:B06
ES 85	M00057100D:B03	ES 109	M00027781D:E04
ES 85	M00057103A:E11	ES 109	M00027786D:B01
ES 85	M00057103A:H09	ES 109	M00027803A:H10
ES 85	M00057104B:F08	ES 109	M00027806C:H05
ES 85	M00057106B:A03	ES 109	M00027808D:G10
ES 85	M00057106C:E02	ES 109	M00027817B:B11
ES 85	M00057106D:B06	ES 109	M00027820C:C02
ES 85	M00057108B:F04	ES 109	M00027823C:G07
ES 85	M00057108D:E09	ES 109	M00027829C:D02
ES 85	M00057108D:E09	ES 109	M00027833C:D01
ES 85	M00057112D:B09	ES 110	M00042345A:F12
ES 85	M00057114D:B10	ES 110	M00042523A:C05
ES 85	M00057117D:G11	ES 110	M00042523C:E08
ES 85	M00057118C:C02	ES 110	M00042525D:E01
ES 85	M00057120D:E12	ES 110	M00042527B:D07
ES 85	M00057124B:D10	ES 110	M00042528C:F11
ES 85	M00057127A:F11	ES 110	M00042529C:G07
ES 85	M00057127B:G07	ES 110	M00042532A:F08
ES 85	M00057130C:H11	ES 110	M00042534A:B07
ES 85	M00057131C:B01	ES 110	M00042536D:F01
ES 85	M00057132C:F08	ES 110	M00042537A:H05
ES 85	M00057133D:F01	ES 110	M00042538B:E06
ES 85	M00057134A:C01	ES 110	M00042538D:A08
ES 85	M00057134C:A01	ES 110	M00042539C:E05
ES 85	M00057134D:G10	ES 110	M00042540A:H06
ES 85	M00057135D:H04	ES 110	M00042540D:F03
ES 85	M00057136A:F01	ES 110	M00042540D:H05
ES 85	M00057141B:B02	ES 110	M00042543C:H02
ES 85	M00057141D:D02	ES 110	M00042544B:D02
ES 85	M00057142A:A07	ES 110	M00042544C:F10
ES 85	M00057143C:E05	ES 110	M00042547A:A02
ES 85	M00057145A:D05	ES 110	M00042547B:D11
ES 85	M00057146D:C09	ES 110	M00042547C:F02

Table 8			
ES No.	Clone Name	ES No.	Clone Name
ES 85	M00057147A:A01	ES 110	M00042551A:D09
ES 85	M00057150A:C10	ES 110	M00042556A:D04
ES 85	M00057151A:B04	ES 110	M00042563C:E02
ES 86	M00057154A:D06	ES 110	M00042563C:E02
ES 86	M00057154C:B04	ES 110	M00042563D:G09
ES 86	M00057161B:E09	ES 110	M00042564B:H11
ES 86	M00057162A:C07	ES 110	M00042565A:H03
ES 86	M00057162B:H02	ES 110	M00042565C:A08
ES 86	M00057162D:D10	ES 110	M00042567D:C01
ES 86	M00057163D:B01	ES 110	M00042570D:H02
ES 86	M00057165D:E12	ES 110	M00042573C:A07
ES 86	M00057167B:E12	ES 110	M00042574B:H08
ES 86	M00057167B:G12	ES 110	M00042575C:D01
ES 86	M00057167D:B07	ES 110	M00042693D:E04
ES 86	M00057170C:H03	ES 110	M00042694C:E02
ES 86	M00057174B:C06	ES 110	M00042695B:H05
ES 86	M00057174B:G12	ES 110	M00042700B:A01
ES 86	M00057174C:H12	ES 110	M00042700B:D03
ES 86	M00057180A:H11	ES 110	M00042700B:D03
ES 86	M00057181C:D06	ES 110	M00042700D:H05
ES 86	M00057182D:B11	ES 110	M00042704A:F04
ES 86	M00057189B:G05	ES 110	M00042704A:F09
ES 86	M00057191A:A03	ES 110	M00042704D:E02
ES 86	M00057192B:E02	ES 110	M00042705A:D02
ES 86	M00057192D:G02	ES 110	M00042706C:A04
ES 86	M00057196A:E03	ES 110	M00054596B:G11
ES 86	M00057196C:F04	ES 110	M00004101C:H01
ES 86	M00057203C:E06	ES 111	M00042711C:G11
ES 86	M00057208A:A02	ES 111	M00042711D:C04
ES 86	M00057208C:C06	ES 111	M00042712B:B10
ES 86	M00057208C:D08	ES 111	M00042717D:D04
ES 86	M00057211B:F07	ES 111	M00042718B:C03
ES 86	M00057211D:A06	ES 111	M00042720C:D06
ES 86	M00057215B:B02	ES 111	M00042720D:G10
ES 86	M00057217B:B07	ES 111	M00042721A:G07
ES 86	M00057218D:C01	ES 111	M00042727C:H12
ES 86	M00057223C:C06	ES 111	M00042728D:E07
ES 86	M00057224B:C10	ES 111	M00042732A:G09
ES 86	M00057226D:C05	ES 111	M00042735C:G02
ES 86	M00057229D:F06	ES 111	M00042735D:A07
ES 86	M00057230C:D12	ES 111	M00042738B:D10
ES 86	M00057231C:G09	ES 111	M00042739D:D01
ES 86	M00057231D:A09	ES 111	M00042741D:D10
ES 86	M00057232B:D06	ES 111	M00042742B:H03
ES 86	M00057233A:F07	ES 111	M00042742C:A06

Table 8			
ES No.	Clone Name	ES No.	Clone Name
ES 86	M00057233B:E04	ES 111	M00042742D:D05
ES 86	M00057236B:H06	ES 111	M00042746B:F02
ES 86	M00057237A:B11	ES 111	M00042746D:B09
ES 86	M00057239A:G08	ES 111	M00042750D:B09
ES 86	M00057241B:B04	ES 111	M00042881D:C08
ES 86	M00057242B:F07	ES 111	M00042883A:F12
ES 87	M00057242D:B09	ES 111	M00042886C:C03
ES 87	M00057242D:H05	ES 111	M00042886C:F01
ES 87	M00057249A:C06	ES 111	M00042887C:D07
ES 87	M00057259A:H10	ES 111	M00042889B:A09
ES 87	M00057259B:B08	ES 111	M00042890D:C08
ES 87	M00057266C:D04	ES 111	M00042891B:C04
ES 87	M00057266C:G12	ES 111	M00042893B:C08
ES 87	M00057268C:E10	ES 111	M00042900C:C07
ES 87	M00057270B:H09	ES 111	M00042901B:A03
ES 87	M00057270C:E04	ES 111	M00042902A:C04
ES 87	M00057271C:E01	ES 111	M00042905A:F11
ES 87	M00057272A:B03	ES 111	M00042905C:C10
ES 87	M00057272C:H04	ES 111	M00042908D:G01
ES 87	M00057272D:A01	ES 111	M00042909B:G04
ES 87	M00057275B:A12	ES 111	M00042911A:H03
ES 87	M00057277B:C09	ES 111	M00042914D:B10
ES 87	M00057277B:E10	ES 111	M00054792D:E09
ES 87	M00057279A:G02	ES 111	M00054793D:B07
ES 87	M00057280C:A06	ES 111	M00054798D:F01
ES 87	M00057283A:E06	ES 111	M00054913C:G03
ES 87	M00057288D:E08	ES 111	M00054915D:E07
ES 87	M00057291C:B06	ES 111	M00054917B:F09
ES 87	M00057297A:F03	ES 111	M00054917D:D12
ES 87	M00057300B:F02	ES 111	M00054918C:D03
ES 87	M00057301B:H12	ES 112	M00054918D:C11
ES 87	M00057304A:E01	ES 112	M00055426B:B02
ES 87	M00057306B:H07	ES 112	M00055426C:H06
ES 87	M00057312B:E11	ES 112	M00055427A:F01
ES 87	M00057318B:B09	ES 112	M00055428C:A02
ES 87	M00057318C:A03	ES 112	M00055429A:H05
ES 87	M00057324A:D12	ES 112	M00055430B:H02
ES 87	M00057325C:C10	ES 112	M00055431C:E09
ES 87	M00057333A:F09	ES 112	M00055438C:C06
ES 87	M00057334B:F01	ES 112	M00055438C:H10
ES 87	M00057337B:G02	ES 112	M00055441B:D02
ES 87	M00057340B:C12	ES 112	M00055445D:G06
ES 87	M00042355A:G02	ES 112	M00055446C:B06
ES 87	M00042355D:C01	ES 112	M00055447D:H04
ES 87	M00042442D:A02	ES 112	M00055447D:H04

Table 8			
ES No.	Clone Name	ES No.	Clone Name
ES 87	M00042444D:G05	ES 112	M00055448A:D08
ES 87	M00042444D:H08	ES 112	M00055448C:E07
ES 87	M00042450D:H10	ES 112	M00055450A:G09
ES 87	M00042453C:E01	ES 112	M00055450D:B08
ES 87	M00042460D:A07	ES 112	M00055451A:F07
ES 87	M00042517C:F07	ES 112	M00055451A:F11
ES 87	M00042518D:A06	ES 112	M00055451C:G11
ES 87	M00042520A:F04	ES 112	M00055453C:E01
ES 88	M00042520A:F09	ES 112	M00055453C:E01
ES 88	M00042520A:F09	ES 112	M00055454A:A07
ES 88	M00043296C:B10	ES 112	M00055454A:H11
ES 88	M00043300A:H11	ES 112	M00055454C:G05
ES 88	M00043301A:F06	ES 112	M00055456D:F12
ES 88	M00043301D:H09	ES 112	M00055463D:H10
ES 88	M00043304A:D01	ES 112	M00055464A:F05
ES 88	M00043304B:C05	ES 112	M00055466D:B08
ES 88	M00043304B:C05	ES 112	M00055470B:G01
ES 88	M00043306D:B07	ES 112	M00055491A:G08
ES 88	M00043309B:H07	ES 112	M00055494D:C09
ES 88	M00043310C:B03	ES 112	M00055495A:G02
ES 88	M00043313A:A03	ES 112	M00055495C:D05
ES 88	M00043313A:G07	ES 112	M00055495C:F03
ES 88	M00043313D:C06	ES 112	M00055495D:E02
ES 88	M00043314C:H04	ES 112	M00055496A:F09
ES 88	M00043317A:H01	ES 112	M00055496B:E07
ES 88	M00043317C:F04	ES 112	M00055496C:C09
ES 88	M00043323C:D04	ES 112	M00055498A:H09
ES 88	M00043324D:D04	ES 112	M00055500D:B05
ES 88	M00043327D:H02	ES 112	M00055504C:D08
ES 88	M00043327D:H02	ES 112	M00055505D:A10
ES 88	M00043336B:E08	ES 112	M00055508D:E03
ES 88	M00043338A:B03	ES 112	M00055509C:H09
ES 88	M00043338B:A03	ES 112	M00055510B:B07
ES 88	M00043345B:C03	ES 113	M00055511D:E09
ES 88	M00043347B:G12	ES 113	M00055512C:G06
ES 88	M00043349A:C08	ES 113	M00055512D:D07
ES 88	M00043350B:H06	ES 113	M00055512D:F08
ES 88	M00043350C:H09	ES 113	M00055513C:D06
ES 88	M00043352A:E09	ES 113	M00055514D:H05
ES 88	M00043352D:B05	ES 113	M00055516B:E08
ES 88	M00043354D:C01	ES 113	M00055517B:D03
ES 88	M00043355D:H11	ES 113	M00055519B:C06
ES 88	M00043361D:D05	ES 113	M00055519C:H07
ES 88	M00043365A:C06	ES 113	M00055520C:A06
ES 88	M00043374A:B02	ES 113	M00055522A:E07

Table 8			
ES No.	Clone Name	ES No.	Clone Name
ES 89	M00054575C:C01	ES 114	M00055583B:B04
ES 89	M00054580C:D11	ES 114	M00055583B:H05
ES 89	M00054583A:F05	ES 114	M00055584A:C11
ES 89	M00054587A:F09	ES 114	M00055584D:G06
ES 89	M00054590C:G02	ES 114	M00055586C:F05
ES 89	M00054591C:H07	ES 114	M00055586D:F02
ES 89	M00054595A:B02	ES 114	M00055591C:H01
ES 89	M00054595B:H09	ES 114	M00055592D:A05
ES 89	M00054596B:B07	ES 114	M00055594B:A01
ES 89	M00054600D:G07	ES 114	M00055597C:E08
ES 89	M00054601A:H10	ES 114	M00055601C:D09
ES 89	M00054601D:E08	ES 114	M00055602B:G10
ES 89	M00054602A:C04	ES 114	M00055602C:E07
ES 90	M00054602B:D02	ES 114	M00055609A:G03
ES 90	M00054604A:D09	ES 114	M00055609D:F12
ES 90	M00054604A:D09	ES 114	M00055613A:D10
ES 90	M00054605C:D01	ES 114	M00055613A:E02
ES 90	M00054609A:F01	ES 114	M00055618C:A06
ES 90	M00054609D:H06	ES 114	M00055628A:A08
ES 90	M00054611C:F02	ES 114	M00055630B:E09
ES 90	M00054613A:D09	ES 114	M00055633D:A02
ES 90	M00054613A:D09	ES 114	M00055633D:G11
ES 90	M00054617B:A09	ES 114	M00055635A:H10
ES 90	M00054621B:C06	ES 114	M00055635B:E10
ES 90	M00054621D:D11	ES 114	M00055635C:G04
ES 90	M00054629C:E09	ES 114	M00055636A:F10
ES 90	M00054636B:B03	ES 114	M00055647C:B04
ES 90	M00054636C:A02	ES 114	M00055653A:H04
ES 90	M00054636C:F02	ES 114	M00055656A:E09
ES 90	M00054638A:D09	ES 114	M00055662C:A04
ES 90	M00054638B:C08	ES 114	M00055664C:A08
ES 90	M00054646C:B01	ES 114	M00055668B:B07
ES 90	M00054647D:H02	ES 114	M00055679A:A07
ES 90	M00054648C:H10	ES 114	M00055681B:G02
ES 90	M00054660D:F05	ES 114	M00055685D:E01
ES 90	M00054665B:H08	ES 114	M00055686D:E11
ES 90	M00054665D:E11	ES 114	M00055687C:F01
ES 90	M00054677C:D02	ES 114	M00055688C:B04
ES 90	M00054678A:E07	ES 114	M00055689A:G12
ES 90	M00054679B:D12	ES 115	M00055689D:F02
ES 90	M00054680B:E06	ES 115	M00055689D:F07
ES 90	M00054680D:B11	ES 115	M00055691B:E07
ES 90	M00054681C:B02	ES 115	M00055692D:E07
ES 90	M00054684C:H12	ES 115	M00055701C:D10
ES 90	M00054689D:E12	ES 115	M00055703A:B08

Table 8			
ES No.	Clone Name	ES No.	Clone Name
ES 90	M00054691A:E05	ES 115	M00055703B:B06
ES 90	M00054692B:D01	ES 115	M00055703B:C05
ES 90	M00054694D:G04	ES 115	M00055703C:G09
ES 90	M00054706B:C09	ES 115	M00055704C:D07
ES 90	M00054707B:B08	ES 115	M00055705C:G07
ES 90	M00054707B:E05	ES 115	M00055706A:A01
ES 90	M00054713A:D12	ES 115	M00055706B:G01
ES 90	M00054720D:D12	ES 115	M00055707D:C08
ES 90	M00054720D:F11	ES 115	M00055709B:G09
ES 90	M00054721C:F11	ES 115	M00055716C:B04
ES 90	M00054722C:D01	ES 115	M00055717B:F04
ES 90	M00054722D:C08	ES 115	M00055718A:F05
ES 90	M00054726A:F08	ES 115	M00055720B:G09
ES 90	M00054727D:E10	ES 115	M00055720C:A06
ES 90	M00054727D:H06	ES 115	M00055720D:A01
ES 90	M00054728B:E08	ES 115	M00055721B:F06
ES 91	M00054728D:B10	ES 115	M00055721B:F06
ES 91	M00054729A:E01	ES 115	M00055721C:E05
ES 91	M00054731C:C12	ES 115	M00055723A:B08
ES 91	M00054732D:E03	ES 115	M00055723D:E05
ES 91	M00054734D:H10	ES 115	M00055724D:D09
ES 91	M00054739A:G03	ES 115	M00055726B:B08
ES 91	M00054739C:D03	ES 115	M00055726C:D12
ES 91	M00054739C:E06	ES 115	M00055726C:G10
ES 91	M00054740A:H08	ES 115	M00055729D:A06
ES 91	M00054741A:C10	ES 115	M00055731A:H12
ES 91	M00054741A:E10	ES 115	M00055733A:G11
ES 91	M00054741D:G10	ES 115	M00055734C:H05
ES 91	M00054743C:E02	ES 115	M00055735C:C07
ES 91	M00054745D:A03	ES 115	M00055735C:G05
ES 91	M00054747A:F01	ES 115	M00055736A:D06
ES 91	M00054747D:C06	ES 115	M00055736B:G03
ES 91	M00054750C:D12	ES 115	M00055736C:G07
ES 91	M00054752B:A07	ES 115	M00055740B:B12
ES 91	M00054755B:H06	ES 115	M00055740B:F09
ES 91	M00054759A:B08	ES 115	M00055743B:C12
ES 91	M00054760A:A12	ES 115	M00055744B:C08
ES 91	M00054762B:F07	ES 115	M00055744C:F08
ES 91	M00054765B:C05	ES 115	M00055744C:F09
ES 91	M00054766C:B04	ES 115	M00055744D:G08
ES 91	M00054769A:F07	ES 115	M00055747C:D09
ES 91	M00054772C:C06	ES 115	M00055749D:H11
ES 91	M00054773A:A12	ES 116	M00055751C:D01
ES 91	M00054776B:F01	ES 116	M00055755C:D02
ES 91	M00054779A:F07	ES 116	M00055755D:H03

Table 8			
ES No.	Clone Name	ES No.	Clone Name
ES 91	M00054780C:G08	ES 116	M00055761D:C03
ES 91	M00054781B:B04	ES 116	M00055763B:E06
ES 91	M00054802A:G02	ES 116	M00055765A:B05
ES 91	M00054804D:H12	ES 116	M00055766A:H03
ES 91	M00054808A:D07	ES 116	M00055768A:B05
ES 91	M00054808B:F08	ES 116	M00055770C:G01
ES 91	M00054810B:H02	ES 116	M00055771A:A11
ES 91	M00054812B:A05	ES 116	M00055771A:D01
ES 91	M00054812D:C07	ES 116	M00055771C:A11
ES 91	M00054812D:C07	ES 116	M00055771C:F05
ES 91	M00054815C:E01	ES 116	M00055771D:D04
ES 91	M00054816C:D11	ES 116	M00055771D:F07
ES 91	M00054821A:C11	ES 116	M00055774C:E01
ES 91	M00054823D:H07	ES 116	M00055774D:G03
ES 91	M00054826B:C10	ES 116	M00055775C:B10
ES 91	M00054826B:E05	ES 116	M00055775D:C06
ES 91	M00054826D:C10	ES 116	M00055778A:F09
ES 91	M00054827B:H01	ES 116	M00055779B:A02
ES 92	M00054832D:E09	ES 116	M00055780B:B07
ES 92	M00054836A:B05	ES 116	M00055780D:G08
ES 92	M00054839B:B02	ES 116	M00055781C:C05
ES 92	M00054839C:F06	ES 116	M00055782A:F02
ES 92	M00054841D:B07	ES 116	M00055783A:C11
ES 92	M00054841D:B07	ES 116	M00055785B:F03
ES 92	M00054842D:C11	ES 116	M00055785C:E08
ES 92	M00054844D:F06	ES 116	M00055786A:D05
ES 92	M00054849D:H11	ES 116	M00055788D:A03
ES 92	M00054851B:E03	ES 116	M00055790C:H02
ES 92	M00054854D:E08	ES 116	M00055791A:D05
ES 92	M00054856D:A02	ES 116	M00055791D:F03
ES 92	M00054857D:E12	ES 116	M00055792B:G09
ES 92	M00054862B:B07	ES 116	M00055792D:E07
ES 92	M00054863B:G03	ES 116	M00055794A:G11
ES 92	M00054865B:H04	ES 116	M00055794C:B06
ES 92	M00054866C:G07	ES 116	M00055796D:E10
ES 92	M00054867A:C07	ES 116	M00055797A:D08
ES 92	M00054867B:B02	ES 116	M00055797B:E07
ES 92	M00054867C:B07	ES 116	M00055798B:C06
ES 92	M00054869C:D01	ES 116	M00055800A:D08
ES 92	M00054870B:D09	ES 116	M00055800B:C08
ES 92	M00054875B:C04	ES 116	M00055802A:D08
ES 92	M00054876B:G03	ES 116	M00055802A:G02
ES 92	M00054877A:H12	ES 116	M00055802B:H04
ES 92	M00054895B:D09	ES 116	M00055802C:F12
ES 92	M00054899D:F07	ES 116	M00055803B:A11

Table 8			
ES No.	Clone Name	ES No.	Clone Name
ES 92	M00054899D:G01	ES 117	M00055803C:D08
ES 92	M00054903D:C12	ES 117	M00055804A:F03
ES 92	M00054908B:F07	ES 117	M00055804B:F01
ES 92	M00054910D:G06	ES 117	M00055805B:C07
ES 92	M00054926D:F01	ES 117	M00055805C:D10
ES 92	M00054927B:E08	ES 117	M00055806A:H12
ES 92	M00054931C:A09	ES 117	M00055806B:F07
ES 92	M00054933A:D07	ES 117	M00055806C:E09
ES 92	M00054934C:D03	ES 117	M00055807B:G10
ES 92	M00054935A:E01	ES 117	M00055807B:G10
ES 92	M00054935A:G04	ES 117	M00055807D:C04
ES 92	M00054937A:B03	ES 117	M00055808C:G11
ES 92	M00054937B:A12	ES 117	M00055811A:A08
ES 92	M00054937B:F03	ES 117	M00055811D:C12
ES 92	M00054937C:B10	ES 117	M00055812A:E01
ES 92	M00054941C:G04	ES 117	M00055814C:D11
ES 92	M00054943C:C04	ES 117	M00055816B:F01
ES 92	M00054943D:C03	ES 117	M00055817B:F01
ES 92	M00054945C:G07	ES 117	M00055817C:C08
ES 92	M00054947B:G12	ES 117	M00055817C:D08
ES 92	M00054949A:E03	ES 117	M00055818A:F12
ES 93	M00054949C:A07	ES 117	M00055818D:E10
ES 93	M00054950D:G06	ES 117	M00055820A:E08
ES 93	M00054952A:F01	ES 117	M00055820B:E05
ES 93	M00054952C:H06	ES 117	M00055820C:C08
ES 93	M00054953D:G10	ES 117	M00055820D:G10
ES 93	M00054954B:C03	ES 117	M00055821A:A06
ES 93	M00054954D:F01	ES 117	M00055821A:G12
ES 93	M00054957A:B02	ES 117	M00055822B:H04
ES 93	M00054959C:C11	ES 117	M00055823B:D03
ES 93	M00054963C:H11	ES 117	M00055823C:D11
ES 93	M00054963D:H04	ES 117	M00055825B:E03
ES 93	M00054964A:H11	ES 117	M00055826A:F04
ES 93	M00054965B:H02	ES 117	M00055827B:D02
ES 93	M00054970D:G03	ES 117	M00055827D:A02
ES 93	M00054973B:A10	ES 117	M00055827D:C06
ES 93	M00054975C:C04	ES 117	M00055827D:E05
ES 93	M00054980D:C02	ES 117	M00055829C:G09
ES 93	M00054981C:E11	ES 117	M00055830A:G10
ES 93	M00054981D:C06	ES 117	M00055832D:E12
ES 93	M00054984D:B12	ES 117	M00055833D:A11
ES 93	M00054984D:C07	ES 117	M00055838B:D12
ES 93	M00054985C:F07	ES 117	M00055838B:G12
ES 93	M00054987D:C02	ES 117	M00055839A:F09
ES 93	M00054988C:G02	ES 117	M00055839B:A10

Table 8			
ES No.	Clone Name	ES No.	Clone Name
ES 93	M00054995A:C10	ES 117	M00055840C:D06
ES 93	M00054996C:B11	ES 117	M00055841A:B09
ES 93	M00054996C:C09	ES 117	M00055841C:D05
ES 93	M00054997C:B12	ES 118	M00055848C:H06
ES 93	M00054997C:H03	ES 118	M00055849C:D08
ES 93	M00055000C:F04	ES 118	M00055850B:F03
ES 93	M00055002D:E04	ES 118	M00055851A:G11
ES 93	M00055005B:H11	ES 118	M00055851C:F12
ES 93	M00055005D:B08	ES 118	M00055851C:F12
ES 93	M00055008A:B08	ES 118	M00055852A:A07
ES 93	M00055008D:B09	ES 118	M00055854A:E04
ES 93	M00055011C:E04	ES 118	M00055856A:F04
ES 93	M00055017A:A11	ES 118	M00055856C:F07
ES 93	M00055021D:D11	ES 118	M00055860D:A08
ES 93	M00055022A:H04	ES 118	M00055861A:D03
ES 93	M00055027B:D07	ES 118	M00055864A:E11
ES 93	M00055027D:F08	ES 118	M00055864A:H02
ES 93	M00055032D:A06	ES 118	M00055866D:A02
ES 93	M00055034C:G01	ES 118	M00055868A:F06
ES 93	M00055034D:H01	ES 118	M00055868D:D03
ES 93	M00055037A:E10	ES 118	M00055868D:F09
ES 93	M00055039A:G01	ES 118	M00055869B:A06
ES 93	M00055039C:E02	ES 118	M00055871A:F05
ES 93	M00055041A:E02	ES 118	M00055871D:G06
ES 94	M00055042A:B01	ES 118	M00055872D:D12
ES 94	M00055046B:C07	ES 118	M00055873A:B11
ES 94	M00055046C:E11	ES 118	M00055873B:E03
ES 94	M00055050C:G04	ES 118	M00055874B:B06
ES 94	M00055053C:B03	ES 118	M00055874D:D03
ES 94	M00055054A:C02	ES 118	M00055879B:E11
ES 94	M00055056D:B06	ES 118	M00055879C:D04
ES 94	M00055057A:F03	ES 118	M00055880D:F12
ES 94	M00055063D:G01	ES 118	M00055882C:A06
ES 94	M00055064A:E12	ES 118	M00055882C:A09
ES 94	M00055071B:A02	ES 118	M00055884A:E10
ES 94	M00055073C:H12	ES 118	M00055884C:B01
ES 94	M00055075B:H05	ES 118	M00055884D:A05
ES 94	M00055077C:F11	ES 118	M00055886D:G09
ES 94	M00055085A:A10	ES 118	M00055887A:C06
ES 94	M00055087A:A10	ES 118	M00055887A:F07
ES 94	M00055088A:A12	ES 118	M00055887B:E04
ES 94	M00055088C:E09	ES 118	M00055888B:B05
ES 94	M00055093B:H05	ES 118	M00055889C:H12
ES 94	M00055094B:H09	ES 118	M00055891B:A04
ES 94	M00055097A:G06	ES 118	M00055893B:C05

Table 8			
ES No.	Clone Name	ES No.	Clone Name
ES 94	M00055100B:D08	ES 118	M00055896C:F11
ES 94	M00055104C:B12	ES 118	M00055900B:B05
ES 94	M00055106A:D07	ES 118	M00055906B:D10
ES 94	M00055111B:D03	ES 118	M00055906C:F12
ES 94	M00055112A:C03	ES 118	M00055908B:H11
ES 94	M00055113B:A11	ES 118	M00055908C:E12
ES 94	M00055114D:A11	ES 122	M00056209B:F12
ES 94	M00055115A:E05	ES 122	M00056210B:E03
ES 94	M00055116B:B02	ES 122	M00056212C:G01
ES 94	M00055117C:C03	ES 122	M00056213A:A04
ES 94	M00055121D:C07	ES 122	M00056215A:E03
ES 94	M00055125B:E06	ES 122	M00056218C:G03
ES 94	M00055125B:F01	ES 122	M00056220D:D02
ES 94	M00055128D:B10	ES 122	M00056220D:D09
ES 94	M00055130D:G01	ES 122	M00056221D:E05
ES 94	M00055131C:B10	ES 122	M00056222C:F02
ES 94	M00055134B:E03	ES 122	M00056223B:G03
ES 94	M00055134B:H02	ES 122	M00056224C:B10
ES 94	M00055134D:B03	ES 122	M00056224D:E08
ES 94	M00055137C:C04	ES 122	M00056225D:G09
ES 94	M00055145A:F07	ES 122	M00056226C:F12
ES 94	M00055148D:D11	ES 122	M00056228B:A07
ES 94	M00055154C:F04	ES 122	M00056231B:G09
ES 94	M00055157A:C11	ES 122	M00056231B:G09
ES 94	M00055161D:A11	ES 122	M00056232C:E06
ES 94	M00055162A:F06	ES 122	M00056232D:G12
ES 94	M00055163A:C02	ES 122	M00056233D:F03
ES 95	M00055170A:F01	ES 122	M00056236D:G01
ES 95	M00055170D:E02	ES 122	M00056238B:E07
ES 95	M00055172D:D04	ES 122	M00056243C:G10
ES 95	M00055179C:D02	ES 122	M00056244A:B08
ES 95	M00055181A:E01	ES 122	M00056244B:C07
ES 95	M00055182B:C07	ES 122	M00056246A:B03
ES 95	M00055185C:B01	ES 122	M00056246C:G07
ES 95	M00055194D:C05	ES 122	M00056247A:G06
ES 95	M00055196B:A09	ES 122	M00056248A:A09
ES 95	M00055198D:F07	ES 122	M00056250B:F01
ES 95	M00055198D:G07	ES 122	M00056251C:A06
ES 95	M00055201D:A03	ES 122	M00056252B:H08
ES 95	M00055201D:B07	ES 122	M00056252D:E11
ES 95	M00055203B:H02	ES 122	M00056253A:F12
ES 95	M00055206A:H04	ES 122	M00056253D:H06
ES 95	M00055207D:A04	ES 122	M00056254A:H02
ES 95	M00055209D:A08	ES 122	M00056256C:H11
ES 95	M00055209D:D10	ES 122	M00056262B:B08

Table 8			
ES No.	Clone Name	ES No.	Clone Name
ES 95	M00055216A:A03	ES 122	M00056263D:C01
ES 95	M00055216A:A03	ES 122	M00056267A:E02
ES 95	M00055222D:H05	ES 122	M00056267C:B02
ES 95	M00055227A:H09	ES 122	M00056268B:B04
ES 95	M00055227D:E02	ES 122	M00056268C:D01
ES 95	M00055227D:E07	ES 122	M00056273B:A01
ES 95	M00055231A:D10	ES 122	M00056281D:E04
ES 95	M00055242A:E06	ES 122	M00056282A:F11
ES 95	M00055242B:A01	ES 122	M00056282B:D04
ES 95	M00055242D:D04	ES 123	M00056282D:C01
ES 95	M00055243A:F04	ES 123	M00056282D:H09
ES 95	M00055243A:G01	ES 123	M00056283A:E02
ES 95	M00055245B:A09	ES 123	M00056283A:E02
ES 95	M00055247B:A11	ES 123	M00056283D:C03
ES 95	M00055252A:C02	ES 123	M00056286A:E08
ES 95	M00055259D:F04	ES 123	M00056286D:A12
ES 95	M00055260B:A05	ES 123	M00056290B:F05
ES 95	M00055260C:F12	ES 123	M00056290D:E08
ES 95	M00055262C:B11	ES 123	M00056290D:H02
ES 95	M00055263A:G09	ES 123	M00056291B:G01
ES 95	M00055271D:C05	ES 123	M00056291D:B05
ES 95	M00055273B:C05	ES 123	M00056292B:E05
ES 95	M00055274C:F02	ES 123	M00056293B:E08
ES 95	M00055279B:G08	ES 123	M00056293C:F05
ES 95	M00055279C:E12	ES 123	M00056293C:G09
ES 95	M00055283B:F05	ES 123	M00056295A:F07
ES 95	M00055283C:H02	ES 123	M00056295C:D06
ES 95	M00055289B:D02	ES 123	M00056300A:A05
ES 95	M00055294B:D04	ES 123	M00056302B:F12
ES 96	M00055302D:F02	ES 123	M00056303A:C03
ES 96	M00055306A:G09	ES 123	M00056303C:B04
ES 96	M00055319B:A01	ES 123	M00056304D:G11
ES 96	M00055322B:E01	ES 123	M00056307A:H12
ES 96	M00055324C:H10	ES 123	M00056310B:G06
ES 96	M00055325C:B12	ES 123	M00056312B:A04
ES 96	M00055327D:H08	ES 123	M00056312D:C03
ES 96	M00055332C:G11	ES 123	M00056313C:F07
ES 96	M00055334C:H09	ES 123	M00056319C:G01
ES 96	M00055335A:H03	ES 123	M00056320C:H02
ES 96	M00055338B:H07	ES 123	M00056323A:H10
ES 96	M00055344C:H09	ES 123	M00056323A:H10
ES 96	M00055345C:H11	ES 123	M00056323C:C12
ES 96	M00055346B:D02	ES 123	M00056323D:A07
ES 96	M00055350A:F01	ES 123	M00056324B:D02
ES 96	M00055356C:C06	ES 123	M00056330C:D03

Table 8			
ES No.	Clone Name	ES No.	Clone Name
ES 96	M00055358B:C01	ES 123	M00056331B:D01
ES 96	M00055361D:H01	ES 123	M00056338B:B06
ES 96	M00055363D:G12	ES 123	M00056338C:B10
ES 96	M00055364D:E01	ES 123	M00056342A:G05
ES 96	M00055368B:C10	ES 123	M00056342B:G03
ES 96	M00055368C:B06	ES 123	M00056342C:F11
ES 96	M00055371B:F01	ES 123	M00056344A:G03
ES 96	M00055373D:D10	ES 123	M00056345D:E03
ES 96	M00055374A:A08	ES 123	M00056437C:H07
ES 96	M00055376B:B01	ES 123	M00056438C:A06
ES 96	M00055379D:C08	ES 123	M00056447B:A04
ES 96	M00055381B:E09	ES 123	M00056448B:C09
ES 96	M00055383B:B04	ES 124	M00056456C:A09
ES 96	M00055383B:B04	ES 124	M00056456C:F02
ES 96	M00055384D:A03	ES 124	M00056456D:F01
ES 96	M00055385C:G06	ES 124	M00056459A:C07
ES 96	M00055388A:G08	ES 124	M00056459A:C07
ES 96	M00055388A:H08	ES 124	M00056459A:D07
ES 96	M00055390B:D08	ES 124	M00056460A:G11
ES 96	M00055391A:G08	ES 124	M00056466A:A03
ES 96	M00055391C:G06	ES 124	M00056466A:E02
ES 96	M00055395A:C02	ES 124	M00056467C:E07
ES 96	M00055396A:G07	ES 124	M00056475B:C12
ES 96	M00055404D:C07	ES 124	M00056475C:F01
ES 96	M00055405A:D09	ES 124	M00056475C:F02
ES 96	M00055405B:H05	ES 124	M00042432C:H10
ES 96	M00055405D:G07	ES 124	M00042440A:E05
ES 96	M00055406B:D05	ES 124	M00042461A:A10
ES 96	M00055408B:E09	ES 124	M00042463A:F09
ES 96	M00055408D:F03	ES 124	M00042466D:H06
ES 96	M00055413A:B07	ES 124	M00042469D:H04
ES 96	M00055414C:A11	ES 124	M00042511A:A04
ES 97	M00055415B:H11	ES 124	M00042513D:A12
ES 97	M00055417A:G08	ES 124	M00042515C:A10
ES 97	M00055419D:G01	ES 124	M00042756B:B01
ES 97	M00055420A:E06	ES 124	M00042758D:H12
ES 97	M00055420B:F10	ES 124	M00042760B:C07
ES 97	M00055420D:G04	ES 124	M00042764B:B04
ES 97	M00055421B:D04	ES 124	M00042767D:D02
ES 97	M00055421C:C11	ES 124	M00042770B:B12
ES 97	M00055423A:A10	ES 124	M00042771B:A03
ES 97	M00055423A:G08	ES 124	M00042777A:D06
ES 97	M00055423C:H10	ES 124	M00042781C:A06
ES 97	M00055425D:C05	ES 124	M00042783C:A03
ES 97	M00055472A:F02	ES 124	M00042787C:E09

Table 8			
ES No.	Clone Name	ES No.	Clone Name
ES 97	M00055472B:H03	ES 124	M00042792C:G10
ES 97	M00055475D:G08	ES 124	M00042792D:F04
ES 97	M00055479A:G02	ES 124	M00042793B:G06
ES 97	M00055479C:C12	ES 124	M00042800A:A03
ES 97	M00055480C:H10	ES 124	M00042801B:B06
ES 97	M00055482D:A01	ES 124	M00042802C:G11
ES 97	M00055484A:G07	ES 124	M00042805A:E06
ES 97	M00055485A:C09	ES 124	M00042805D:H08
ES 97	M00055487B:F06	ES 124	M00042814D:B11
ES 97	M00001340A:E01	ES 124	M00042816B:F04
ES 97	M00001470C:G01	ES 124	M00042818A:E12
ES 97	M00001470C:G01	ES 124	M00042823B:G04
ES 97	M00001491B:C08	ES 124	M00042826B:C05
ES 97	M00001537D:F10	ES 124	M00042826D:C03
ES 97	M00001537D:F10	ES 124	M00042833D:G01
ES 97	M00001561B:G01	ES 125	M00042834C:B06
ES 97	M00001625A:B08	ES 125	M00042835C:C01
ES 97	M00001637A:D09	ES 125	M00042835D:D02
ES 97	M00003792B:A11	ES 125	M00042838D:E11
ES 97	M00003794C:D07	ES 125	M00042842A:C01
ES 97	M00003804D:A09	ES 125	M00042842D:E08
ES 97	M00003922B:H03	ES 125	M00042844C:C12
ES 97	M00003948A:B12	ES 125	M00042846C:D09
ES 97	M00003986D:G12	ES 125	M00042848D:G12
ES 97	M00003986D:G12	ES 125	M00042849D:F11
ES 97	M00004054C:G05	ES 125	M00042850B:C04
ES 97	M00004066C:D02	ES 125	M00042850C:C10
ES 97	M00004080A:A05	ES 125	M00042853A:G03
ES 97	M00004087D:B11	ES 125	M00042853D:A04
ES 97	M00004093D:C10	ES 125	M00042855A:B09
ES 97	M00004167C:D11	ES 125	M00042856C:F07
ES 97	M00004167C:D11	ES 125	M00042864A:E05
ES 97	M00004198B:A11	ES 125	M00042867D:H01
ES 97	M00004296D:G11	ES 125	M00042869C:E06
ES 98	M00004304A:D07	ES 125	M00042875C:E04
ES 98	M00004842C:B07	ES 125	M00042879B:F09
ES 98	M00004850C:G05	ES 125	M00056346C:C12
ES 98	M00004852D:A04	ES 125	M00056351B:D06
ES 98	M00004868B:D12	ES 125	M00056356B:F04
ES 98	M00004869D:D06	ES 125	M00056359C:A11
ES 98	M00004971B:G04	ES 125	M00056362D:G05
ES 98	M00004972C:E01	ES 125	M00056363A:B06
ES 98	M00005000B:H08	ES 125	M00056368C:F04
ES 98	M00005019D:D02	ES 125	M00056369B:D12
ES 98	M00005293B:D06	ES 125	M00056370B:G02

Table 8			
ES No.	Clone Name	ES No.	Clone Name
ES 98	M00005309D:E05	ES 125	M00056371B:F12
ES 98	M00005312A:D10	ES 125	M00056372B:C10
ES 98	M00005313C:B02	ES 125	M00056374B:H02
ES 98	M00005359A:A06	ES 125	M00056382C:H02
ES 98	M00005373D:H06	ES 125	M00056383A:C10
ES 98	M00005385C:A10	ES 125	M00056410B:E04
ES 98	M00005389C:C11	ES 125	M00056411C:E04
ES 98	M00005395A:D09	ES 125	M00056414B:A05
ES 98	M00005406C:A11	ES 125	M00056416C:B12
ES 98	M00005407B:E12	ES 125	M00056420C:D07
ES 98	M00005411C:C07	ES 125	M00056421A:F12
ES 98	M00005413B:F03	ES 125	M00056424A:F12
ES 98	M00005415C:F12	ES 125	M00056424B:H06
ES 98	M00005420B:C01	ES 125	M00056424D:A10
ES 98	M00005438B:A06	ES 125	M00056425A:H08
ES 98	M00005445C:A02	ES 125	M00056425D:B03
ES 98	M00005447C:D01	ES 125	M00056434A:C08
ES 98	M00005449C:E10	ES 125	M00056434D:E07
ES 98	M00005454B:C03	ES 126	M00056480B:C12
ES 98	M00005459B:B01	ES 126	M00056480D:A10
ES 98	M00005469B:A07	ES 126	M00056481A:F02
ES 98	M00005481D:C06	ES 126	M00056483D:F06
ES 98	M00005485B:B05	ES 126	M00056484B:G02
ES 98	M00005485D:A09	ES 126	M00056485B:B12
ES 98	M00005491B:H12	ES 126	M00056490D:E02
ES 98	M00005491D:B03	ES 126	M00056491D:G08
ES 98	M00005500B:E03	ES 126	M00056496B:A01
ES 98	M00005501B:E05	ES 126	M00056496C:H09
ES 98	M00005501D:G09	ES 126	M00056499C:F05
ES 98	M00005513B:F09	ES 126	M00056501C:H07
ES 98	M00005514C:A06	ES 126	M00056503B:G11
ES 98	M00005515B:H04	ES 126	M00056503B:G11
ES 98	M00005516D:H06	ES 126	M00056505B:H02
ES 98	M00005517B:F04	ES 126	M00056505D:D07
ES 98	M00005520C:E12	ES 126	M00056506C:G12
ES 98	M00005530C:A07	ES 126	M00056507D:B10
ES 98	M00005545B:A08	ES 126	M00056508B:B10
ES 99	M00005546A:G02	ES 126	M00056511A:H12
ES 99	M00005548A:A02	ES 126	M00056512B:C06
ES 99	M00005563C:B12	ES 126	M00056512C:E09
ES 99	M00005565A:F05	ES 126	M00056512D:C12
ES 99	M00005568C:B09	ES 126	M00056514B:E08
ES 99	M00007926A:A07	ES 126	M00056514C:G01
ES 99	M00007926D:A05	ES 126	M00056515C:C05
ES 99	M00007927C:C01	ES 126	M00056517B:G03

Table 8			
ES No.	Clone Name	ES No.	Clone Name
ES 99	M00007931A:A10	ES 126	M00056519C:H01
ES 99	M00007935D:A05	ES 126	M00056526C:E11
ES 99	M00007936D:B09	ES 126	M00056529D:F12
ES 99	M00007936D:B09	ES 126	M00056529D:H09
ES 99	M00007939B:A03	ES 126	M00056530A:D01
ES 99	M00007943A:C02	ES 126	M00056532B:G06
ES 99	M00007951C:A05	ES 126	M00056534A:D11
ES 99	M00007953B:A01	ES 126	M00056537B:H05
ES 99	M00007953D:H09	ES 126	M00056537C:A09
ES 99	M00007954C:B04	ES 126	M00056541B:A08
ES 99	M00007961B:F05	ES 126	M00056547A:C04
ES 99	M00007964B:G01	ES 126	M00056548A:C11
ES 99	M00007965A:G10	ES 126	M00056551A:F02
ES 99	M00007965B:C03	ES 126	M00056552A:A10
ES 99	M00007965B:C03	ES 126	M00056552D:B10
ES 99	M00007981D:B04	ES 126	M00056555A:F09
ES 99	M00007982A:F11	ES 126	M00056556C:G01
ES 99	M00007983B:D03	ES 126	M00056557C:D02
ES 99	M00007983D:H06	ES 126	M00056561C:D08
ES 99	M00007990D:D03	ES 126	M00056564C:E09
ES 99	M00007991D:G01	ES 126	M00056566C:H01
ES 99	M00007992D:G08	ES 127	M00056574B:A07
ES 99	M00007994A:C11	ES 127	M00056580B:F10
ES 99	M00007994D:A05	ES 127	M00056591C:E03
ES 99	M00007998C:F07	ES 127	M00056592A:F04
ES 99	M00005589C:F07	ES 127	M00056592C:C03
ES 99	M00005610D:B11	ES 127	M00056592D:D07
ES 99	M00005619B:A09	ES 127	M00056592D:D07
ES 99	M00005621A:H08	ES 127	M00056593B:E05
ES 99	M00005627B:B10	ES 127	M00056594C:C06
ES 99	M00005628B:C10	ES 127	M00056594C:C10
ES 99	M00005632A:H02	ES 127	M00056595A:A02
ES 99	M00005650C:A06	ES 127	M00056595A:C07
ES 99	M00005650C:D04	ES 127	M00056595B:F02
ES 99	M00005655B:F08	ES 127	M00056596A:E02
ES 99	M00005675A:G02	ES 127	M00056596C:E06
ES 99	M00005685D:D12	ES 127	M00056596C:H08
ES 99	M00005704C:D10	ES 127	M00056597A:F07
ES 99	M00005708B:B07	ES 127	M00056597D:C02
ES 100	M00042455C:D11	ES 127	M00056599D:D11
ES 100	M00054826A:B05	ES 127	M00056600D:H07
ES 100	M00055281A:E08	ES 127	M00056603C:D01
ES 100	M00005657D:A12	ES 127	M00056608C:E04
ES 100	M00005710A:D01	ES 127	M00056610B:H12
ES 100	M00005765D:F07	ES 127	M00056613A:A05

Table 8			
ES No.	Clone Name	ES No.	Clone Name
ES 100	M00005766C:F10	ES 127	M00056616B:C08
ES 100	M00005769B:A03	ES 127	M00056616D:A10
ES 100	M00005782A:B10	ES 127	M00056617B:H06
ES 100	M00005800D:D11	ES 127	M00056618A:B02
ES 100	M00005802B:H10	ES 127	M00056618B:F06
ES 100	M00005810B:F07	ES 127	M00056618D:F11
ES 100	M00005810B:G10	ES 127	M00056620D:E12
ES 100	M00005813B:E10	ES 127	M00056622D:C03
ES 100	M00005818D:B09	ES 127	M00056624D:H05
ES 100	M00005819C:B11	ES 127	M00056628C:F01
ES 100	M00005826D:G10	ES 127	M00056631B:G05
ES 100	M00005830C:D10	ES 127	M00056631D:C08
ES 100	M00006576A:B04	ES 127	M00056631D:D03
ES 100	M00006583B:H03	ES 127	M00056633B:B07
ES 100	M00006587B:A08	ES 127	M00056635A:A11
ES 100	M00006588A:H06	ES 127	M00056635A:E09
ES 100	M00006590A:C10	ES 127	M00056638A:D08
ES 100	M00006610C:D08	ES 127	M00056638B:B01
ES 100	M00006630D:C11	ES 127	M00056639A:E02
ES 100	M00006638A:G02	ES 127	M00056643D:G06
ES 100	M00006641C:H03	ES 127	M00056645C:B11
ES 100	M00006641C:H03	ES 127	M00056645D:F06
ES 100	M00006648B:A05	ES 127	M00056646C:C02
ES 100	M00006649D:B11	ES 127	M00056646D:G05
ES 100	M00006650A:A03	ES 128	M00056652D:F04
ES 100	M00006650D:D05	ES 128	M00056656C:H03
ES 100	M00006664A:B09	ES 128	M00056659C:G08
ES 100	M00006679D:C04	ES 128	M00056661B:A09
ES 100	M00006686B:B07	ES 128	M00056661D:E05
ES 100	M00006695D:H08	ES 128	M00056662B:F03
ES 100	M00006695D:H08	ES 128	M00056664B:G06
ES 100	M00006704C:G06	ES 128	M00056664C:B07
ES 100	M00006705B:A09	ES 128	M00056665B:A11
ES 100	M00006705C:G09	ES 128	M00056665C:E05
ES 100	M00006712C:F02	ES 128	M00056666A:C08
ES 100	M00006719A:E12	ES 128	M00056669B:G07
ES 100	M00006719A:H07	ES 128	M00056670A:A11
ES 100	M00006731B:B02	ES 128	M00056673D:E06
ES 100	M00006731B:C08	ES 128	M00056674B:E05
ES 100	M00006731B:D03	ES 128	M00056674D:H04
ES 100	M00006731C:E01	ES 128	M00056682D:F10
ES 100	M00006734C:A08	ES 128	M00056683C:B09
ES 100	M00006737D:A11	ES 128	M00056684D:A05
ES 100	M00006740B:G01	ES 128	M00056684D:F11
ES 100	M00006745C:A02	ES 128	M00056688B:F05

Table 8			
ES No.	Clone Name	ES No.	Clone Name
ES 101	M00006979D:B10	ES 129	M00056729B:D04
ES 101	M00006987A:G11	ES 129	M00056729C:H12
ES 101	M00006989C:E04	ES 129	M00056733C:D09
ES 101	M00006990D:E02	ES 129	M00056735D:B08
ES 102	M00006996C:F10	ES 129	M00056737B:G07
ES 102	M00006997A:A03	ES 129	M00056739A:D11
ES 102	M00007006B:A01	ES 129	M00056739B:D08
ES 102	M00007007B:H05	ES 129	M00056740C:B05
ES 102	M00007028C:C04	ES 129	M00056741B:C06
ES 102	M00007028C:C04	ES 129	M00056746D:A02
ES 102	M00007032C:F09	ES 129	M00056746D:D06
ES 102	M00007034B:B06	ES 129	M00056747A:D05
ES 102	M00007035C:E06	ES 129	M00056752A:E01
ES 102	M00007065C:F11	ES 129	M00056753D:A10
ES 102	M00007084B:G04	ES 129	M00056754A:A04
ES 102	M00007092D:F03	ES 129	M00056754B:D09
ES 102	M00007096A:E02	ES 129	M00056754B:H04
ES 102	M00007096C:E01	ES 129	M00056754D:A05
ES 102	M00007096D:H02	ES 129	M00056756B:A05
ES 102	M00007097A:B04	ES 129	M00056756D:B08
ES 102	M00007097D:D07	ES 129	M00056757B:F03
ES 102	M00007098A:C05	ES 129	M00056758B:C05
ES 102	M00007105D:C12	ES 129	M00056759A:F11
ES 102	M00007108A:D01	ES 129	M00056759B:G03
ES 102	M00007110C:F03	ES 129	M00056760D:A04
ES 102	M00007112A:A12	ES 129	M00056761A:F05
ES 102	M00007117D:H03	ES 129	M00056762C:E05
ES 102	M00007121C:G08	ES 129	M00056763C:D05
ES 102	M00007128B:G06	ES 129	M00056764A:E08
ES 102	M00007129A:F08	ES 129	M00056765A:A10
ES 102	M00007131C:A01	ES 130	M00056765C:E12
ES 102	M00007135D:B11	ES 130	M00056765D:D10
ES 102	M00007135D:B11	ES 130	M00056766B:A10
ES 102	M00007136C:C05	ES 130	M00056771C:F12
ES 102	M00007146D:F11	ES 130	M00056771D:C12
ES 102	M00007151A:B11	ES 130	M00056772D:A04
ES 102	M00007156A:E06	ES 130	M00056772D:A04
ES 102	M00007156D:F08	ES 130	M00056772D:E08
ES 102	M00007166A:E06	ES 130	M00056773A:H11
ES 102	M00007172B:C03	ES 130	M00056774B:A02
ES 102	M00007174C:D06	ES 130	M00056775D:A07
ES 102	M00007177A:E11	ES 130	M00056775D:C01
ES 102	M00007178C:D03	ES 130	M00056775D:C08
ES 102	M00007192A:E06	ES 130	M00056776D:A06
ES 102	M00007194A:E06	ES 130	M00056776D:D09

ES No.	Clone Name	ES No.	Clone Name
ES 102	M00007194B:B04	ES 130	M00056777B:C03
ES 102	M00007204C:G12	ES 130	M00056777D:B02
ES 102	M00007204D:D01	ES 130	M00056777D:F07
ES 102	M00008014A:B01	ES 130	M00056779A:E12
ES 102	M00008015D:B10	ES 130	M00056779D:H10
ES 102	M00008015D:F08	ES 130	M00056779D:H10
ES 102	M00008020C:C03	ES 130	M00056780D:C02
ES 103	M00008023B:D12	ES 130	M00056780D:F09
ES 103	M00008043B:B11	ES 130	M00056781C:E12
ES 103	M00008059D:B08	ES 130	M00056782D:B06
ES 103	M00008065A:B05	ES 130	M00056783B:G11
ES 103	M00008065C:F02	ES 130	M00056784A:B05
ES 103	M00008075C:A12	ES 130	M00056785B:F08
ES 103	M00008076C:F02	ES 130	M00056789A:C04
ES 103	M00008079C:C03	ES 130	M00056789D:E10
ES 103	M00008085B:C09	ES 130	M00056791D:F12
ES 103	M00008089A:E09	ES 130	M00056793C:H07
ES 103	M00008098D:H01	ES 130	M00056796A:H05
ES 103	M00008099B:G08	ES 130	M00056799B:E11
ES 103	M00021620B:F10	ES 130	M00056802B:H01
ES 103	M00021626C:C04	ES 130	M00056802B:H01
ES 103	M00021626D:F04	ES 130	M00056804B:E06
ES 103	M00021628B:B11	ES 130	M00056805D:B09
ES 103	M00021628B:D07	ES 130	M00056808B:B12
ES 103	M00021649A:E12	ES 130	M00056811A:C04
ES 103	M00021654A:A04	ES 130	M00056812C:E08
ES 103	M00021654A:A04	ES 130	M00056815A:B01
ES 103	M00021655C:H02	ES 130	M00056816B:A10
ES 103	M00021670D:G05	ES 130	M00056817C:C03
ES 103	M00021681D:C02	ES 130	M00056821D:C09
ES 103	M00021681D:C02	ES 130	M00056822C:G11
ES 103	M00022189A:B03	ES 130	M00056823A:B05
ES 103	M00022216D:D06	ES 130	M00056823C:A07
ES 103	M00022221A:D06	ES 131	M00056824B:C10
ES 103	M00022221D:D06	ES 131	M00056824D:E01
ES 103	M00022231D:E12	ES 131	M00056826A:B12
ES 103	M00022234B:D05	ES 131	M00056830C:G02
ES 103	M00022235C:C11	ES 131	M00056833C:C01
ES 103	M00022236A:A02	ES 131	M00056839A:G01
ES 103	M00022246A:H08	ES 131	M00056839A:G02
ES 103	M00022251C:A09	ES 131	M00056839C:F01
ES 103	M00022253A:E03	ES 131	M00056840D:H09
ES 103	M00022259C:B07	ES 131	M00056841D:G09
ES 103	M00022273B:A09	ES 131	M00056842B:F12
ES 103	M00022279B:H04	ES 131	M00056842B:F12

Table 8			
ES No.	Clone Name	ES No.	Clone Name
ES 103	M00022280A:G11	ES 131	M00056843B:H09
ES 103	M00022370A:G02	ES 131	M00056844A:E07
ES 103	M00022411D:G12	ES 131	M00056844C:A10
ES 103	M00022415C:B06	ES 131	M00056848B:C07
ES 103	M00022420B:H03	ES 131	M00056850B:E11
ES 103	M00022430B:D10	ES 131	M00056850B:E11
ES 103	M00022430C:D04	ES 131	M00056857B:C09
ES 103	M00022440D:D01	ES 131	M00056858A:B03
ES 103	M00022444A:C11	ES 131	M00056858B:A12
ES 103	M00022452A:B07	ES 131	M00056859A:D12
ES 104	M00022453B:H04	ES 131	M00056860A:F12
ES 104	M00022453B:H04	ES 131	M00056863C:E03
ES 104	M00022457C:G05	ES 131	M00056864B:H09
ES 104	M00022465D:F05	ES 131	M00056866B:E05
ES 104	M00022468A:E12	ES 131	M00056868D:E09
ES 104	M00022468C:E10	ES 131	M00056870A:E10
ES 104	M00022470B:G01	ES 131	M00056872A:A06
ES 104	M00022470B:G01	ES 131	M00056873C:E06
ES 104	M00022472D:E11	ES 131	M00056874B:H06
ES 104	M00022473D:B06	ES 131	M00056874C:D05
ES 104	M00022496D:F04	ES 131	M00056874D:G01
ES 104	M00022508A:C02	ES 131	M00056879A:E05
ES 104	M00022509A:B06	ES 131	M00056879B:H11
ES 104	M00022516B:E09	ES 131	M00056879D:A02
ES 104	M00022517B:E03	ES 131	M00056880D:B04
ES 104	M00022528A:H12	ES 131	M00056883D:A07
ES 104	M00022533C:E06	ES 131	M00056884B:C06
ES 104	M00022537A:C11	ES 131	M00056885C:C06
ES 104	M00022550C:B04	ES 131	M00056886A:C11
ES 104	M00022559D:D09	ES 131	M00056887B:F08
ES 104	M00022561A:A06	ES 131	M00056892C:A01
ES 104	M00022565A:A05	ES 131	M00056893B:H06
ES 104	M00022565A:A05	ES 131	M00056894D:G06
ES 104	M00022569A:A07	ES 131	M00056895B:A07
ES 104	M00022571C:D11	ES 131	M00056896A:F05
ES 104	M00021854C:E07	ES 131	M00056896A:F10
ES 104	M00021864A:E07	ES 132	M00056898D:D04
ES 104	M00021869D:D01	ES 132	M00056901A:A06
ES 104	M00021886D:F06	ES 132	M00056902A:H12
ES 104	M00021911A:H03	ES 132	M00056909B:E11
ES 104	M00021915B:E10	ES 132	M00056909C:D09
ES 104	M00021925C:H10	ES 132	M00056911B:F02
ES 104	M00021947B:C06	ES 132	M00056913B:G10
ES 104	M00022010B:H01	ES 132	M00056914D:B09
ES 104	M00022013D:H05	ES 132	M00056916C:B02

Table 8			
ES No.	Clone Name	ES No.	Clone Name
ES 104	M00022015D:F11	ES 132	M00056916C:F04
ES 104	M00022015D:F11	ES 132	M00056921A:C07
ES 104	M00022025C:D02	ES 132	M00056923C:E09
ES 104	M00022049C:B07	ES 132	M00056924D:B06
ES 104	M00022050C:D04	ES 132	M00056925D:C07
ES 104	M00022052D:A08	ES 132	M00056939A:F08
ES 104	M00022058D:A01	ES 132	M00056939D:B02
ES 104	M00022060B:F09	ES 132	M00056941D:E02
ES 104	M00022106B:D04	ES 132	M00056945A:B11
ES 104	M00022123A:D05	ES 132	M00056947D:F09
ES 104	M00022129A:E12	ES 132	M00056949C:F06
ES 104	M00022132A:D10	ES 132	M00056951B:F09
ES 104	M00022132C:F04	ES 132	M00056952C:A06
ES 105	M00022137B:G04	ES 132	M00056952D:H04
ES 105	M00022143A:C10	ES 132	M00056953B:A06
ES 105	M00022143A:D01	ES 132	M00056955B:G09
ES 105	M00022143A:D01	ES 132	M00056956B:F01
ES 105	M00022148A:A06	ES 132	M00056960A:C05
ES 105	M00022149C:C01	ES 132	M00056961A:B08
ES 105	M00022149D:C06	ES 132	M00056961C:G12
ES 105	M00022151A:D11	ES 132	M00056964B:A02
ES 105	M00022151A:G05	ES 132	M00056966D:A11
ES 105	M00022163A:C08	ES 132	M00056967A:D02
ES 105	M00022598B:E12	ES 132	M00056967A:E07
ES 105	M00022598C:D05	ES 132	M00056969B:C08
ES 105	M00022617B:C02	ES 132	M00056969D:B01
ES 105	M00022624C:C02	ES 132	M00056972A:F05
ES 105	M00022641A:C10	ES 132	M00056973D:B08
ES 105	M00022641A:E06	ES 132	M00056974C:F04
ES 105	M00022641B:F02	ES 132	M00056976C:F10
ES 105	M00022645D:A05	ES 132	M00056977A:G03
ES 105	M00022645D:C07	ES 132	M00056985B:C05
ES 105	M00022651D:B04	ES 132	M00056986A:F11
ES 105	M00022651D:C01	ES 132	M00056986D:G01
ES 105	M00022655A:D10	ES 132	M00056990C:B09
ES 105	M00022656D:E11	ES 132	M00056990D:C11
ES 105	M00022660A:B04	ES 132	M00056993A:B06
ES 105	M00022667A:C05	ES 132	M00056993D:D03
ES 105	M00022667D:E11	ES 132	M00056994B:F07
ES 105	M00022681D:E06	ES 133	M00056994C:C03
ES 105	M00022697A:D12	ES 133	M00056996D:A12
ES 105	M00022702B:B04	ES 133	M00056997C:H09
ES 105	M00022716C:C06	ES 133	M00056998A:E08
ES 105	M00022716C:C06	ES 133	M00057002D:B05
ES 105	M00022719A:F12	ES 133	M00057002D:B06

Table 8			
ES No.	Clone Name	ES No.	Clone Name
ES 105	M00022720B:A11	ES 133	M00057003B:B09
ES 105	M00022720C:C09	ES 133	M00057005B:C01
ES 105	M00022724C:D04	ES 133	M00057005C:D03
ES 105	M00022738B:D06	ES 133	M00057007C:B12
ES 105	M00022741B:B11	ES 133	M00057008C:E09
ES 105	M00022745C:C07	ES 133	M00057011A:D03
ES 105	M00022750A:A07	ES 133	M00057013B:D01
ES 105	M00022750A:A07	ES 133	M00057015A:C12
ES 105	M00022791B:F11	ES 133	M00057019C:H02
ES 105	M00022813B:A08	ES 133	M00057023A:H09
ES 105	M00022820D:C06	ES 133	M00057024A:E02
ES 105	M00022823A:D03	ES 133	M00057024A:G05
ES 105	M00022828A:C06	ES 133	M00057024D:H08
ES 105	M00022829A:H06	ES 133	M00057025C:A08
ES 105	M00022829C:H10	ES 133	M00057027C:G06
ES 105	M00022831B:H07	ES 133	M00057028D:D09
ES 106	M00022831C:A09	ES 133	M00057029A:C12
ES 106	M00022831D:C04	ES 133	M00057029D:A06
ES 106	M00022834C:G01	ES 133	M00057033A:F09
ES 106	M00022836A:G03	ES 133	M00057035B:C09
ES 106	M00022853C:C11	ES 133	M00057041D:B11
ES 106	M00022861D:B10	ES 133	M00057044C:F06
ES 106	M00022872A:B05	ES 133	M00057047B:C02
ES 106	M00022876B:B05	ES 133	M00057049A:G06
ES 106	M00022876D:D08	ES 133	M00057049C:H05
ES 106	M00022880C:G09	ES 133	M00057052D:B11
ES 106	M00022892C:G07	ES 133	M00057052D:G09
ES 106	M00022895B:B11	ES 133	M00057055B:G08
ES 106	M00022897D:H03	ES 133	M00057055B:G08
ES 106	M00022898C:F04	ES 133	M00057058C:F09
ES 106	M00022899A:C09	ES 133	M00057059D:F06
ES 106	M00022901D:E11	ES 133	M00057059D:H09
ES 106	M00022901D:E11	ES 133	M00057060B:A12
ES 106	M00022902C:H10	ES 133	M00057061C:D04
ES 106	M00022908B:H03	ES 133	M00057063A:C08
ES 106	M00022911B:G01	ES 133	M00057065C:D04
ES 106	M00022928A:F03	ES 133	M00057066A:A04
ES 106	M00022934D:B03	ES 133	M00057070D:B08
ES 106	M00022956B:B09	ES 133	M00057072B:E02
ES 106	M00022961A:B11	ES 133	M00057073D:A05
ES 106	M00022973A:G07	ES 133	M00057074D:C09
ES 106	M00022973C:G08	ES 133	M00057074D:C09
ES 106	M00022974D:D10	ES 134	M00055909B:G01
ES 106	M00022995C:E02	ES 134	M00055909C:E08
ES 106	M00022997A:C08	ES 134	M00055911B:E06

Table 8			
ES No.	Clone Name	ES No.	Clone Name
ES 106	M00022998B:C08	ES 134	M00055912C:E10
ES 106	M00023002D:G10	ES 134	M00055912D:C05
ES 106	M00023015A:D10	ES 134	M00055913B:D05
ES 106	M00023015C:D02	ES 134	M00055919A:A06
ES 106	M00023020D:G09	ES 134	M00055921A:E03
ES 106	M00023023C:F03	ES 134	M00055921B:B11
ES 106	M00023029A:E06	ES 134	M00055922A:C02
ES 106	M00023331D:A11	ES 134	M00055924A:H11
ES 106	M00023347D:C12	ES 134	M00055930A:B08
ES 106	M00023377D:C09	ES 134	M00055931A:A03
ES 106	M00023393D:C02	ES 134	M00055931A:C01
ES 106	M00023393D:E12	ES 134	M00055931B:E01
ES 106	M00023399C:C08	ES 134	M00055936B:E07
ES 106	M00023409A:G08	ES 134	M00055937B:C02
ES 106	M00023414B:F03	ES 134	M00055941B:B12
ES 106	M00023428C:D03	ES 134	M00055941B:B12
ES 106	M00023428D:F11	ES 134	M00055945A:H11
ES 106	M00023430B:D10	ES 134	M00055945B:E10
ES 106	M00023518C:A04	ES 134	M00055946D:G07
ES 107	M00023520A:G07	ES 134	M00055951C:C02
ES 107	M00026804D:D03	ES 134	M00055956C:E02
ES 107	M00026805B:B04	ES 134	M00055958D:F02
ES 107	M00026848C:G11	ES 134	M00055959D:A12
ES 107	M00026854A:E07	ES 134	M00055966C:A03
ES 107	M00026856C:C11	ES 134	M00055966C:D06
ES 107	M00026860D:E01	ES 134	M00055971C:E07
ES 107	M00026861D:A09	ES 134	M00055973A:D04
ES 107	M00026865D:G11	ES 134	M00055976B:F01
ES 107	M00026866A:H08	ES 134	M00055979B:B09
ES 107	M00026873B:E11	ES 134	M00055980A:A10
ES 107	M00026873D:B08	ES 134	M00055981D:A07
ES 107	M00026879A:B02	ES 134	M00055984C:C02
ES 107	M00026879C:D10	ES 134	M00055985D:D01
ES 107	M00026890C:D02	ES 134	M00055990C:B05
ES 107	M00026893C:A01	ES 134	M00055992C:E11
ES 107	M00026896D:E10	ES 134	M00056139D:E04
ES 107	M00026899C:G11	ES 134	M00056139D:G01
ES 107	M00026899C:G11	ES 134	M00056140B:H07
ES 107	M00026900B:C02	ES 134	M00056140D:E07
ES 107	M00026902A:G04	ES 134	M00056141A:D05
ES 107	M00026906B:C10	ES 134	M00056141D:B09
ES 107	M00026909A:G03	ES 134	M00056143A:E09
ES 107	M00026917D:H03	ES 134	M00056144B:C09
ES 107	M00026926D:C05	ES 134	M00056145C:B04
ES 107	M00026934D:E09	ES 134	M00056149C:B01

Table 8			
ES No.	Clone Name	ES No.	Clone Name
ES 107	M00026936D:C12	ES 135	M00056150B:C12
ES 107	M00026937C:B08	ES 135	M00056153C:D01
ES 107	M00026938A:F04	ES 135	M00056156D:A12
ES 107	M00026938A:F04	ES 135	M00056160D:A08
ES 107	M00026949B:H10	ES 135	M00056161D:G04
ES 107	M00026950A:F12	ES 135	M00056162B:F08
ES 107	M00026950D:H01	ES 135	M00056162B:F08
ES 107	M00026951A:G06	ES 135	M00056162D:D06
ES 107	M00026951A:G11	ES 135	M00056162D:E09
ES 107	M00026951A:G11	ES 135	M00056167D:B08
ES 107	M00026951C:D03	ES 135	M00056169A:F06
ES 107	M00026975C:B03	ES 135	M00056171C:H11
ES 107	M00026977A:E09	ES 135	M00056171C:H12
ES 107	M00026984A:D10	ES 135	M00056180B:H09
ES 107	M00026985C:B05	ES 135	M00056184B:D08
ES 107	M00026986B:H10	ES 135	M00056184C:H03
ES 107	M00026993B:H06	ES 135	M00056184D:F01
ES 107	M00026994C:A07	ES 135	M00056185D:A03
ES 107	M00026996D:A06	ES 135	M00056185D:D06
ES 107	M00027000C:F05	ES 135	M00056186C:F02
ES 107	M00027006B:H01	ES 135	M00056190D:G02
ES 107	M00027013D:E10	ES 135	M00056192D:E04
ES 108	M00027014C:G04	ES 135	M00056192D:H02
ES 108	M00027014D:G04	ES 135	M00056195B:C08
ES 108	M00027016D:G06	ES 135	M00056198A:D07
ES 108	M00027021D:H11	ES 135	M00056199D:A09
ES 108	M00027028D:C07	ES 135	M00056201C:H08
ES 108	M00027030C:C08	ES 135	M00056203A:H10
ES 108	M00027034B:D09	ES 135	M00056204B:A04
ES 108	M00027034C:D11	ES 135	M00056205B:D01
ES 108	M00027035D:H09	ES 135	M00056206A:E06
ES 108	M00027039A:F06	ES 136	M00055997C:G11
ES 108	M00027039B:E09	ES 136	M00055999C:G10
ES 108	M00027042C:G11	ES 136	M00055999D:G06
ES 108	M00027046B:E05	ES 136	M00056000A:F12
ES 108	M00027051A:A07	ES 136	M00056000C:D09
ES 108	M00027054B:B03	ES 136	M00056001A:B06
ES 108	M00027076D:F07	ES 136	M00056001A:B07
ES 108	M00027084C:H10	ES 136	M00056001C:E09
ES 108	M00027088D:H06	ES 136	M00056003A:E06
ES 108	M00027090A:E08	ES 136	M00056005B:E05
ES 108	M00027093C:B08	ES 136	M00056005D:C04
ES 108	M00027096A:G07	ES 136	M00056007A:A11
ES 108	M00027097C:G11	ES 136	M00056007C:F06
ES 108	M00027111A:H04	ES 136	M00056016D:D06

ES No.	Clone Name	ES No.	Clone Name
ES 108	M00027134A:G02	ES 136	M00056018B:G05
ES 108	M00027139D:C06	ES 136	M00056020A:D10
ES 108	M00027140A:C11	ES 136	M00056020D:D07
ES 108	M00027163A:D11	ES 136	M00056028C:F03
ES 108	M00027165C:F11	ES 136	M00056036D:B06
ES 108	M00027168C:H10	ES 136	M00056037C:B02
ES 108	M00027171D:B07	ES 136	M00056038D:F04
ES 108	M00027172A:C03	ES 136	M00056041A:C04
ES 108	M00027173D:D08	ES 136	M00056042A:A01
ES 108	M00027183B:B01	ES 136	M00056045D:H01
ES 108	M00027193C:C05	ES 136	M00056050C:A03
ES 108	M00027194D:A05	ES 136	M00056053A:A09
ES 108	M00027197A:G07	ES 136	M00056053A:D12
ES 108	M00027197B:F07	ES 136	M00056055A:A07
ES 108	M00027203B:H08	ES 136	M00056055B:B01
ES 108	M00027207B:E09	ES 136	M00056055C:D03
ES 108	M00027217A:G03	ES 136	M00056058A:H04
ES 108	M00027220A:B12	ES 136	M00056060B:B10
ES 108	M00027222A:C09	ES 136	M00056061B:F06
ES 108	M00027229D:E06	ES 136	M00056066D:H07
ES 108	M00027231D:A03	ES 136	M00056067B:D08
ES 108	M00027524B:B11	ES 136	M00056074D:G10
ES 108	M00027527A:G04	ES 136	M00056077D:E06
ES 108	M00027532C:C02	ES 136	M00056077D:E12
ES 108	M00027535D:E08	ES 136	M00056077D:E12
ES 109	M00027536D:G12	ES 136	M00056079B:D12
ES 109	M00027543C:B09	ES 136	M00056079B:F07
ES 109	M00027543D:G07	ES 136	M00056079C:C11
ES 109	M00027556D:G10	ES 136	M00056081D:B05
ES 109	M00027561C:C04	ES 136	M00056081D:B09
ES 109	M00027562B:C02	ES 136	M00056082C:F06
ES 109	M00027564A:D03	ES 136	M00056085D:H11
ES 109	M00027571C:C11	ES 136	M00056094A:H07
ES 109	M00027573A:F09	ES 136	M00056098A:H01
ES 109	M00027578B:F05	ES 136	M00056099B:G09
ES 109	M00027578C:E04	ES 136	M00056099B:H11
ES 109	M00027580C:E10	ES 136	M00056099B:H11
ES 109	M00027581B:E01	ES 136	M00056103A:D12
ES 109	M00027588A:C01	ES 136	M00056103C:H12
ES 109	M00027588C:A06	ES 136	M00056107B:E06
ES 109	M00027594B:C03	ES 136	M00056108D:B12
ES 109	M00027604A:G10	ES 136	M00056108D:B12
ES 109	M00027604A:G10	ES 136	M00056110C:D09
ES 109	M00027605C:E05	ES 136	M00056111D:H02
ES 109	M00027607A:H05	ES 136	M00056112A:H02

Table 8			
ES No.	Clone Name	ES No.	Clone Name
ES 109	M00027608C:H07	ES 136	M00056114C:C06
ES 109	M00027616C:G12	ES 136	M00056125B:D09
ES 109	M00027628C:A01	ES 136	M00056128C:B10
ES 109	M00027639B:E11	ES 136	M00056131B:C12
ES 109	M00027641B:A01	ES 136	M00056133D:D09
ES 109	M00027652B:G03	ES 136	M00056136A:B11

Table 9 PatientID	Path Report ID	Anatomical Loc	Primary Tumor Size	Primary Tumor Grade	Histopath Grade	Local Invasion	Lymphnode Met	Incidence Lymph	Regional Lymph	Distant Met & Loc	Descript Distant Met	Dist Met Grade	Comment
15	21	Ascending colon	4.0	T3	G2	extending into subserosal adipose tissue	positive	3/8	N1	negative		MX	invasive adenocarcinoma, moderately differentiated; focal perineural invasion is seen
52	71	Ascending colon	9.0	T3	G3	Invasion through muscularis propria,	negative	0/12	N0	negative		M0	Hyperplastic polyp in appendix.
121	140	Sigmoid	6	T4	G2	Invasion of muscularis propria into serosa, involving	negative	0/34	N0	negative		M0	Perineural invasion; donut anastomosis negative. One tubulovillous
125	144	Cecum	6	T3	G2	Invasion through the muscularis propria into subserosal adipose tissue. ileocecal junction.	negative	0/19	N0	negative		M0	patient history of metastatic melanoma
128	147	Transverse colon	5.0	T3	G2	Invasion of muscularis propria into pericolic fat	positive	1/5	N1	negative		M0	
130	149	Splenic flexure	5.5	T3		through wall and into surrounding adipose tissue	positive	10/24	N2	negative		M1	

Table 9 PatientID	Path Report ID	Anatomical Loc	Primary Tumor Size	Primary Tumor Grade	Histopath Grade	Local Invasion	Lymph node Met	Incidence Lymph	Regional Lymph	Distant Met & Loc	Descript Distant Met	Dist Met Grade	Comment
133	152	Rectum	5.0	T3	G2	Invasion through muscularis propria into non-peritonealized pericolic tissue; gross configuration is annular.	negative	0/9	N0	negative		M0	Small separate tubular adenoma (0.4 cm)
141	160	Cecum	5.5	T3	G2	Invasion of muscularis propria into pericolic adipose tissue, but not through serosa. Arising from tubular adenoma.	positive	7/21	N2	positive (Liver)	adenocarcinoma consistent with primary	M1	Perineural invasion identified adjacent to metastatic adenocarcinoma.
156	175	Hepatic flexure	3.8	T3	G2	Invasion through muscularis propria into subserosa/pericolic adipose, no serosal involvement. Gross configuration annular.	positive	2/13	N1	negative		M0	Separate tubulovillous and tubular adenomas

Table 9 PatientID	Path Report ID	Anatomical Loc	Primary Tumor Size	Primary Tumor Grade	Histopath Grade	Local Invasion	Lymphnode Met	Incidence Lymph	Regional Lymph	Distant Met & Loc	Descript Distant Met	Dist Met Grade	Comment
228	247	Rectum	5.8	T3	G2 to G3	Invasion through muscularis propria to involve subserosal, perirectal adipose, and serosa	positive	1/8	N1	negative		MX	Hyperplastic polyps
264	283	Ascending colon	5.5	T3	G2	Invasion through muscularis propria into subserosal adipose tissue.	negative	0/10	N0	negative		M0	Tubulovillous adenoma with high grade dysplasia
266	285	Transverse colon	9	T3	G2	Invades through muscularis propria to involve pericolic adipose, extends to serosa.	negative	0/15	N1	positive (Mesenteric deposit)	0.4 cm, may represent lymph node completely replaced by tumor	MX	
268	287	Cecum	6.5	T2	G2	Invades full thickness of muscularis propria, but mesenteric adipose free of malignancy	negative	0/12	N0	negative		M0	
278	297	Rectum	4	T3	G2	Invasion into perirectal adipose tissue.	positive	7/10	N2	negative		M0	Descending colon polyps, no HGD or carcinoma identified..

Table 9 PatientID	Path Report ID	Anatomical Loc	Primary Tumor Size	Primary Tumor Grade	Histopath Grade	Local Invasion	Lymph node Met	Incidence Lymph	Regional Lymph	Distant Met & Loc	Descript Distant Met	Dist Met Grade	Comment
295	314	Ascending colon	5.0	T3	G2	Invasion through muscularis propria into pericolic adipose tissue.	negative	0/12	N0	negative		M0	Melanosis coli and diverticular disease.
339	358	Rectosigmoid	6	T3	G2	Extends into perirectal fat but does not reach serosa	negative	0/6	N0	negative		M0	1 hyperplastic polyp identified
341	360	Ascending colon	2 cm invasive	T3	G2	Invasion through muscularis propria to involve pericolonic fat. Arising from villous adenoma.	negative	0/4	N0	negative		MX	
356	375	Sigmoid	6.5	T3	G2	Through colon wall into subserosal adipose tissue. No serosal spread seen.	negative	0/4	N0	negative		M0	Two mucosal polyps
360	412	Ascending colon	4.3	T3	G2	Invasion through muscularis propria to pericolonic fat	positive	1/5	N1	negative		M0	Tumor arising at prior ileocolic surgical anastomosis.
392	444	Ascending colon	2	T3	G2	Invasion through muscularis propria into subserosal adipose tissue, not serosa.	positive	1/6	N1	positive (Liver)	Macrovesicular and microvesicular steatosis	M1	

Table 9 Patient ID	Path Report ID	Anatomical Loc	Primary Tumor Size	Primary Tumor Grade	Histopath Grade	Local Invasion	Lymph node Met	Incidence Lymph	Regional Lymph	Distant Met & Loc	Descript Distant Met	Dist Met Grade	Comment
393	445	Cecum	6.0	T3	G2	Cecum, invades through muscularis propria to involve subserosal adipose tissue but not serosa.	negative	0/21	N0	negative		M0	redagnosis of oophorectomy path to metastatic colon cancer.
413	465	Ascending colon	4.8	T3	G2	Invasive through muscularis to involve periserosal fat; abutting ileocecal junction.	negative	0/7	N0	positive (Liver)	adenocarcinoma in multiple slides	M1	
505	383		7.5 cm max dim	T3	G2	Invasion through muscularis propria involving pericolic adipose, serosal surface uninvolved	positive	2/17	N1	positive (Liver)	moderately differentiated adenocarcinoma, consistent with primary	M1	Anatomical location of primary not noted in report. Evidence of chronic colitis.
517	395	Sigmoid	3	T3	G2	penetrates muscularis propria, involves pericolic fat.	positive	6/6	N2	negative		M0	No mention of distant met in report

Table 9 PatientID	Path Report ID	Anatomical Loc	Primary Tumor Size	Primary Tumor Grade	Histopath Grade	Local Invasion	Lymphnode Met	Incident Lymph	Regional Lymph	Distant Met & Loc	Descript Distant Met	Dist Met Grade	Comment
534	553	Ascending colon	12	T3	G3	Invasion through the muscularis propria involving pericolic fat. Serosa free of tumor.	negative	0/8	N0	negative		M0	Omentum with fibrosis and fat necrosis. Small bowel with acute and chronic serositis, focal abscess and adhesions.
546	565	Ascending colon	5.5	T3	G2	Invasion through muscularis propria extensively through submucosal and extending to serosa.	positive	6/12	N2	positive (Liver)	metastatic adenocarcinoma	M1	Appendix dilated and fibrotic, but not involved by tumor
577	596	Cecum	11.5	T3	G2	Invasion through the bowel wall, into subserosal adipose. Serosal surface free of tumor.	negative	0/58	N0	negative		M0	

Table 9

Table 9 PatientID	Path Report ID	Anatomical Loc	Primary Tumor Size	Primary Tumor Grade	Histopath Grade	Local Invasion	Lymphnode Met	Incidence Lymph	Regional Lymph	Distant Met & Loc	Descript Distant Met	Dist Met Grade	Comment
695	714	Cecum	14	T3	G2	extending through bowel wall into serosal fat	negative	0/22	N0	negative		MX	tubular adenoma and hyperplastic polyps present, moderately differentiated adenoma with mucinous differentiation (% not stated)
784	803	Ascending colon	3.5	T3	G3	through muscularis propria into pericolic soft tissues	positive	5/17	N2	positive (Liver)		M1	invasive poorly differentiated adenocarcinoma
786	805	Descending colon	9.5	T3	G2	through muscularis propria into pericolic fat, but not at serosal surface	negative	0/12	N0	positive (Liver)		M1	moderately differentiated invasive adenocarcinoma
791	810	Ascending colon	5.8	T3	G3	through the muscularis propria into pericolic fat	positive	13/25	N2	positive (Liver)		M1	poorly differentiated invasive colonic adenocarcinoma

Table 9

Table 9 PatientID	Path Report ID	Anatomical Loc	Primary Tumor Size	Primary Tumor Grade	Histopath Grade	Local Invasion	Lymphnode Met	Incidence Lymph	Regional Lymph	Distant Met & Loc	Descrip Distant Met	Dist Met Grade	Comment
888	908	Ascending colon	2.0	T2	G1	into muscularis propria		positive	3/21	N0	positive (Liver)	M1	well- to moderately- differentiated adenocarcinoma; this patient has tumors of the ascending colon and the sigmoid colon
889	909	Cecum	4.8	T3	G2	through muscularis propria int	positive	1/4	N1	positive (Liver)		M1	moderately differentiated adenocarcinoma

Table 10

SEQ ID NO	%Pts ≥2x T/N	% Pts ≥2_5x T/N	% Pts ≥5x T/N	P15	P52	P121	P125
18	30.3	15.2	3.0	1.855	2.705	1.000	2.280
22	45.5	39.4	18.2	2.196	1.719	0.604	2.388
127	27.3	18.2	6.1	1.000	1.620	1.822	1.692
139	21.2	18.2	15.2	1000.000	0.001	2.345	1.000
148	27.3	18.2	6.1	1.000	1.620	1.822	1.692
155	45.5	12.1	3.0	1.870	3.104	1.361	2.388
246	42.4	9.1	0.0	2.211	2.347	1.000	1.493
272	48.5	27.3	12.1	1.735	3.110	1.379	2.277
273	21.2	18.2	18.2	1.000	1.000	0.330	1.349
279	24.2	12.1	0.0	1.614	2.348	1.498	1.916
298	21.2	18.2	18.2	1.000	1.000	0.330	1.349
329	21.2	9.1	6.1	1.000	1.000	2.211	1.182
353	45.5	12.1	3.0	1.870	3.104	1.361	2.388
354	48.5	30.3	3.0	1.000	1.592	2.248	2.315
381	27.3	18.2	6.1	1.000	1.620	1.822	1.692
389	21.2	9.1	6.1	1.000	1.000	2.211	1.182
405	21.2	9.1	3.0	1.000	2.366	1.546	1.562
406	21.2	9.1	3.0	1.000	2.366	1.546	1.562
412	36.4	18.2	0.0	2.584	1.332	1.952	1.641
421	51.5	24.2	3.0	2.481	2.253	2.234	1.431
465	21.2	18.2	15.2	1000.000	0.001	2.345	1.000
534	21.2	9.1	3.0	1.000	2.366	1.546	1.562
538	42.4	15.2	0.0	1.489	2.019	3.022	1.121
565	45.5	12.1	3.0	1.870	3.104	1.361	2.388
657	45.5	30.3	3.0	1.512	2.748	0.784	2.162
670	24.2	6.1	0.0	1.190	1.000	0.656	1.456
739	21.2	12.1	0.0	1.936	1.830	0.831	1.347
741	48.5	18.2	0.0	2.750	2.458	1.485	1.151
744	48.5	21.2	0.0	2.069	3.002	1.229	1.631
755	30.3	18.2	3.0	1.000	1.414	1.236	1.738
757	21.2	15.2	6.1	1.000	0.839	2.032	2.557
810	30.3	18.2	3.0	1.000	1.414	1.236	1.738
811	30.3	18.2	3.0	1.000	1.414	1.236	1.738
845	30.3	15.2	9.1	1.000	0.271	0.860	1.310
861	24.2	21.2	15.2	1000.000	1000.000	1.000	1.320
915	30.3	15.2	3.0	1.855	2.705	1.000	2.280
954	24.2	21.2	15.2	1000.000	1000.000	1.000	1.320
955	39.4	21.2	3.0	1.612	2.281	0.785	2.045
991	39.4	21.2	3.0	1.612	2.281	0.785	2.045
1035	24.2	6.1	0.0	1.190	1.000	0.656	1.456
1049	21.2	12.1	0.0	1.936	1.830	0.831	1.347
1050	39.4	21.2	3.0	1.612	2.281	0.785	2.045
1235	45.5	12.1	3.0	1.870	3.104	1.361	2.388
1292	21.2	3.0	0.0	1.558	2.014	2.250	1.643

Table 10

SEQ ID NO	%Pts ≥2x T/N	% Pts ≥2_5x T/N	% Pts ≥5x T/N	P15	P52	P121	P125
1313	24.2	6.1	0.0	1.190	1.000	0.656	1.456
1331	27.3	9.1	3.0	1.327	3.749	1.000	2.045
1334	48.5	30.3	3.0	1.000	1.592	2.248	2.315
1418	30.3	15.2	3.0	1.855	2.705	1.000	2.280
1419	45.5	12.1	3.0	1.870	3.104	1.361	2.388
1420	39.4	18.2	3.0	1.759	1.566	1.000	2.302
1477	39.4	18.2	3.0	1.759	1.566	1.000	2.302
1554	33.3	15.2	0.0	1.829	1.622	1.882	1.957
1579	42.4	9.1	0.0	2.211	2.347	1.000	1.493
1600	45.5	12.1	3.0	1.870	3.104	1.361	2.388
1639	48.5	27.3	12.1	1.735	3.110	1.379	2.277
1657	42.4	24.2	0.0	1.000	1.908	2.267	1.188
1679	33.3	15.2	0.0	1.829	1.622	1.882	1.957
1744	42.4	15.2	3.0	2.059	2.753	1.679	1.587
1847	78.8	63.6	9.1	2.625	4.493	1.642	2.743
1877	45.5	12.1	3.0	1.870	3.104	1.361	2.388
1880	66.7	48.5	6.1	1.000	4.075	1.754	2.436
1889	45.5	12.1	3.0	1.870	3.104	1.361	2.388
2009	30.3	15.2	3.0	1.855	2.705	1.000	2.280
2023	30.3	18.2	0.0	1.285	2.400	0.767	1.270
2029	42.4	9.1	0.0	2.211	2.347	1.000	1.493
2071	24.2	6.1	0.0	1.190	1.000	0.656	1.456
2077	24.2	6.1	0.0	1.190	1.000	0.656	1.456
2103	27.3	21.2	0.0	3.505	0.793	0.809	1.348
2109	24.2	6.1	0.0	1.190	1.000	0.656	1.456
2138	33.3	21.2	9.1	1.000	0.296	3.016	0.794
2143	60.6	48.5	12.1	6.263	1.000	1.832	1.937
2183	63.6	45.5	12.1	1.945	2.010	0.547	3.325
2185	30.3	18.2	3.0	1.000	1.414	1.236	1.738
2190	24.2	6.1	0.0	1.190	1.000	0.656	1.456
2200	45.5	12.1	3.0	1.870	3.104	1.361	2.388
2206	60.6	27.3	3.0	2.256	2.228	1.673	1.937
2220	33.3	24.2	3.0	2.591	0.483	2.580	1.440
2224	48.5	36.4	3.0	1.602	3.209	1.000	2.942
2249	45.5	12.1	3.0	1.870	3.104	1.361	2.388
2255	24.2	3.0	0.0	1.985	2.261	1.000	0.904
2265	54.5	42.4	6.1	1.886	1.000	1.503	3.375
2267	84.8	57.6	18.2	2.529	3.042	2.471	1.669
2281	54.5	36.4	3.0	2.008	0.686	3.104	1.362
2294	30.3	15.2	3.0	1.855	2.705	1.000	2.280
2300	30.3	15.2	3.0	1.855	2.705	1.000	2.280
2307	42.4	9.1	0.0	2.211	2.347	1.000	1.493
2309	42.4	21.2	9.1	2.497	1.837	3.249	1.497
2313	57.6	48.5	9.1	2.603	2.642	1.000	1.939

Table 10

SEQ ID NO	%Pts ≥2x T/N	% Pts ≥2_5x T/N	% Pts ≥5x T/N	P15	P52	P121	P125
2314	48.5	27.3	12.1	1.735	3.110	1.379	2.277
2316	42.4	9.1	0.0	2.211	2.347	1.000	1.493
2327	39.4	24.2	3.0	2.006	1.692	1.778	1.662
2348	72.7	45.5	0.0	2.961	3.152	2.712	1.346

Table 11

SEQ ID NO	P128	P130	P133	P141	P156	P228	P264	P266
18	0.713	1.800	1.955	0.663	0.466	1.457	2.262	1.236
22	1.594	6.800	1.340	1.131	1.000	2.647	1.628	1.190
127	3.761	1.000	1.000	1.587	2.127	1.000	1.000	1.000
139	1000.000	1.000	1000.000	0.482	2.846	0.767	1.631	1.000
148	3.761	1.000	1.000	1.587	2.127	1.000	1.000	1.000
155	2.062	1.781	2.302	1.000	1.000	1.306	2.099	1.357
246	1.779	1.337	2.865	1.515	1.617	1.301	2.098	1.733
272	2.044	2.219	4.257	0.744	1.000	1.127	1.588	1.634
273	1000.000	1000.000	1.000	1.000	0.566	1.554	1.000	1.000
279	1.202	1.852	2.370	1.000	1.000	1.114	1.399	1.239
298	1000.000	1000.000	1.000	1.000	0.566	1.554	1.000	1.000
329	3.234	0.001	1.000	8.480	2.077	1.000	0.001	1.445
353	2.062	1.781	2.302	1.000	1.000	1.306	2.099	1.357
354	1.664	1.987	2.307	2.728	1.000	1.239	1.469	2.059
381	3.761	1.000	1.000	1.587	2.127	1.000	1.000	1.000
389	3.234	0.001	1.000	8.480	2.077	1.000	0.001	1.445
405	1.531	1.553	1.854	2.044	1.363	1.786	1.877	1.644
406	1.531	1.553	1.854	2.044	1.363	1.786	1.877	1.644
412	1.831	1.503	2.326	1.130	1.773	1.379	2.318	2.019
421	2.209	1.889	3.114	1.776	1.788	1.879	2.666	2.257
465	1000.000	1.000	1000.000	0.482	2.846	0.767	1.631	1.000
534	1.531	1.553	1.854	2.044	1.363	1.786	1.877	1.644
538	1.559	1.000	1.740	3.133	2.186	1.869	2.023	2.483
565	2.062	1.781	2.302	1.000	1.000	1.306	2.099	1.357
657	1.524	1.770	2.846	1.185	1.000	1.460	1.831	2.261
670	1.182	1.636	1.418	1.298	1.000	1.000	1.127	0.774
739	0.845	1.286	1.872	1.000	1.000	1.295	1.722	1.785
741	1.819	1.801	3.227	1.457	2.960	1.388	2.086	2.410
744	2.515	1.605	2.399	1.803	2.524	1.551	2.284	1.574
755	1.000	0.754	2.234	3.723	1.000	1.285	1.771	2.246
757	0.745	1.332	1000.000	1.000	1.000	1.781	1.515	1.747
810	1.000	0.754	2.234	3.723	1.000	1.285	1.771	2.246
811	1.000	0.754	2.234	3.723	1.000	1.285	1.771	2.246
845	2.331	1.641	1000.000	1.252	1.000	0.595	1.950	0.616
861	2.888	1.000	0.001	1.000	1.694	0.001	1000.000	1.423
915	0.713	1.800	1.955	0.663	0.466	1.457	2.262	1.236
954	2.888	1.000	0.001	1.000	1.694	0.001	1000.000	1.423
955	1.415	2.042	2.733	0.898	1.431	1.000	1.459	2.009
991	1.415	2.042	2.733	0.898	1.431	1.000	1.459	2.009
1035	1.182	1.636	1.418	1.298	1.000	1.000	1.127	0.774
1049	0.845	1.286	1.872	1.000	1.000	1.295	1.722	1.785
1050	1.415	2.042	2.733	0.898	1.431	1.000	1.459	2.009
1235	2.062	1.781	2.302	1.000	1.000	1.306	2.099	1.357
1292	1.804	1.641	1.876	1.335	0.766	1.245	1.500	1.000
1313	1.182	1.636	1.418	1.298	1.000	1.000	1.127	0.774

Table 11

1331	1.427	1.669	1.837	1.265	1.000	1.667	1.000	1.374
1334	1.664	1.987	2.307	2.728	1.000	1.239	1.469	2.059
1418	0.713	1.800	1.955	0.663	0.466	1.457	2.262	1.236
1419	2.062	1.781	2.302	1.000	1.000	1.306	2.099	1.357
1420	1.518	1.997	2.298	2.273	1.000	1.234	1.186	1.730
1477	1.518	1.997	2.298	2.273	1.000	1.234	1.186	1.730
1554	2.959	1.821	2.234	1.181	1.827	1.000	2.042	1.970
1579	1.779	1.337	2.865	1.515	1.617	1.301	2.098	1.733
1600	2.062	1.781	2.302	1.000	1.000	1.306	2.099	1.357
1639	2.044	2.219	4.257	0.744	1.000	1.127	1.588	1.634
1657	2.160	1.416	1.000	3.531	2.974	1.798	1.899	2.065
1679	2.959	1.821	2.234	1.181	1.827	1.000	2.042	1.970
1744	1.479	1.669	2.442	1.352	1.367	1.605	2.145	2.098
1847	1.839	2.548	2.954	2.234	1.816	1.352	3.390	2.541
1877	2.062	1.781	2.302	1.000	1.000	1.306	2.099	1.357
1880	2.762	2.081	4.111	2.306	2.391	1.675	2.572	3.031
1889	2.062	1.781	2.302	1.000	1.000	1.306	2.099	1.357
2009	0.713	1.800	1.955	0.663	0.466	1.457	2.262	1.236
2023	1.871	1.869	2.588	1.834	1.718	1.197	1.965	2.023
2029	1.779	1.337	2.865	1.515	1.617	1.301	2.098	1.733
2071	1.182	1.636	1.418	1.298	1.000	1.000	1.127	0.774
2077	1.182	1.636	1.418	1.298	1.000	1.000	1.127	0.774
2103	2.297	0.855	1.659	1.607	0.252	1.602	2.866	1.292
2109	1.182	1.636	1.418	1.298	1.000	1.000	1.127	0.774
2138	2.074	1.438	1.552	2.403	0.647	0.605	0.469	0.528
2143	2.828	2.795	2.732	2.548	0.073	1.201	1.722	1.181
2183	1.714	3.061	4.635	1.688	1.230	1.241	1.237	1.852
2185	1.000	0.754	2.234	3.723	1.000	1.285	1.771	2.246
2190	1.182	1.636	1.418	1.298	1.000	1.000	1.127	0.774
2200	2.062	1.781	2.302	1.000	1.000	1.306	2.099	1.357
2206	2.229	2.131	2.194	2.235	2.121	1.388	3.468	2.115
2220	2.650	0.815	1.629	1.586	0.155	1.408	2.830	1.636
2224	1.385	2.044	2.510	0.628	1.763	1.000	1.000	1.687
2249	2.062	1.781	2.302	1.000	1.000	1.306	2.099	1.357
2255	1.454	1.000	1.567	2.350	1.729	2.071	1.439	1.540
2265	2.843	2.931	1.690	1.678	0.724	2.656	2.035	3.526
2267	2.490	1.937	3.729	2.105	2.224	2.547	2.605	4.402
2281	3.412	2.374	1.404	4.761	3.241	2.253	1.384	1.912
2294	0.713	1.800	1.955	0.663	0.466	1.457	2.262	1.236
2300	0.713	1.800	1.955	0.663	0.466	1.457	2.262	1.236
2307	1.779	1.337	2.865	1.515	1.617	1.301	2.098	1.733
2309	1.496	1.483	2.427	1.764	1.000	1.231	1.413	1.000
2313	1.452	1.915	2.252	1.342	2.516	1.278	2.179	4.223
2314	2.044	2.219	4.257	0.744	1.000	1.127	1.588	1.634
2316	1.779	1.337	2.865	1.515	1.617	1.301	2.098	1.733
2327	1.778	1.200	2.169	1.462	1.570	1.784	1.937	2.633
2348	2.064	1.288	2.075	2.527	2.239	1.745	3.772	3.393

Table 11

2384	2.340	0.001	0.001	2.927	4.830	1.708	1.651	1.586
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Table 12

SEQ ID NO	P268	P278	P295	P339	P341	P356	P360	P392
18	1.000	2.819	1.000	1.589	1.238	1.784	0.748	2.486
22	1.194	1.000	1.000	1.474	3.006	2.766	1.622	10.061
127	2.953	2.030	8.118	1.000	2.854	1.000	1000.000	0.001
139	1000.000	1.332	1.000	0.344	1.537	1.000	0.001	0.464
148	2.953	2.030	8.118	1.000	2.854	1.000	1000.000	0.001
155	1.187	1.447	1.000	1.484	3.621	3.844	1.995	1.313
246	1.422	2.018	2.385	1.218	2.039	3.486	1.636	1.623
272	1.268	1.563	1.870	2.056	6.240	6.491	2.230	1.427
273	1.000	1000.000	1.000	1.196	2.209	1000.000	0.001	1.000
279	1.000	1.000	1.000	1.737	2.382	3.061	2.679	1.361
298	1.000	1000.000	1.000	1.196	2.209	1000.000	0.001	1.000
329	2.467	2.166	21.707	0.615	1.616	1.000	1.000	1.000
353	1.187	1.447	1.000	1.484	3.621	3.844	1.995	1.313
354	2.359	1.552	2.918	1.647	4.706	3.623	1.979	1.677
381	2.953	2.030	8.118	1.000	2.854	1.000	1000.000	0.001
389	2.467	2.166	21.707	0.615	1.616	1.000	1.000	1.000
405	1.221	1.796	1.995	1.780	1.726	2.970	1.792	1.581
406	1.221	1.796	1.995	1.780	1.726	2.970	1.792	1.581
412	2.677	2.809	2.969	1.373	2.087	3.804	1.612	1.163
421	2.468	5.262	4.008	1.487	4.366	2.078	1.781	1.332
465	1000.000	1.332	1.000	0.344	1.537	1.000	0.001	0.464
534	1.221	1.796	1.995	1.780	1.726	2.970	1.792	1.581
538	2.565	1.856	1.000	1.000	2.449	1.000	2.097	2.647
565	1.187	1.447	1.000	1.484	3.621	3.844	1.995	1.313
657	1.369	1.000	1.000	1.679	3.084	2.855	2.104	0.927
670	1.677	2.420	2.263	1.314	1.473	2.523	1.776	2.244
739	1.412	1.431	3.103	1.000	2.847	2.621	1.000	1.117
741	2.240	2.040	1.000	1.000	2.450	3.440	2.045	1.998
744	1.837	2.201	2.518	1.604	2.248	2.989	1.570	1.409
755	1.000	1.320	0.556	1.385	1.321	1.000	1.000	6.185
757	0.713	1000.000	0.632	2.389	0.202	1.000	1.000	0.356
810	1.000	1.320	0.556	1.385	1.321	1.000	1.000	6.185
811	1.000	1.320	0.556	1.385	1.321	1.000	1.000	6.185
845	2.151	2.384	2.417	0.573	1.451	2.652	1.000	0.734
861	1.000	1.509	9.879	1000.000	2.327	0.001	1.236	0.870
915	1.000	2.819	1.000	1.589	1.238	1.784	0.748	2.486
954	1.000	1.509	9.879	1000.000	2.327	0.001	1.236	0.870
955	1.657	1.732	3.510	1.652	4.946	4.071	2.194	1.932
991	1.657	1.732	3.510	1.652	4.946	4.071	2.194	1.932
1035	1.677	2.420	2.263	1.314	1.473	2.523	1.776	2.244
1049	1.412	1.431	3.103	1.000	2.847	2.621	1.000	1.117
1050	1.657	1.732	3.510	1.652	4.946	4.071	2.194	1.932
1235	1.187	1.447	1.000	1.484	3.621	3.844	1.995	1.313
1292	0.718	1.000	1.000	1.675	2.301	1.361	2.161	1.825
1313	1.677	2.420	2.263	1.314	1.473	2.523	1.776	2.244

Table 12

1331	0.789	1.609	1.000	0.797	1.000	2.075	2.491	2.505
1334	2.359	1.552	2.918	1.647	4.706	3.623	1.979	1.677
1418	1.000	2.819	1.000	1.589	1.238	1.784	0.748	2.486
1419	1.187	1.447	1.000	1.484	3.621	3.844	1.995	1.313
1420	1.864	1.428	2.631	1.854	3.430	3.182	1.892	1.581
1477	1.864	1.428	2.631	1.854	3.430	3.182	1.892	1.581
1554	2.495	2.090	3.320	1.000	3.907	2.976	1.875	1.000
1579	1.422	2.018	2.385	1.218	2.039	3.486	1.636	1.623
1600	1.187	1.447	1.000	1.484	3.621	3.844	1.995	1.313
1639	1.268	1.563	1.870	2.056	6.240	6.491	2.230	1.427
1657	2.183	2.285	3.554	1.247	2.093	1.840	1.855	1.504
1679	2.495	2.090	3.320	1.000	3.907	2.976	1.875	1.000
1744	2.006	1.696	2.261	1.611	2.154	3.791	1.816	1.356
1847	1.535	2.851	4.154	2.055	6.047	4.103	3.367	2.029
1877	1.187	1.447	1.000	1.484	3.621	3.844	1.995	1.313
1880	2.274	1.266	4.526	2.591	5.409	3.138	2.675	1.391
1889	1.187	1.447	1.000	1.484	3.621	3.844	1.995	1.313
2009	1.000	2.819	1.000	1.589	1.238	1.784	0.748	2.486
2023	1.971	1.699	2.355	1.453	3.122	2.528	1.949	1.326
2029	1.422	2.018	2.385	1.218	2.039	3.486	1.636	1.623
2071	1.677	2.420	2.263	1.314	1.473	2.523	1.776	2.244
2077	1.677	2.420	2.263	1.314	1.473	2.523	1.776	2.244
2103	2.516	0.852	1.775	0.818	4.294	2.281	1.119	0.890
2109	1.677	2.420	2.263	1.314	1.473	2.523	1.776	2.244
2138	1.794	1.486	5.006	0.398	4.768	0.001	2.344	2.434
2143	2.079	1.664	1.000	1.871	2.812	2.693	5.094	1.947
2183	2.325	2.043	2.530	2.411	5.749	5.509	3.490	2.008
2185	1.000	1.320	0.556	1.385	1.321	1.000	1.000	6.185
2190	1.677	2.420	2.263	1.314	1.473	2.523	1.776	2.244
2200	1.187	1.447	1.000	1.484	3.621	3.844	1.995	1.313
2206	1.977	1.676	1.774	1.542	2.538	1.867	2.312	1.000
2220	2.942	0.729	1.772	0.861	15.794	2.349	1.363	0.808
2224	1.457	1.690	2.551	1.860	4.114	3.548	3.125	0.792
2249	1.187	1.447	1.000	1.484	3.621	3.844	1.995	1.313
2255	1.586	1.943	1.000	0.699	1.593	2.039	1.798	0.774
2265	2.157	1.922	3.895	4.143	2.655	1.914	2.159	3.312
2267	3.442	3.933	5.994	1.448	8.695	7.488	2.687	2.449
2281	2.467	1.000	7.584	1.417	3.693	1.947	1.539	4.429
2294	1.000	2.819	1.000	1.589	1.238	1.784	0.748	2.486
2300	1.000	2.819	1.000	1.589	1.238	1.784	0.748	2.486
2307	1.422	2.018	2.385	1.218	2.039	3.486	1.636	1.623
2309	2.485	2.369	1.000	1.820	3.354	5.046	1.820	0.703
2313	3.203	1.593	4.012	1.593	6.374	6.940	3.158	0.947
2314	1.268	1.563	1.870	2.056	6.240	6.491	2.230	1.427
2316	1.422	2.018	2.385	1.218	2.039	3.486	1.636	1.623
2327	2.439	1.482	2.156	1.390	3.500	3.654	1.655	0.771
2348	2.448	2.617	4.003	1.289	2.940	3.894	2.277	1.202



2384	2.328	1.359	9.253	0.383	1.835	0.001	1.000	0.714
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Table 13

SEQ ID NO	P393	P413	P505	P517	P534	P546	P577	P695
18	1.058	2.471	1.583	1.726	0.506	1.431	2.632	5.930
22	14.260	2.516	1.498	3.747	1.300	5.779	11.202	0.001
127	1.000	0.001	1.000	1.000	0.001	1.000	3.303	1.000
139	1.000	1.000	0.458	1.249	0.001	1000.000	0.702	1.000
148	1.000	0.001	1.000	1.000	0.001	1.000	3.303	1.000
155	1.137	2.268	2.414	1.382	2.107	2.210	2.384	5.256
246	0.741	2.181	2.494	1.504	1.511	1.831	2.064	4.421
272	1.348	2.222	2.506	1.355	1.670	2.535	1.556	8.411
273	1.000	1.000	1000.000	1.477	1.645	1.000	1.389	1.000
279	0.914	1.603	1.936	1.485	2.430	1.999	1.647	4.375
298	1.000	1.000	1000.000	1.477	1.645	1.000	1.389	1.000
329	1.000	1.000	1.436	0.517	1.000	1.469	1.000	1.000
353	1.137	2.268	2.414	1.382	2.107	2.210	2.384	5.256
354	1.224	3.432	2.806	1.328	2.470	2.592	1.929	6.973
381	1.000	0.001	1.000	1.000	0.001	1.000	3.303	1.000
389	1.000	1.000	1.436	0.517	1.000	1.469	1.000	1.000
405	1.241	1.841	1.470	1.000	1.672	2.218	1.649	7.555
406	1.241	1.841	1.470	1.000	1.672	2.218	1.649	7.555
412	1.258	2.153	1.849	1.445	1.000	1.531	1.637	3.302
421	1.000	1.327	2.871	1.116	1.903	2.200	2.644	0.001
465	1.000	1.000	0.458	1.249	0.001	1000.000	0.702	1.000
534	1.241	1.841	1.470	1.000	1.672	2.218	1.649	7.555
538	1.560	1.982	2.159	1.278	1.425	1.204	3.046	2.068
565	1.137	2.268	2.414	1.382	2.107	2.210	2.384	5.256
657	0.763	1.602	2.797	1.265	2.765	2.236	2.548	5.071
670	1.710	2.337	1.898	0.892	1.347	1.908	1.136	3.404
739	2.102	1.689	4.429	0.830	1.000	1.000	2.108	2.208
741	1.935	1.911	2.812	1.000	1.854	1.793	2.441	0.001
744	1.320	1.404	1.553	1.000	1.957	1.816	2.156	3.745
755	1.219	2.547	1.288	2.539	3.936	3.625	2.363	1.955
757	0.851	0.750	0.815	0.258	0.712	1.229	0.190	1.000
810	1.219	2.547	1.288	2.539	3.936	3.625	2.363	1.955
811	1.219	2.547	1.288	2.539	3.936	3.625	2.363	1.955
845	2.765	1.000	2.202	0.472	0.490	1.417	0.725	0.001
861	1.000	1.000	1.000	1.000	1.000	1.530	0.769	1.000
915	1.058	2.471	1.583	1.726	0.506	1.431	2.632	5.930
954	1.000	1.000	1.000	1.000	1.000	1.530	0.769	1.000
955	1.322	2.608	1.910	1.199	1.635	1.893	1.473	5.842
991	1.322	2.608	1.910	1.199	1.635	1.893	1.473	5.842
1035	1.710	2.337	1.898	0.892	1.347	1.908	1.136	3.404
1049	2.102	1.689	4.429	0.830	1.000	1.000	2.108	2.208
1050	1.322	2.608	1.910	1.199	1.635	1.893	1.473	5.842
1235	1.137	2.268	2.414	1.382	2.107	2.210	2.384	5.256
1292	1.000	1.518	1.980	1.518	2.526	1.588	1.865	2.251
1313	1.710	2.337	1.898	0.892	1.347	1.908	1.136	3.404

Table 13

1331	0.743	2.126	1.613	1.177	2.128	1.000	1.951	6.931
1334	1.224	3.432	2.806	1.328	2.470	2.592	1.929	6.973
1418	1.058	2.471	1.583	1.726	0.506	1.431	2.632	5.930
1419	1.137	2.268	2.414	1.382	2.107	2.210	2.384	5.256
1420	1.205	3.301	2.749	1.256	2.474	2.345	1.826	8.108
1477	1.205	3.301	2.749	1.256	2.474	2.345	1.826	8.108
1554	1.000	1.793	2.719	1.679	1.000	1.549	2.076	0.001
1579	0.741	2.181	2.494	1.504	1.511	1.831	2.064	4.421
1600	1.137	2.268	2.414	1.382	2.107	2.210	2.384	5.256
1639	1.348	2.222	2.506	1.355	1.670	2.535	1.556	8.411
1657	2.809	1.534	1.366	1.197	2.545	1.964	1.506	0.001
1679	1.000	1.793	2.719	1.679	1.000	1.549	2.076	0.001
1744	1.249	2.009	1.832	1.488	1.379	1.975	2.128	13.930
1847	1.781	2.929	2.183	2.759	3.853	3.092	2.051	7.549
1877	1.137	2.268	2.414	1.382	2.107	2.210	2.384	5.256
1880	1.000	3.187	2.564	0.756	1.226	3.841	3.201	16.724
1889	1.137	2.268	2.414	1.382	2.107	2.210	2.384	5.256
2009	1.058	2.471	1.583	1.726	0.506	1.431	2.632	5.930
2023	1.952	1.472	1.917	1.516	2.305	2.677	2.620	2.660
2029	0.741	2.181	2.494	1.504	1.511	1.831	2.064	4.421
2071	1.710	2.337	1.898	0.892	1.347	1.908	1.136	3.404
2077	1.710	2.337	1.898	0.892	1.347	1.908	1.136	3.404
2103	0.537	1.790	0.727	0.750	0.329	1.100	1.239	0.001
2109	1.710	2.337	1.898	0.892	1.347	1.908	1.136	3.404
2138	0.852	1.789	3.765	0.686	3.176	1.591	1.852	0.001
2143	2.044	17.760	4.034	1.988	0.026	3.908	2.394	42.662
2183	1.088	5.833	3.519	1.572	2.641	4.011	1.695	7.783
2185	1.219	2.547	1.288	2.539	3.936	3.625	2.363	1.955
2190	1.710	2.337	1.898	0.892	1.347	1.908	1.136	3.404
2200	1.137	2.268	2.414	1.382	2.107	2.210	2.384	5.256
2206	1.000	3.033	1.912	1.699	2.147	2.780	2.155	2.518
2220	0.337	2.339	0.768	0.563	0.359	1.242	1.492	1.000
2224	1.000	2.266	2.040	1.000	2.747	2.620	1.718	14.145
2249	1.137	2.268	2.414	1.382	2.107	2.210	2.384	5.256
2255	1.243	1.766	1.547	0.843	1.000	1.498	2.122	4.421
2265	5.268	1.518	2.253	3.678	0.766	1.565	1.000	1.853
2267	0.815	2.497	3.234	2.275	2.344	3.596	5.023	12.124
2281	1.128	0.885	1.237	1.434	3.327	3.206	1.355	0.001
2294	1.058	2.471	1.583	1.726	0.506	1.431	2.632	5.930
2300	1.058	2.471	1.583	1.726	0.506	1.431	2.632	5.930
2307	0.741	2.181	2.494	1.504	1.511	1.831	2.064	4.421
2309	1.240	2.239	2.841	1.000	2.270	2.614	0.583	5.244
2313	0.633	2.821	2.976	1.253	1.675	3.657	2.284	8.587
2314	1.348	2.222	2.506	1.355	1.670	2.535	1.556	8.411
2316	0.741	2.181	2.494	1.504	1.511	1.831	2.064	4.421
2327	1.000	1.801	1.978	1.000	3.188	1.607	2.276	13.068
2348	0.790	3.524	3.377	2.062	2.123	1.959	1.626	1.000

Table 13

2384	0.001	1.346	1.831	1.000	1.646	1.944	1.549	1.000
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Table 14

SEQ ID NO	P784	P786	P791	P888	P889
18	1.000	1.000	4.202	1.464	2.147
22	1.000	1.276	14.034	4.139	3.640
127	1.708	2.247	1.000	0.441	0.001
139	1.391	1.857	1.000	0.402	1.000
148	1.708	2.247	1.000	0.441	0.001
155	1.328	1.421	2.456	1.910	2.069
246	1.243	1.679	2.228	2.333	1.774
272	0.819	1.632	2.808	5.465	2.307
273	1000.000	0.758	1.000	1.000	1.000
279	1.000	1.000	1.834	2.776	1.636
298	1000.000	0.758	1.000	1.000	1.000
329	1.000	1.000	1.000	0.642	1.000
353	1.328	1.421	2.456	1.910	2.069
354	1.000	1.416	2.862	2.690	1.645
381	1.708	2.247	1.000	0.441	0.001
389	1.000	1.000	1.000	0.642	1.000
405	1.000	1.821	1.628	2.276	2.501
406	1.000	1.821	1.628	2.276	2.501
412	1.000	1.888	1.915	2.276	1.481
421	3.336	1.677	2.208	1.000	1.976
465	1.391	1.857	1.000	0.402	1.000
534	1.000	1.821	1.628	2.276	2.501
538	1.000	1.629	2.152	1.000	1.792
565	1.328	1.421	2.456	1.910	2.069
657	1.000	1.997	2.083	3.178	3.444
670	1.000	1.780	1.000	2.177	2.258
739	1.356	0.696	1.000	1.000	1.463
741	2.324	1.000	2.379	1.407	2.833
744	2.137	1.934	2.482	2.035	3.980
755	0.796	1.000	1.737	1.000	2.218
757	2.531	3.138	0.395	1.000	1.000
810	0.796	1.000	1.737	1.000	2.218
811	0.796	1.000	1.737	1.000	2.218
845	1000.000	1.984	1000.000	1.374	1.000
861	3.031	1.000	1.000	1.000	1.000
915	1.000	1.000	4.202	1.464	2.147
954	3.031	1.000	1.000	1.000	1.000
955	0.876	1.781	2.424	4.143	1.977
991	0.876	1.781	2.424	4.143	1.977
1035	1.000	1.780	1.000	2.177	2.258
1049	1.356	0.696	1.000	1.000	1.463
1050	0.876	1.781	2.424	4.143	1.977
1235	1.328	1.421	2.456	1.910	2.069
1292	1.000	1.000	1.992	2.144	1.615
1313	1.000	1.780	1.000	2.177	2.258

Table 14

1331	1.290	1.000	1.000	1.995	2.203
1334	1.000	1.416	2.862	2.690	1.645
1418	1.000	1.000	4.202	1.464	2.147
1419	1.328	1.421	2.456	1.910	2.069
1420	0.816	1.000	2.196	2.446	1.518
1477	0.816	1.000	2.196	2.446	1.518
1554	1.585	1.889	2.178	1.806	1.867
1579	1.243	1.679	2.228	2.333	1.774
1600	1.328	1.421	2.456	1.910	2.069
1639	0.819	1.632	2.808	5.465	2.307
1657	2.810	2.638	1.976	1.491	2.955
1679	1.585	1.889	2.178	1.806	1.867
1744	1.253	1.994	1.874	3.193	2.663
1847	1.559	2.762	5.043	4.135	3.753
1877	1.328	1.421	2.456	1.910	2.069
1880	1.306	1.940	2.293	3.897	1.624
1889	1.328	1.421	2.456	1.910	2.069
2009	1.000	1.000	4.202	1.464	2.147
2023	1.511	1.357	1.632	1.891	1.895
2029	1.243	1.679	2.228	2.333	1.774
2071	1.000	1.780	1.000	2.177	2.258
2077	1.000	1.780	1.000	2.177	2.258
2103	0.573	2.678	1.000	2.507	3.278
2109	1.000	1.780	1.000	2.177	2.258
2138	7.866	1.000	1000.000	1.719	1.000
2143	2.625	2.744	4.155	2.105	4.438
2183	1.000	2.139	3.014	3.159	3.381
2185	0.796	1.000	1.737	1.000	2.218
2190	1.000	1.780	1.000	2.177	2.258
2200	1.328	1.421	2.456	1.910	2.069
2206	1.489	2.750	2.910	5.049	4.006
2220	0.419	3.014	0.575	2.397	3.558
2224	1.000	1.815	2.513	3.487	2.180
2249	1.328	1.421	2.456	1.910	2.069
2255	1.000	1.493	2.186	1.000	2.222
2265	1.267	3.638	1.623	5.889	3.339
2267	1.746	2.363	5.515	2.674	3.637
2281	2.399	3.587	3.625	2.567	2.417
2294	1.000	1.000	4.202	1.464	2.147
2300	1.000	1.000	4.202	1.464	2.147
2307	1.243	1.679	2.228	2.333	1.774
2309	0.397	1.000	1.472	5.315	2.250
2313	1.000	1.939	2.505	4.525	2.674
2314	0.819	1.632	2.808	5.465	2.307
2316	1.243	1.679	2.228	2.333	1.774
2327	1.295	1.658	2.836	2.766	2.873
2348	2.167	2.157	3.410	2.828	3.794

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